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CC EMBL; X05630; CAA29117.1; -.
CC EMBL; X03476; CAA27195.1; -.
CC PIR; B29336; B29336.
CC PIR; S09373; S09373.
CC PIR; B25405; B25405.
CC InterPro: IPR000179; Cyt_b_b6.
CC Pfam; PF00032; cytochrome_b_c_2.
CC Pfam; PF00033; cytochrome_b_n_1.
CC PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
CC PROSITE; PS00193; CYTOCHROME_B_QQ; 1.
CC Electron transport; Respiratory chain; Heme; Transmembrane.
CC INIT_MET 0
CC METAL 96 96 IRON 1 (HEME B566 AXIAL LIGAND).
CC METAL 110 110 IRON 2 (HEME B566 AXIAL LIGAND).
CC METAL 197 197 IRON 2 (HEME B566 AXIAL LIGAND).
CC METAL 211 211 IRON 1 (HEME B566 AXIAL LIGAND).
CC VARIANT 66 67 MH -> ID (IN STRAIN GA).
CC VARIANT 280 280 V -> I (IN STRAIN GA).
CC MUTAGEN 143 143 F->L,S: LOSS OF BINDING AFFINITY
FOR UBIQUINONE AND UBIQUINOL.
CC SEQUENCE 436 AA; 49218 MW; CLEAF62733087CA7 CRC64;

Query Match 62.0%; Score 44; DB 1; Length 436;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKQOQFWLW 11
DB 359 RPKFRWFWEFL 369

RESULT 10
ID VEF_GVHA STANDARD; PRT; 902 AA.
AC P54232;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE VIRAL ENHANCING FACTOR (VEF) (ENHANCIN) (104 KDA GLYCOPROTEIN)
DE (SYNERGISTIC FACTOR).
GN VEF
OS Heliothis armigera granulosis virus (HaGV) (Heliothis armigera
granulovirus).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
ON NCBI_TaxID=45440;
RX SEQUENCE FROM N.A.
MEDLINE=96068802; PubMed=7595376;
RA Roelvink P.W., Corsaro B.G., Granados R.R.;
RT "Characterization of the Helicoverpa armigera and Pseudaletia
unipuncta granulovirus enhancin genes.";
RL J. Gen. Virol. 76:2693-2705(1995).
CC -!- FUNCTION: INVOLVED IN DISRUPTION OF THE PERITROPHIC MEMBRANE AND
FUSION OF NUCLEOCAPSIDS WITH MIDGUT CELLS (BY SIMILARITY).
CC -!- SIMILARITY: TO TNGV AND PUGV VEF.
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CC EMBL; D28558; BAA05908.1; -.
CC Glycoprotein; Late protein.
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 278 278 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 540 540 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 593 593 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 782 782 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 840 840 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 902 AA; 104791 MW; D8E45BAA5F675FDE CRC64;

Query Match 60.6%; Score 43; DB 1; Length 902;
Best Local Similarity 70.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQOQFWLW 11
DB 353 PYPQIWAFLW 362

RESULT 11
ID DCHS_ENTAE STANDARD; PRT; 377 AA.
AC P28577;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE HISTIDINE DECARBOXYLASE (EC 4.1.1.22) (HDC).
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_TaxID=548;
RN [1]
RX SEQUENCE FROM N.A.
MEDLINE=91236707; PubMed=2033044;
RA Kamath A.V., Vaaler G.L., Snell E.E.;
RT "Pyridoxal phosphate-dependent histidine decarboxylases. Cloning,
sequencing, and expression of genes from Klebsiella planticola and
Enterobacter aerogenes and properties of the overexpressed enzymes.";
RL J. Biol. Chem. 266:9432-9437(1991).
CC -!- CATALYTIC ACTIVITY: HISTIDINE = HISTAMINE + CO(2).
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
TYRDC).
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CC EMBL; M62745; AAA24802.1; -.
CC PIR; A40004; A40004.
CC InterPro: IPR002129; Pyridoxal_dec.
CC Pfam; PF00282; pyridoxal_dec; 1.
CC PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
CC Lyase; Decarboxylase; Pyridoxal phosphate.
FT INIT_MET 0 BY SIMILARITY.
FT BINDING 232 232 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 377 AA; 42303 MW; 4C7A3334ACA7D6AE CRC64;

Query Match 59.2%; Score 42; DB 1; Length 377;
Best Local Similarity 62.5%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 PKPOQWFW 9
    |||:|
Db 338 PKPSEWVW 335

RESULT 12
ATP8_SQUAC
ID ATP8_SQUAC STANDARD; PRT; 55 AA.
AC Q92250;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (ATPASE SUBUNIT 8) (A6L).
GN MTATP8 OR ATP8.
OS Squalus acanthias (Spiny dogfish).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99091711; PubMed=9873084;
RA Rasmussen A.S., Arnsdon U.;
RT "Phylogenetic studies of complete mitochondrial DNA molecules place
RT cartilaginous fishes within the tree of bony fishes.";
RL J. Mol. Evol. 48:118-123(1999).
CC -1- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
CC (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
CC -1- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
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CC or send an email to license@isb-sib.ch).
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DR EMBL; Y18134; CAA77053.1; -
DR InterPro; IPR001421; ATP-synt_8.
DR Pfam; PF00895; ATP-synt_8; 1.
DR Hydrogen Ion transport; CF(0); Mitochondrion; Transmembrane.
FT TRANSMEM 6 26 POTENTIAL.
SQ SEQUENCE 55 AA; 6587 MW; 3FB9F843CEFA54EE CRC64;

Query Match 57.7%; Score 41; DB 1; Length 55;
Best Local Similarity 55.6%; Pred. No. 6.8;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RKPOQWFW 9
    |||:|
Db 44 KKPPEWVW 52

RESULT 13
CIW2_MOUSE
ID CIW2_MOUSE STANDARD; PRT; 411 AA.
AC P97438;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTWARD RECTIFYING POTASSIUM
DE CHANNEL PROTEIN TREK-1) (TWO-PORE POTASSIUM CHANNEL TPCK1) (TREK-1 K+
DE CHANNEL SUBUNIT).
GN KCNK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RP TISSUE=Brain;
RX MEDLINE=97157476; PubMed=9003761;
RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA Lazdunski M.;
RT "Cloning, functional expression and brain localization of a novel
RT unconventional outward rectifier K+ channel.";
RL EMBO J. 15:6854-6862(1996).
RN [2]
RP REVISIONS.
RP TISSUE=Brain;
RC Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA Lazdunski M.;
RN Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP ACTIVATION.
RX MEDLINE=98254548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+
RT channels.";
RL Nat. Neurosci. 2:422-426(1999).
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO
CC DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN
CC LIVER. IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB,
CC HIPPOCAMPUS AND CEREBELLUM.
CC -1- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL
CC ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
CC ISOFLURANE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
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DR EMBL; U73488; AAC53005.2; -
DR MGD; MGI:109366; Kcnk2.
DR InterPro; IPR003280; 2porek_channel.
DR InterPro; IPR001622; Channel_pore_k.
DR InterPro; IPR000099; TWIK_channel.
DR Pfam; PF02034; TWIK_channel; 1.
DR PRINTS; PR01333; 2PORECHANNEL.
DR Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 47 67 POTENTIAL.
FT DOMAIN 129 155 PORE-FORMING (POTENTIAL).
FT TRANSMEM 157 177 POTENTIAL.
FT DOMAIN 178 207 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 208 228 POTENTIAL.
FT DOMAIN 238 268 PORE-FORMING (POTENTIAL).
FT TRANSMEM 273 293 POTENTIAL.
FT DOMAIN 294 411 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 378 411 ESSENTIAL FOR CHLOROFORM AND HALOTHANE
SENSITIVITY.
FT DOMAIN 354 411 REQUIRED FOR BASAL CHANNEL ACTIVITY.
FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 411 AA; 45297 MW; 8F976DDDD103EFA05 CRC64;

Query Match 56.3%; Score 40; DB 1; Length 411;
Best Local Similarity 55.6%; Pred. No. 58;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQOWFWLW 11
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Db 271 KPWWFWIL 279
|| |||:
FT CONFLICT 309 311 RLV -> DWL (IN REF. 2).
FT CONFLICT 391 S -> N (IN REF. 2).
FT CONFLICT 411 A -> T (IN REF. 2).
SQ SEQUENCE 426 AA: 47016 MW: 2ABA2336D4009F4E CRC64;

Query Match 56.3%; Score 40; DB 1; Length 426;
Best Local Similarity 55.6%; Pred. No. 60;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPQOWFWIL 11
Db 286 KPWWFWIL 294
|| |||:

RESULT 15
CIWA_HUMAN STANDARD; PRT; 538 AA.
AC P57789; Q9HB59;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-1) (TREK-1 K+ CHANNEL SUBUNIT).
DE KCNK10 OR TREK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9254548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+ channels.";
RL Nat. Neurosci. 2:422-426(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANAESTHETICS SUCH AS CHLOROFORM, HALOTHANE AND ISOFLURANE.
CC -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.
CC
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CC
CC EMBL: AF129399; AAD47569.1; -.
CC EMBL: AF004711; AAD01203.1; -.
CC MIM: 603219; -.
CC InterPro: IPR003280; 2poreK_channel.
CC InterPro: IPR001622; Channel_pore_k.
CC InterPro: IPR000099; TWIK_channel.
CC Pfam: PF02034; TWIK_channel.1.
CC PRINTS: PR01333; 2POREKCHANNEL.
CC Ionic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein.
KW DOMAIN 1 61 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 62 82 POTENTIAL.
FT DOMAIN 144 170 PORE-FORMING (BY SIMILARITY).
FT TRANSMEM 172 192 POTENTIAL.
FT DOMAIN 193 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 244 POTENTIAL.
FT DOMAIN 253 283 PORE-FORMING (BY SIMILARITY).
FT TRANSMEM 288 308 POTENTIAL.
FT DOMAIN 309 426 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 378 426 ESSENTIAL FOR CHLOROFORM AND HALOTHANE SENSITIVITY (BY SIMILARITY).
FT DOMAIN 354 426 REQUIRED FOR BASAL CHANNEL ACTIVITY (BY SIMILARITY).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 2 16 MISSING (IN REF. 2).

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CC
CC EMBL: AF279890; AAG15191.1; -.
CC InterPro: IPR003280; 2poreK_channel.
CC InterPro: IPR001622; Channel_pore_k.
CC InterPro: IPR000099; TWIK_channel.
CC Pfam: PF02034; TWIK_channel.1.
CC Ionic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein.
KW DOMAIN 1 71 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 72 92 POTENTIAL.
FT DOMAIN 154 180 PORE-FORMING (BY SIMILARITY).
FT TRANSMEM 182 202 POTENTIAL.
FT DOMAIN 203 233 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 234 254 POTENTIAL.
FT DOMAIN 263 294 PORE-FORMING (BY SIMILARITY).
FT TRANSMEM 299 319 POTENTIAL.
FT DOMAIN 320 538 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 148 148 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 538 AA; 59764 MW; 8EA615B08D147FBC CRC64;

Query Match 56.3%; Score 40; DB 1; Length 538;
Best Local Similarity 55.6%; Pred. No. 74;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFWM 11
   || |||::
Db 297 KPLVWFIL 305

RESULT 16
CIWA_RAT STANDARD; PRT; 538 AA.
AC Q9JIS4;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2) (TREK-2 K+ CHANNEL SUBUNIT).
GN KCNK10 OR TREK2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20298807; PubMed=10747911;
RA Bang H., Kim Y., Kim D.;
RT "TREK-2, a new member of the mechanosensitive tandem-pore K+ channel family."
RL J. Biol. Chem. 275:17412-17419(2000).
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.
CC ACTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING UNSATURATED FREE FATTY ACIDS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: EXPRESSED MAINLY IN THE CEREBELLUM, SPLEEN, AND TESTIS.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.
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EMBL; AF196965; AAF75132.1; -
DR InterPro; IPR003280; 2poreK_channel.
DR InterPro; IPR001622; Channel_pore_K.
DR InterPro; IPR000099; TWIK_channel.
DR Pfam; PF02034; TWIK_channel; 1.
DR PRINTS; PR01333; 2PORECHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein.
FT DOMAIN 1 71 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 72 92 POTENTIAL.
FT DOMAIN 154 180 PORE-FORMING (BY SIMILARITY).
FT TRANSMEM 182 202 POTENTIAL.
FT DOMAIN 203 233 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 234 254 POTENTIAL.
FT DOMAIN 263 294 PORE-FORMING (BY SIMILARITY).
FT TRANSMEM 299 319 POTENTIAL.
FT DOMAIN 320 538 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 538 AA; 59800 MW; 1FF33F0AA52B97E4 CRC64;

Query Match 56.3%; Score 40; DB 1; Length 538;
Best Local Similarity 55.6%; Pred. No. 74;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFWM 11
   || |||::
Db 297 KPLVWFIL 305

RESULT 17
CNG_DROME STANDARD; PRT; 665 AA.
AC Q24278;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL (CNG CHANNEL).
GN CNG.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95045396; PubMed=7957070;
RA Baumann A., Frings S., Godde M., Seifert R., Kaupp U.B.;
RT "Primary structure and functional expression of a Drosophila cyclic nucleotide-gated channel present in eyes and antennae."
RL EMBO J. 13:5040-5050(1994).
CC -1- FUNCTION: APPROXIMATELY 50-FOLD MORE SENSITIVE TO cGMP THAN TO cAMP. MAY BE INVOLVED IN TRANSDUCTION CASCADES OF BOTH INVERTEBRATE PHOTORECEPTORS AND OLFACTORY SENSILLAE.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ANTENNAE AND THE VISUAL SYSTEM.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL FAMILY.
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EMBL; X89601; CAA61760.1; -
DR Flybase; FBgn0014462; Cng.
DR InterPro; IPR002025; CNG_membrane.
DR InterPro; IPR000595; cNMP_binding.
DR Pfam; PF00914; CNG_membrane; 1.
DR Pfam; PF00027; cNMP_binding; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; 1.
DR PROSITE; PS00889; cNMP_BINDING_2; 1.
DR PROSITE; PS00442; cNMP_BINDING_3; 1.
DR KW Ionic channel; Ion transport; cAMP-binding; Transmembrane.
FT DOMAIN 1 110 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 111 131 H1 (POTENTIAL).
FT DOMAIN 132 138 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 139 159 H2 (POTENTIAL).
FT DOMAIN 160 186 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 187 207 H3 (POTENTIAL).
FT DOMAIN 208 253 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 254 274 H4 (POTENTIAL).
FT DOMAIN 275 325 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 326 346 H5 (POTENTIAL).
FT DOMAIN 347 481 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 482 502 H6 (POTENTIAL).
FT DOMAIN 503 665 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 437 559 CAMP (BY SIMILARITY).
FT BINDING 496 496 CAMP (POTENTIAL).
FT BINDING 511 511 CAMP (POTENTIAL).
```

FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 665 AA; 75922 MW; 9FLBDC5D9581C8DB CRC64;

Query Match 56.3%; Score 40; DB 1; Length 665;
Best Local Similarity 75.0%; Pred. NO. 90;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQWF 8
||||| II
Db 52 RPKPPDWF 59

RESULT 18
FUT3 HUMAN
ID FUT3_HUMAN STANDARD; PRT; 361 AA.
AC P21217; Q99448; 099449;
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GALACTOSIDE 3(4)-L-FUCOSYLTRANSFERASE (EC 2.4.1.65) (BLOOD GROUP LEWIS
DE ALPHA-4-FUCOSYLTRANSFERASE) (LEWIS FT) (FUCOSYLTRANSFERASE 3) (FUC-
DE III).
GN FUT3 OR LE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE-91032981; PubMed-1977660;
RX Kulkowska-Latallo J.F., Larsen R.D., Nair R.P., Lowe J.B.;
RA "A cloned human cDNA determines expression of a mouse stage-specific
RT embryonic antigen and the Lewis blood group
RT alpha(1,3/1,4)fucosyltransferase.";
RL Genes Dev. 4:1288-1303(1990).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE-95378269; PubMed-7650030;
RA Cameron H.S., Szczepaniak D., Weston W.;
RT "Expression of human chromosome 19p alpha(1,3)-fucosyltransferase
RT genes in normal tissues. Alternative splicing, polyadenylation, and
RT isoforms.";
RL J. Biol. Chem. 270:20112-20122(1995).
[3]
RN VARIANT LE(-) MET-105.
RP MEDLINE-94059067; PubMed-8240322;
RX Elmgren A., Rydberg L., Larson G.;
RA "Genotypic heterogeneity among Lewis negative individuals.";
RT Biochem. Biophys. Res. Commun. 196:515-520(1993).
[4]
RN VARIANT LE(-) ARG-20; SER-170 AND ALA-336.
RX MEDLINE-94059082; PubMed-8240337;
RA Nishihara S., Yazawa S., Iwasaki H., Nakazato M., Kudo T., Ando T.,
RA Narimatsu H.;
RT "Alpha (1,3/1,4)fucosyltransferase (FucT-III) gene is inactivated by
RT a single amino acid substitution in Lewis histo-blood type negative
RT individuals.";
RL Biochem. Biophys. Res. Commun. 196:624-631(1993).
[5]
RN VARIANT LE(-) ARG-20 AND SER-170.
RX MEDLINE-94033579; PubMed-8219240;
RA Koda Y., Kimura H., Mekada E.;
RT "Analysis of Lewis fucosyltransferase genes from the human gastric
RT mucosa of Lewis-positive and -negative individuals.";
RL Blood 82:2915-2919(1993).
[6]
RN VARIANT LE(-) ARG-20 AND LYS-356.
RX MEDLINE-94342259; PubMed-8063716;
RA Mollicone R., Reuguine I., Kelly R.J., Fletcher A., Watt J.,
RA Chatfield S., Aziz A., Cameron H.S., Weston B.W., Lowe J.B., Oriol R.;
RT "Molecular basis for Lewis alpha(1,3/1,4)-fucosyltransferase gene

deficiency (FUT3) found in Lewis-negative Indonesian pedigrees.";
J. Biol. Chem. 269:20987-20994(1994).
[7]
RN VARIANT LE(-) LYS-356.
RX MEDLINE-95050753; PubMed-7961897;
RA Nishihara S., Narimatsu H., Iwasaki H., Yazawa S., Akamatsu S.,
RA Ando T., Seno T., Narimatsu I.;
RT "Molecular genetic analysis of the human Lewis histo-blood group
RT system.";
RL J. Biol. Chem. 269:29271-29278(1994).
[8]
RN VARIANT LE(-) ARG-20; ARG-68; MET-105 AND LYS-356.
RX MEDLINE-96243526; PubMed-8801770;
RA Elmgren A., Boerjeson C., Svensson L., Rydberg L., Larson G.;
RT "DNA sequencing and screening for point mutations in the human Lewis
RT 'FUT3' gene enables molecular genotyping of the human Lewis blood
RT group system.";
RL Vox Sang. 70:97-103(1996).
[9]
RN VARIANT LE(-) ARG-68 AND MET-105.
RX MEDLINE-974113801; PubMed-9268337;
RA Elmgren A., Mollicone R., Costache M., Boerjeson C., Oriol R.,
RA Harrington J., Larson G.;
RT "Significance of individual point mutations, T202C and C314T, in the
RT human Lewis 'FUT3' gene for expression of Lewis antigens by the human
RT alpha'1,3/1,4'-fucosyltransferase, Fuc-TIII.";
RL J. Biol. Chem. 272:21994-21998(1997).
[10]
RN VARIANT LE(+) K-102; A-124, AND VARIANTS LE(-) N-162; R-223; M-270.
RX MEDLINE-98366989; PubMed-9703429;
RA Pang H., Liu Y., Koda Y., Soejima M., Jia J., Schlaphoff T.,
RA du Toit E.D., Kimura H.;
RT "Five novel missense mutations of the Lewis gene 'FUT3' in African
RT 'Xhosa' and Caucasian populations in South Africa.";
RL Hum. Genet. 102:675-680(1998).
CC -!- FUNCTION: MAY CATALYZE ALPHA-1,3 AND ALPHA-1,4 GLYCOSIDIC LINKAGES
CC INVOLVED IN THE EXPRESSION OF VIM-2, LEWIS A, LEWIS B, STALYL
CC LEWIS X AND LEWIS X/SSSEA-1 ANTIGENS, MAY BE INVOLVED IN BLOOD
CC GROUP LEWIS DETERMINATION; LEWIS-POSITIVE (LE(+)) INDIVIDUALS
CC HAVE AN ACTIVE ENZYME WHILE LEWIS-NEGATIVE (LE(-)) INDIVIDUALS
CC HAVE AN INACTIVE ENZYME.
CC -!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-
CC N-ACETYL-D-GLUCOSAMINYL-R = GDP + 1,3-BETA-D-GALACTOSYL-
CC (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
CC -!- PATHWAY: GLYCOSYLATION.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC FORM IN TRANS CISTERNAE OF GOLGI.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN STOMACH, COLON, SMALL
CC INTESTINE, LUNG AND KIDNEY AND TO A LESSER EXTENT IN SALIVARY
CC GLAND, BLADDER, UTERUS AND LIVER.
CC -!- MISCELLANEOUS: ALSO ACTS ON THE CORRESPONDING 1,4-GALACTOSYL
CC DERIVATIVE, FORMING 1,3-L-FUCOSYL LINKS.
CC -!- SIMILARITY: STRUCTURAL SIMILARITY WITH THE OTHER MAMMALIAN
CC GLYCOSYLTRANSFERASES.
CC
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CC
CC EMBL; X53578; CAA37641.1; -
DR EMBL; U27328; AAC50187.1; -
DR EMBL; U27326; AAC50185.1; -
DR EMBL; U27327; AAC50186.1; -
DR EMBL; D89324; BAAL3941.1; -
DR EMBL; D89325; BAAL3942.1; -
DR EMBL; A36669; A36669.
DR MIR; 111100; -
DR InterPro; IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.

KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane;
KW Signal-anchor; Golgi stack; Polymorphic; Blood group antigen.
FT DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
FT TRANSFER 16 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT TRANSFER 35 361 LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (PROBABLE).
FT VARIANT 20 20 L -> R (IN LE(-)).
FT VARIANT 68 68 W -> R (IN LE(-)).
FT VARIANT 102 102 /FTID=VAR_007959.
FT VARIANT 102 102 Q -> K (IN LE(+)).
FT VARIANT 105 105 /FTID=VAR_007960.
FT VARIANT 105 105 T -> M (IN LE(-)).
FT VARIANT 124 124 /FTID=VAR_003427.
FT VARIANT 124 124 S -> A (IN LE(+)).
FT VARIANT 162 162 /FTID=VAR_007961.
FT VARIANT 162 162 D -> N (IN LE(-)).
FT VARIANT 170 170 /FTID=VAR_007962.
FT VARIANT 170 170 G -> S (IN LE(-)); COMPLETELY INACTIVE).
FT VARIANT 223 223 /FTID=VAR_003428.
FT VARIANT 270 270 G -> R (IN LE(-)).
FT VARIANT 270 270 /FTID=VAR_007963.
FT VARIANT 336 336 V -> M (IN LE(-)).
FT VARIANT 336 336 D -> A (IN LE(-)).
FT VARIANT 356 356 /FTID=VAR_003429.
FT VARIANT 356 356 I -> K (IN LE(-)); LESS THAN 10% REDUCTION
IN ACTIVITY).
FT SEQUENCE 361 AA; 42117 MW; BF4398044F19C284 CRC64;

Query Match 54.98; Score 39; DB 1; Length 361;
Best Local Similarity 55.68; Pred. No. 71;
Matches 5; Conservative 2; Mismatches 0; Indels 2; Gaps 0;
QY 1 RPKPQQWF 9
DB 126 RPOGQRW 134
II: I: I: I

RESULT 19
FUT3_PANTR STANDARD; PRT; 372 AA.
AC O19058;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE GALACTOSIDE 3(4)-L-FUCOSYLTRANSFERASE (EC 2.4.1.65) (BLOOD GROUP LEWIS
DE ALPHA-4-FUCOSYLTRANSFERASE) (LEWIS PT) (FUCOSYLTRANSFERASE 3) (FUCT-
DE III) (ALPHA-3/4-FUCOSYLTRANSFERASE).
GN FUT3.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98037800; PubMed=9368041;
RA Costache M., Apoll P.-A., Cailliau A., Elmgren A., Larson G.,
RA Henry S., Blancher A., Iordachescu D., Oriol R., Mollicone R.;
RA "Evolution of fucosyltransferase genes in vertebrates.";
RL J. Biol. Chem. 272:29721-29728(1997).
CC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 AND ALPHA-1,4 GLYCOSIDIC LINKAGES
INVOLVED IN THE EXPRESSION OF STAYL LEWIS X AND LEWIS X/SSEA-1
CC ANTIGENS. IT MAY BE INVOLVED IN BLOOD GROUP LEWIS DETERMINATION
(BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-
N-ACETYL-D-GLUCOSAMINYL-R -> GDP + 1,3-BETA-D-GALACTOSYL-
CC (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
CC -1- PATHWAY: GLYCOSYLATION.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND

CC FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
CC -1- POLYMORPHISM: THERE ARE TWO ALLELES (A AND B). ALLELE A HAS ARG-
CC 162 AND VAL-304. ALLELE B HAS GLY-162 AND MET-304.
CC -1- MISCELLANEOUS: ALSO ACTS ON THE CORRESPONDING 1,4-GALACTOSYL
CC DERIVATIVE, FORMING 1,3-L-FUCOSYL LINKS.
CC -1- SIMILARITY: STRUCTURAL SIMILARITY WITH THE OTHER MAMMALIAN
CC GLYCOSYLTRANSFERASES.
CC -----
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CC -----
CC EMBL: Y14033; CAA74360.1;
CC InterPro: IPR001503; Glyco_transf_10.
CC Pfam: PF00852; Glyco_transf_10; 1.
CC Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane;
KW Signal-anchor; Golgi stack; Polymorphic.
FT DOMAIN 1 14 CYTOPLASMIC (POTENTIAL).
FT TRANSFER 15 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 35 372 LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 162 162 R -> G (IN ALLELE B).
FT VARIANT 304 304 V -> M (IN ALLELE B).
FT SEQUENCE 372 AA; 43233 MW; 649CBFB8CA7BD74C CRC64;

Query Match 54.98; Score 39; DB 1; Length 372;
Best Local Similarity 55.68; Pred. No. 73;
Matches 5; Conservative 2; Mismatches 0; Indels 2; Gaps 0;
QY 1 RPKPQQWF 9
DB 137 RPOGQRW 145
II: I: I: I

RESULT 20
FUT5_HUMAN STANDARD; PRT; 374 AA.
AC Q11128;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.65) (GALACTOSIDE 3-L-
DE FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 5) (FUCT-V).
GN FUT5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood leukocytes;
RX MEDLINE=92156161; PubMed=1740457;
RA Weston B.W., Nair R.P., Larsen R.D., Lowe J.B.;
RA "Isolation of a novel human alpha (1,3)fucosyltransferase gene and
RA molecular comparison to the human Lewis blood group alpha
RA (1,3/4)fucosyltransferase gene. Syntenic, homologous, nonallelic
RA genes encoding enzymes with distinct acceptor substrate
RA specificities.";
RL J. Biol. Chem. 267:4152-4160(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, Kidney, and Liver;
RX MEDLINE=95378269; PubMed=7650030;
RA Cameron H.S., Szczepaniak D., Weston B.W.;
RA "Expression of human chromosome 19p alpha(1,3)-fucosyltransferase
RA genes in normal tissues. Alternative splicing, polyadenylation, and

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CC -----
DR EMBL; M17522; AAA25572.1; -;
DR EMBL; X05799; CAA29244.1; -;
DR PIR; B29413; B29413.
DR InterPro; IPR000179; Cyt_b6.
DR Pfam; PF00032; cytochrome_b_c; 2.
DR Pfam; PF00033; cytochrome_b_n; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_OO; 1.
KW Electron transport; Respiratory chain; Heme; Transmembrane.
FT METAL 97 97
FT METAL 111 111 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 198 198 IRON 2 (HEME B566 AXIAL LIGAND).
FT METAL 212 212 IRON 1 (HEME B566 AXIAL LIGAND).
SQ SEQUENCE 440 AA; 50116 MW; 8D211B8614920C63 CRC64;

Query Match 54.9%; Score 39; DB 1; Length 440;
Best Local Similarity 54.5%; Pred. No. 85;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKQOQFWLM 11
|| : ||||
DB 360 RPLFKWFWLL 370

RESULT 23

NP2_MOUSE
ID NP2_MOUSE STANDARD; PRT; 816 AA.
AC P97460;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE NEURONAL PAS DOMAIN PROTEIN 2 (NEURONAL PAS2).
GN NPAS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97165088; PubMed=9012850;
RA Zhou Y.-D., Barnard M., Tian H., Li X., Ring H.Z., Francke U.,
RA Shelton J., Richardson J., Russell D.W., McKnight S.L.;
RT "Molecular characterization of two mammalian bHLH-PAS domain proteins
RT selectively expressed in the central nervous system.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:713-718(1997).
CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
CC bHLH PROTEIN. INTERACTS WITH HSP90.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- TISSUE SPECIFICITY: IN BRAIN, EXCLUSIVELY NEURONAL. ALSO FOUND IN
CC SPINAL CORD, AND IN A LESSER EXTENT IN COLON, SMALL INTESTINE AND
CC UTERUS.
CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED 3 DAYS AFTER BIRTH.
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (bHLH) FAMILY OF
CC TRANSCRIPTION FACTORS.
CC -1- SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.
CC -----
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DR EMBL; U77969; AAB47249.1; -;
DR MGD; MGI:109232; Npas2.
DR InterPro; IPR003015; HLH_Myc.
DR InterPro; IPR001092; HLH_dim.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
KW Repeat; DNA-binding; Nuclear protein; Transcription regulation.
FT DNA_BIND 10 22
FT DOMAIN 23 60
FT REPEAT 84 150
FT REPEAT 239 305
FT DOMAIN 311 354
FT PAC MOTIF.
SQ SEQUENCE 816 AA; 90915 MW; 7E5CF0641CFDC1DD CRC64;

Query Match 54.9%; Score 39; DB 1; Length 816;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQFWL 10
| ||| |
DB 319 KGQQIWL 326

RESULT 24

NP2_HUMAN
ID NP2_HUMAN STANDARD; PRT; 824 AA.
AC Q99743; Q99629;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE NEURONAL PAS DOMAIN PROTEIN 2 (NEURONAL PAS2) (MEMBER OF PAS PROTEIN
DE 4) (MOP4).
GN NPAS2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97165088; PubMed=9012850;
RA Zhou Y.-D., Barnard M., Tian H., Li X., Ring H.Z., Francke U.,
RA Shelton J., Richardson J., Russell D.W., McKnight S.L.;
RT "Molecular characterization of two mammalian bHLH-PAS domain proteins
RT selectively expressed in the central nervous system.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:713-718(1997).
CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
CC bHLH PROTEIN. INTERACTS WITH HSP90.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (bHLH) FAMILY OF
CC TRANSCRIPTION FACTORS.
CC -1- SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.
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EMBL; U77970; AAB47250.1; -
MIM; 603347; -
InterPro; IPR003015; HLH_MYC.
InterPro; IPR001092; HLH_dlm.
InterPro; IPR001610; PAC.
Pfam; PF00010; HLH; 1.
Pfam; PF00785; PAC; 2.
Pfam; PF00989; PAS; 2.
SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
Repeat; DNA-binding; Nuclear protein; Transcription regulation.
DNA_BIND 10 22
DOMAIN 23 60
REPEAT 84 150
REPEAT 239 305
DOMAIN 311 354
CONFLICT 51 51 K -> E (IN REF. 2).
CONFLICT 164 164 S -> G (IN REF. 2).
CONFLICT 308 308 T -> K (IN REF. 2).
CONFLICT 471 471 L -> S (IN REF. 2).
SEQUENCE 824 AA; 91759 MW; 249A4C4687B328A5 CRC64;

Query Match 54.9%; Score 39; DB 1; Length 824;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 KPQWFNL 10
Db 319 KGQWIWL 326

RESULT 25
CLOC_HUMAN STANDARD; PRT; 846 AA.
AC O15516; O14516; Q9UIT8;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CIRCADIAN LOCOMOTOR OUTPUT CYCLES KAPUT PROTEIN (HCLOCK).
GN CLOC OR KIAA0334.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA King D.P., Steeves T.D.L., Zhao Y., Sangoram A.M., Takahashi J.S.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99216412; PubMed=10198158;
RA Steeves T.D.L., King D.P., Zhao Y., Sangoram A.M., Du F.,
RA Bowcock A.M., Moore R.Y., Takahashi J.S.;
RT "Molecular cloning and characterization of the human CLOCK gene:
RT expression in the suprachiasmatic nuclei.";
RL Genomics 57:189-200(1999).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97349984; PubMed=9205841;
RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. VII.
RT The complete sequences of 100 new cDNA clones from brain which can

RT code for large proteins in vitro.";
RL DNA Res. 4:141-150(1997).
RN [4]
RP SEQUENCE OF 1-349 FROM N.A.
RC TISSUE=Brain;
RA Ikeda M., Takehara N., Ebisawa T., Yamauchi T., Nomura M.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: CIRCADIAN REGULATOR THAT ACTS AS A TRANSCRIPTION FACTOR.
CC CLOCK-BMAL1 HETERODIMERS BIND TO AN E-BOX ELEMENT (3'-CACGTG-5'),
CC THEREBY ACTIVATING TRANSCRIPTION OF PER1, AND POSSIBLY OF OTHER
CC CIRCADIAN CLOCK PROTEINS. MUTANT CLOCK AND BMAL1 FORM HETERODIMER
CC THAT BIND DNA, BUT FAIL TO ACTIVATE TRANSCRIPTION (BY SIMILARITY).
CC !- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
CC HLH PROTEIN. HETERODIMERS WITH BMAL1, AND LESS EFFICIENTLY WITH
CC ARNT AND ARNT2. HETERODIMERS WITH ARNT OR ARNT2 BIND POORLY TO THE
CC E-BOX MOTIF (BY SIMILARITY).
CC !- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC !- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS.
CC !- SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.
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EMBL; AF011568; AAB83969.1; -
EMBL; AF097458; AAF13733.1; -
EMBL; AF097442; AAF13733.1; JOINED.
EMBL; AF097443; AAF13733.1; JOINED.
EMBL; AF097444; AAF13733.1; JOINED.
EMBL; AF097445; AAF13733.1; JOINED.
EMBL; AF097446; AAF13733.1; JOINED.
EMBL; AF097447; AAF13733.1; JOINED.
EMBL; AF097448; AAF13733.1; JOINED.
EMBL; AF097449; AAF13733.1; JOINED.
EMBL; AF097450; AAF13733.1; JOINED.
EMBL; AF097451; AAF13733.1; JOINED.
EMBL; AF097452; AAF13733.1; JOINED.
EMBL; AF097453; AAF13733.1; JOINED.
EMBL; AF097454; AAF13733.1; JOINED.
EMBL; AF097455; AAF13733.1; JOINED.
EMBL; AF097456; AAF13733.1; JOINED.
EMBL; AF097457; AAF13733.1; JOINED.
EMBL; AB002332; BAA20792.1; -
EMBL; AB005535; BAA21774.1; -
MIM; 601851; -
InterPro; IPR003015; HLH_MYC.
InterPro; IPR001092; HLH_dlm.
InterPro; IPR001067; Nucleinslocatr.
InterPro; IPR001610; PAC.
Pfam; PF00785; PAC; 1.
Pfam; PF00989; PAS; 2.
PRINTS; PR00785; NCTRNLOCATR.
SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
Transcription regulation; Nuclear protein; Repeat; Biological rhythms;
DNA-binding.
DNA_BIND 35 47
DOMAIN 48 85
REPEAT 109 175
REPEAT 264 330
DOMAIN 514 564
DOMAIN 744 760
DOMAIN 819 828
CONFLICT 440 440 S -> P (IN REF. 2).

SQ SEQUENCE 846 AA; 95303 MW; C292B451A33B4CBF CRC64;

Query Match 54.9%; Score 39; DB 1; Length 846;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFWL 10
| |||||
Db 344 KGOQWIWL 351

RESULT 26
CLOC_MOUSE STANDARD: PRT; 855 AA.
AC O08785;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CIRCADIAN LOCOMOTOR OUTPUT CYCLES RAPUT PROTEIN (MCLOCK).
GN CLOCK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=97304393; PubMed=9160756;
RA Antoch M.P., Song E.J., Chang A.M., Vitaterna M.H., Zhao Y.,
RA Wilsbacher L.D., Sangoram A.M., King D.P., Pinto L.H., Takahashi J.S.;
RT "Functional identification of the mouse circadian clock gene by
RT transgenic BAC rescue";
RL Cell 89:655-667(1997).
RN [2]
RP SEQUENCE FROM N.A., AND IDENTIFICATION OF CLOCK MUTANT.
RC STRAIN=BALB/C X C57BL/6; Tissue-Suprachiasmatic nucleus;
RX MEDLINE=97304392; PubMed=9160755;
RA King D.P., Zhao Y., Sangoram A.M., Wilsbacher L.D., Tanaka M.,
RA Antoch M.P., Steeves J.D.L., Vitaterna M.H., Kornhauser J.M.,
RA Lowrey P.L., Turek F.W., Takahashi J.S.;
RT "Positional cloning of the mouse circadian clock gene";
RL Cell 89:641-653(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Wilsbacher L.D., Sangoram A.M., Antoch M.P., Takahashi J.S.;
RT "The mouse clock locus: Sequence and analysis of 204 kb from mouse
RT chromosome 5";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP INTERACTION WITH BMAL1.
RX MEDLINE=98279137; PubMed=9616112;
RA Gekakis N., Staknis D., Nguyen H.B., Davis F.C., Wilsbacher L.D.,
RA King D.P., Takahashi J.S., Weitz C.J.;
RT "Role of the clock protein in the mammalian circadian mechanism";
RL Science 280:1564-1569(1998).
CC -1- FUNCTION: CIRCADIAN REGULATOR THAT ACTS AS A TRANSCRIPTION FACTOR.
CC CLOCK-BMAL1 HETERODIMERS BIND TO AN E-BOX ELEMENT (3'-CACGTG-5'),
CC THEREBY ACTIVATING TRANSCRIPTION OF PER1, AND POSSIBLY OF OTHER
CC CIRCADIAN CLOCK PROTEINS. MUTANT CLOCK AND BMAL1 FORM HETERODIMER
CC THAT BIND DNA, BUT FAIL TO ACTIVATE TRANSCRIPTION. IN HOMOZYGOUS
CC CLOCK MUTANTS, THE CIRCADIAN PERIOD IS INCREASED FROM 3 TO 4 HOURS
CC AND USUALLY THE CIRCADIAN RHYTHMICITY IS LOST AT CONSTANT
CC DARKNESS. EXPRESSION OF CLOCK IS ALSO REDUCED.
CC -1- SUBUNIT: HETERODIMER WITH BMAL1, AND LESS EFFICIENTLY WITH ARNT
CC AND ARNT2. HETERODIMERS WITH ARNT OR ARNT2 BIND POORLY TO THE E-
CC BOX MOTIF.
CC -1- TISSUE SPECIFICITY: EXPRESSED EQUALLY IN BRAIN, EYE, TESTES,
CC OVARIES, LIVER, HEART, LUNG, KIDNEY. IN THE BRAIN, EXPRESSION IS
CC ABUNDANT IN THE SUPRACHIASMATIC NUCLEI (SCN), IN THE PYRIFORM
CC CORTEX, AND IN THE HIPPOCAMPUS. LOW EXPRESSION THROUGHOUT THE REST
CC OF THE BRAIN. EXPRESSION DOES NOT APPEAR TO UNDERGO CIRCADIAN

CC -1- DOMAIN: CONTAINS A GLN-RICH C-TERMINAL DOMAIN WHICH COULD
CC CORRESPOND TO THE TRANSACTIVATION DOMAIN. IN MUTANT CLOCK,
CC DELETION OF THIS REGION LEADS TO AN INCREASED CIRCADIAN PERIOD
CC FROM 3 TO 4 HOURS AS WELL AS TO THE LOSS OF CIRCADIAN RHYTHMICITY
CC AND ALTERED LIGHT RESPONSE.
CC -1- DISEASE: DEFECTS IN CLOCK AFFECT TWO PROPERTIES OF THE CIRCADIAN
CC SYSTEM: THE LENGTH OF THE FREE-RUNNING PERIOD AND THE PERSISTENCE
CC OF CIRCADIAN RHYTHMICITY IN CONSTANT DARKNESS.
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (3HLH) FAMILY OF
CC TRANSCRIPTION FACTORS.
CC -1- SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.
CC
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CC
CC EMBL; AF000998; AAC53200.1; -;
CC EMBL; AF146793; AAD30565.1; -;
CC MGD; MG1:99698; Clock.
CC InterPro; IPR003015; HLH_MVC.
CC InterPro; IPR001092; HLH_dim.
CC InterPro; IPR001067; Nucleoslocatr.
CC InterPro; IPR001610; PAC.
CC InterPro; IPR000014; PAS.
CC InterPro; IPR003617; TFS2_N.
CC Pfam; PF00785; PAC; 1.
CC Pfam; PF00989; PAS; 2.
CC PRINTS; PR00785; NCTRNSLOCATR.
CC SMART; SM00353; HLH; 1.
CC SMART; SM00086; PAC; 1.
CC SMART; SM00509; TFS2N; 1.
CC SMART; SM00091; PAS; 2.
CC PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
KW Transcription regulation; Nuclear protein; Repeat; Biological rhythms;
KW DNA-binding; Alternative splicing.
FT DNA_BIND 35 47 BASIC DOMAIN.
FT DOMAIN 48 85 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT REPEAT 109 175 PAS-1.
FT REPEAT 264 330 PAS-2.
FT DOMAIN 484 855 GLN-RICH.
FT DOMAIN 740 745 POLY-GLN.
FT DOMAIN 751 759 POLY-GLN.
FT DOMAIN 762 769 POLY-GLN.
FT DOMAIN 828 837 POLY-GLN.
FT DOMAIN 514 564 IMPLICATED IN THE CIRCADIAN RHYTHMICITY.
FT VARSPLIC 484 513 MISSING (IN SHORT ISOFORM).
SQ SEQUENCE 855 AA; 96393 MW; 9864D947049742F4 CRC64;

Query Match 54.9%; Score 39; DB 1; Length 855;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFWL 10
| |||||
Db 344 KGOQWIWL 351

RESULT 27
CLOC_MOUSE STANDARD: PRT; 1023 AA.
AC O61735; O76342; O77137;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CIRCADIAN LOCOMOTOR OUTPUT CYCLES RAPUT PROTEIN (DCLOCK) (DPAS1).
GN CLK OR JRK OR CLOCK OR PAS1.
OS Drosophila melanogaster (Fruit fly).

RA Engel H., Smink A.J., van Wijngaarden L., Keck W.;
 RT "Murein-metabolizing enzymes from *Escherichia coli*: existence of a
 RT second lytic transglycosylase";
 RL J. Bacteriol. 174:6394-6403(1992).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick J.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12";
 RL Science 277:1453-1474(1997).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP STRAIN=K12;
 RX MEDLINE=97251358; PubMed=9097040;
 RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
 RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Saito N., Sempel G., Seki Y., Sivasubramanian S., Tagami H.,
 RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
 RT "A 460-kb DNA sequence of the *Escherichia coli* K-12 genome
 RT corresponding to the 40.1-50.0 min region on the linkage map";
 RL DNA Res. 3:379-392(1996).
 RN [5]
 RN FUNCTION, AND CHARACTERIZATION.
 RP MEDLINE=97256743; PubMed=9099672;
 RX Clementz T., Zhou Z., Raetz C.R.H.;
 RA "Function of the *Escherichia coli* msbB gene, a multicopy suppressor
 RT of htrB knockouts, in the acylation of lipid A. Acylation by MsbB
 RT follows laurate incorporation by HtrB";
 RL J. Biol. Chem. 272:10353-10360(1997).
 CC -!- FUNCTION: TRANSFERS MYRISTATE OR LAURATE, ACTIVATED ON ACP, TO THE
 CC LIPID IVA MOIETY OF (KDO)2-(LAUROYL)-LIPID IVA. DECANOYL,
 CC PALMITOYL, PALMITOLEYL, AND (R)-3-HYDROXYMYRISTOYL-ACP ARE POOR
 CC ACYL DONORS. FUNCTIONS OPTIMALLY AFTER LAURATE INCORPORATION BY
 CC HTRB HAS TAKEN PLACE. ACYLATES (KDO)2-(LAUROYL)-LIPID IVA ABOUT
 CC 100 TIMES FASTER THAN (KDO)2-LIPID IVA. DISPLAYS A PREFERENCE FOR
 CC MYRISTOYL-ACP OVER LAUROYL-ACP.
 CC -!- PATHWAY: LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
 CC -!- SIMILARITY: BELONGS TO THE HTRB/MSBB FAMILY.
 CC -!- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE MEMBRANE-BOUND
 CC LYTIC MUREIN TRANSGLYCOSYLASE (MLT).
 CC -----
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 CC -----
 DR EMBL; M77039; AAA24181.1; -;
 DR EMBL; M87660; AAA96706.1; -;
 DR EMBL; AE000279; AAC74925.1; -;
 DR EMBL; D90828; BAA15663.1; -;
 DR PIR; A42608; A42608.
 DR ECoGene; EG10614; msbB.
 KW Lipopolysaccharide biosynthesis; Transferase; Acyltransferase;
 KW Transmembrane; Inner membrane; Complete proteome.
 FT TRANSMEM 23 43 POTENTIAL.
 FT TRANSMEM 85 105 POTENTIAL.
 FT TRANSMEM 133 153 POTENTIAL.
 SQ SEQUENCE 323 AA; 37410 MW; 94DAF38A757D20CD CRC64;

Query Match 53.5%; Score 38; DB 1; Length 323;
 Best Local Similarity 40.0%; Pred. No. 89;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPOOWFLWM 11
 Db 291 PRPEQYTWIL 300
 RESULT 29
 LSPL_MOUSE
 ID LSPL_MOUSE STANDARD; PRT; 330 AA.
 AC P19373; Q04950;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PHOSPHO-PROTEIN (LYMPHOCYTE-SPECIFIC ANTIGEN WP34) (S37 PROTEIN).
 DE LYSOPHOSPHO-PROTEIN (LYMPHOCYTE-SPECIFIC ANTIGEN WP34) (S37 PROTEIN).
 GN LSPL OR WP34 OR S37 OR PP52.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (LSPL1).
 RC STRAIN=BA1B/C;
 RX MEDLINE=89035543; PubMed=3263441;
 RA Jongstra J., Tidmarsh G.F., Jongstra-Bilen J., Davis M.M.;
 RT "A new lymphocyte-specific gene which encodes a putative Ca2+-binding
 RT protein is not expressed in transformed T lymphocyte lines";
 RL J. Immunol. 141:3999-4004(1988).
 RN [2]
 RP SEQUENCE FROM N.A. (S37).
 RX MEDLINE=93107706; PubMed=8417117;
 RA Gimble J.M., Dorheim M.-A., Youkhana K., Hudson J., Nead M.,
 RA Gilly M., Wood W.J. Jr., Hermanson G.G., Kuehl M., Wall R.,
 RA Kincade P.W.;
 RT "Alternatively spliced pp52 mRNA in nonlymphoid stromal cells";
 RL J. Immunol. 150:115-121(1993).
 RN [3]
 RP SEQUENCE FROM N.A. (LSPL1).
 RC STRAIN=BA1B/C;
 RX MEDLINE=95021322; PubMed=7935501;
 RA Jongstra J., Ittel M.E., Iscoe N., Brady G.;
 RT "The LSPL gene is expressed in cultured normal and transformed mouse
 RT macrophages";
 RL Mol. Immunol. 31:1125-1131(1994).
 CC -!- FUNCTION: NOT KNOWN. THE AUTHORS BELIEVE THAT IT MAY BE INVOLVED
 CC IN TRANSMEMBRANE SIGNAL TRANSDUCTION THROUGH A POSTULATED CALCIUM-
 CC BINDING FUNCTION, BUT THE EVIDENCE FOR THE EXISTENCE OF A CALCIUM-
 CC BINDING REGION IS WEAK.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF THE PLASMA MEMBRANE.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; LYMPHOID LSPL (SHOWN HERE) AND
 CC STROMAL S37; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: LSPL IS EXPRESSED IN NORMAL MOUSE B AND T
 CC LYMPHOCYTES AND IN TRANSFORMED B-CELLS BUT NOT (OR IN SMALLER
 CC AMOUNTS) IN NINE T LYMPHOMA LINES TESTED. S37 IS EXPRESSED IN
 CC NONLYMPHOID CELL LINES (MYOCYTES, STROMAL CELLS, FIBROBLASTS).
 CC -!- PTM: PHOSPHORYLATED BY CASEIN KINASE II.
 CC -----
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 CC -----
 DR EMBL; M90316; AAA65108.1; -;
 DR EMBL; S74179; AAB32257.1; -;
 DR EMBL; M89956; AAB48537.1; -;
 DR PIR; A30533; A30533.
 DR MGD; MGI:96832; Lspl.
 DR InterPro; IPR002211; Lymphspecific.
 DR PRINTS; PR01083; LYMPHSPECIFIC.
 KW T-cell; Alternative splicing; Phosphorylation.

```
FT MOD_RES 77 77 PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT MOD_RES 78 78 PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT VARSPLIC 1 23 MAERAIIDRCOEDELHEDSEG -> MNGPALLRRNAS
FT CONFLICT 155 156 KRGLKLLR (IN ISOFORM S37).
FT CONFLICT 160 160 AE -> PK (IN REF. 1).
FT CONFLICT 160 160 I -> T (IN REF. 1).
FT CONFLICT 168 168 S -> N (IN REF. 1).
FT CONFLICT 253 253 S -> G (IN REF. 1).
SQ SEQUENCE 330 AA; 36714 MW; CCC27150F02859FB CRC64;

Query Match 53.5%; Score 38; DB 1; Length 330;
Best Local Similarity 55.6%; Pred. No. 90;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQQFW 9
Db 92 KPEPRQQFW 100

RESULT 30
FUT4_HUMAN
ID FUT4_HUMAN STANDARD; PRT; 405 AA.
AC P22083;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-
DE FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV) (ELAM-1 LIGAND
DE FUCOSYLTRANSFERASE).
GN FUT4 OR ELFT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Peripheral blood leukocytes;
RX MEDLINE=91373370; PubMed=1716630;
RA Lowe J.B., Kukowska-Latallo J.F., Nair R.P., Larsen R.D., Marks R.M.,
RA Macher B.A., Kelly R.J., Ernst L.K.;
RT "Molecular cloning of a human fucosyltransferase gene that determines
RT expression of the Lewis x and VIM-2 epitopes but not ELAM-1-dependent
RT cell adhesion."
RL J. Biol. Chem. 266:17467-17477(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91084863; PubMed=1702034;
RA Goelz S.E., Hession C., Goff D., Griffiths B., Tizard R., Newman B.,
RA Chi-Rosso G., Lobb R.;
RT "ELFT: a gene that directs the expression of an ELAM-1 ligand."
RL Cell 63:1349-1356(1990).
RN [3]
RP SEQUENCE OF 1-400 FROM N.A.
RX MEDLINE=92042084; PubMed=1718983;
RA Kumar R., Potvin B., Muller W.A., Stanley P.;
RT "Cloning of a human alpha(1,3)-fucosyltransferase gene that encodes
RT ELFT but does not confer ELAM-1 recognition on Chinese hamster ovary
RT cell transfectants."
RL J. Biol. Chem. 266:21777-21783(1991).
CC -1- FUNCTION: MAY CATALYSE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
CC THE EXPRESSION OF LEWIS X/SSSEA-1 AND VIN-2 ANTIGENS.
CC -1- PATHWAY: GLYCOSYLATION.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC FORM IN TRANS CISTERNAE OF GOLGI.
CC
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CC -----
DR EMBL: M65030; AAA92977.1; -
DR EMBL: M58596; AAA63172.1; -
DR EMBL: M58597; AAA63173.1; ALT_INIT.
DR EMBL: S65161; AAB20349.1; -
DR PIR: A36340; A36340.
DR MIM: 104230; -
DR InterPro: IPR001503; Glyco.transf_10.
DR Pfam: PF00852; Glyco.transf_10; 1.
KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
KW Signal-anchor; Golgi stack.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 47 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT FT 48 405 LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 87 87 P -> R (IN REF. 2 AND 3).
FT CONFLICT 241 241 E -> D (IN REF. 3).
SQ SEQUENCE 405 AA; 45569 MW; DE72E1FDC390268D CRC64;

Query Match 53.5%; Score 38; DB 1; Length 405;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQQFWL 10
Db 161 RPPGQRWVWM 170

RESULT 31
FUT4_MOUSE
ID FUT4_MOUSE STANDARD; PRT; 433 AA.
AC Q11127;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-
DE FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV).
GN FUT4 OR ELFT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96027607; PubMed=7559635;
RA Gersten K.M., Natsuka S., Trinchera M., Petryniak B., Kelly R.J.,
RA Hiraawa N., Jenkins N.A., Gilbert D.J., Copeland N.G., Lowe J.B.;
RT "Molecular cloning, expression, chromosomal assignment, and tissue-
RT specific expression of a murine alpha-(1,3)-fucosyltransferase locus
RT corresponding to the human ELAM-1 ligand fucosyl transferase."
RL J. Biol. Chem. 270:25047-25056(1995).
RN [2]
RP SEQUENCE FROM N.A. (SHORT FORM).
RC STRAIN=129/SV; TISSUE=Liver;
RX MEDLINE=97037075; PubMed=8882722;
RA Ozawa M., Muramatsu T.;
RT "Molecular cloning and expression of a mouse alpha-1,3
RT fucosyltransferase gene that shows homology with the human alpha-1,3
RT fucosyltransferase IV gene."
RL J. Biochem. 119:302-308(1996).
CC -1- FUNCTION: MAY CATALYSE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
CC THE EXPRESSION OF LEWIS X/SSSEA-1 AND VIN-2 ANTIGENS.
CC -1- PATHWAY: GLYCOSYLATION.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC FORM IN TRANS CISTERNAE OF GOLGI.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN STOMACH AND COLON.
CC IT ALSO EXPRESSED IN THE LUNG, TESTIS, UTERUS, SMALL INTESTINE
CC AND TO A LESSER EXTENT IN SPLEEN, AND OVARY. PRESENT IN TRACE
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CC AMOUNTS IN BRAIN, THYMUS, HEART, SMOOTH MUSCLE, KIDNEY AND BONE
CC MARROW. NOT FOUND IN LIVER, SALIVARY GLAND AND PANCREAS.
CC -----
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CC -----
CC EMBL: U33457; AAC5269.1; -
CC DR EMBL: D63380; BAA09697.1; -
CC DR EMBL: D63379; BAA09696.1; -
CC DR MGI: 95594; Fut4.
CC DR InterPro: IPR001503; Glyco_transf_10.
CC DR Pfam: PF00852; Glyco_transf_10; 1.
CC KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
CC KW Signal-anchor; Golgi stack; Alternative splicing.
CC FT DOMAIN 1 52 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 53 74 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC (POTENTIAL).
CC FT DOMAIN 75 433 LUMENAL, CATALYTIC (POTENTIAL).
CC FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT VARSPLIC 218 218 MISSING (IN SHORT ISOFORM).
CC FT CONFLICT 252 252 Q -> P (IN REF. 2).
CC FT CONFLICT 257 257 R -> Q (IN REF. 2).
CC FT CONFLICT 260 260 V -> E (IN REF. 2).
CC FT CONFLICT 273 273 R -> Q (IN REF. 2).
CC SQ SEQUENCE 433 AA; 49481 MW; 2401622F02B5D021 CRC64;

Query Match 53.5%; Score 38; DB 1; Length 433;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQFWL 10
|| | | |
DB 189 RPPGQRVWM 198

RESULT 32
FUT4_RAT
ID FUT4_RAT STANDARD; PRT; 433 AA.
AC Q62994;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALPHA-(1.3)-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-
DE FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV).
GN FUT4 OR RFUC-T.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Kidney;
RX MEDLINE=97265205; PubMed=911142;
RA Szejda-Sulkowska E.M., Smith F.I., Wiedersheim G., McCluer R.H.;
RT "Cloning of a rat alpha1,3-fucosyltransferase gene: a member of the
RT fucosyltransferase IV family.";
RL Glycoconj. J. 14:249-258(1997).
CC -1- FUNCTION: MAY CATALYSE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
CC THE EXPRESSION OF LEWIS X/SSA-1 AND VIM-2 ANTIGENS.
CC -1- PATHWAY: GLYCOSYLATION.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC FORM IN TRANS CISTERNAE OF GOLGI.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: IN ADULT, HIGHEST EXPRESSION IN SPLEEN,
CC TESTIS, BRAIN, LUNG, KIDNEY AND SKELETAL MUSCLE AND TO A LESSER

CC EXTENT IN LIVER AND HEART.
CC -----
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CC -----
CC EMBL: U58860; AAB97609.1; -
CC DR InterPro: IPR001503; Glyco_transf_10.
CC DR Pfam: PF00852; Glyco_transf_10; 1.
CC KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
CC KW Signal-anchor; Golgi stack; Alternative splicing.
CC FT DOMAIN 1 54 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 55 74 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC (POTENTIAL).
CC FT DOMAIN 75 433 LUMENAL, CATALYTIC (POTENTIAL).
CC FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT VARSPLIC 218 218 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CONFLICT 33 33 MISSING (IN SHORT ISOFORM).
CC SQ SEQUENCE 433 AA; 48779 MW; 75B0E569B72FD2F8 CRC64;
Query Match 53.5%; Score 38; DB 1; Length 433;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQFWL 10
|| | | |
DB 189 RPPGQRVWM 198

RESULT 33
YADC_SCHPO
ID YADC_SCHPO STANDARD; PRT; 533 AA.
AC Q09837;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HYPOTHETICAL 62.2 KDA PROTEIN C4G8.12C IN CHROMOSOME I.
GN SPAC4G8.12C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OC NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Badcock K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: TO YEAST SMP3.
CC -1- SIMILARITY: SOME, TO YEAST YGL142C.
CC -----
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CC -----
CC EMBL: Z56276; CAA91213.1; -
CC DR Hypothetical protein; Transmembrane.
CC TRANSMEM 8 28 POTENTIAL.
CC TRANSMEM 61 81 POTENTIAL.
CC TRANSMEM 91 111 POTENTIAL.
CC TRANSMEM 144 164 POTENTIAL.
CC TRANSMEM 175 195 POTENTIAL.
CC TRANSMEM 216 236 POTENTIAL.

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FT TRANSMEM 274 294 POTENTIAL.
FT TRANSMEM 297 317 POTENTIAL.
FT TRANSMEM 338 358 POTENTIAL.
FT TRANSMEM 496 516 POTENTIAL.
SQ SEQUENCE 533 AA; 62200 MW; F14519C995884687 CRC64;

Query Match 53.5%; Score 38; DB 1; Length 533;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RPKQWFWLM 11
   |||||
Db 296 KPATWLWL 304

RESULT 34
ARNT_HUMAN
ID ARNT_HUMAN STANDARD; PRT; 789 AA.
AC P27540;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR (ARNT PROTEIN) (DIOXIN
DE RECEPTOR, NUCLEAR TRANSLOCATOR) (HYPOXIA-INDUCIBLE FACTOR 1 BETA)
DE (HIF-1 BETA).
GN ARNT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91240280; PubMed=1852076;
RA Hofman E.C., Reyes H., Chu F.-F., Sander F., Conley L.H.,
RA Brooks B.A., Hankinson O.;
RT "Cloning of a factor required for activity of the Ah (dioxin)
RT receptor."
RL Science 252:954-958(1991).
RN [2]
RP SEQUENCE OF 186-203 AND 662-694.
RX MEDLINE=95296340; PubMed=7539918;
RA Wang G.L., Jiang B.-H., Rue E.A., Semenza G.L.;
RT "Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS
RT heterodimer regulated by cellular O2 tension."
RL Proc. Natl. Acad. Sci. U.S.A. 92:5510-5514(1995).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=92271249; PubMed=1317062;
RA Reyes H., Reisz-Porszasz S., Hankinson O.;
RT "Identification of the Ah receptor nuclear translocator protein
RT (Arnt) as a component of the DNA binding form of the Ah receptor."
RL Science 256:1193-1195(1992).
CC -!- FUNCTION: REQUIRED FOR ACTIVITY OF THE AH (DIOXIN) RECEPTOR. THIS
CC PROTEIN IS REQUIRED FOR THE LIGAND-BINDING SUBUNIT TO TRANSLOCATE
CC FROM THE CYTOSOL TO THE NUCLEUS AFTER LIGAND BINDING. THE COMPLEX
CC THEN INITIATES TRANSCRIPTION OF A GENES INVOLVED IN THE ACTIVATION
CC OF PAH PROCARCINOGENS.
CC -!- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
CC BHLH PROTEIN. FORMS AN HETERODIMER WITH AHR, WITH HIF1A AS WELL AS
CC WITH OTHER BHLH PROTEINS. INTERACTS WITH TRANSFORMING ACIDIC
CC COILED-COIL CONTAINING PROTEIN 3 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND
CC A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS.
CC -!- SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.
CC -----
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EMBL; M69238; AA51777.1; -.
DR HSSP; P22415; IANA.
DR TRANSFAC; T01346; -.
DR MIM; 126110; -.
DR InterPro; IPR003015; HLH_Myc.
DR InterPro; IPR001092; HLH_dim.
DR InterPro; IPR001067; Nucleinslocatr.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00989; PAS; 2.
DR PRINTS; PR00785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
KW Nuclear protein; DNA-binding; Transcription regulation; Activator;
KW Alternative splicing; Repeat.
FT DNA_BIND 90 102 BASIC DOMAIN.
FT DOMAIN 103 143 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT REPEAT 163 230 PAS-1.
FT REPEAT 351 417 PAS-2.
FT DOMAIN 424 467 PAC MOTIF.
FT DOMAIN 710 769 GLN-RICH.
FT DOMAIN 99 102 POLY-ARG.
FT DOMAIN 503 507 POLY-GLN.
FT DOMAIN 738 741 POLY-SER.
FT VARSPIC 77 91 MISSING (IN SHORT ISOFORM).
SQ SEQUENCE 789 AA; 86636 MW; 2E278F8E62BFBF6D CRC64;

Query Match 53.5%; Score 38; DB 1; Length 789;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKQWFWLM 10
   |||||
Db 430 RSKNOEWLWM 439

RESULT 35
VEF_GVPV
ID VEF_GVPV STANDARD; PRT; 901 AA.
AC P41723;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE VIRAL ENHANCING FACTOR (VEF) (ENHANCIN) (104 KDA GLYCOPROTEIN)
DE (SYNERGISTIC FACTOR).
GN VEF.
OS Pseudolatia unipuncta granulosis virus (puGV) (Pseudolatia unipuncta
OS granulovirus).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX NCBI_TaxID=36355;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HAWAII;
RX MEDLINE=96068802; PubMed=7595376;
RA Roelvik P.W., Corsaro B.G., Granados R.R.;
RT "Characterization of the Helicoverpa armigera and Pseudolatia
RT unipuncta granulovirus enhancer genes."
RL J. Gen. Virol. 76:2693-2705(1995).
CC -!- FUNCTION: INVOLVED IN DISRUPTION OF THE PERITROPIC MEMBRANE AND
CC FUSION OF NUCLEOCAPSIDS WITH MIDGUT CELLS (BY SIMILARITY).
CC -!- SIMILARITY: TO TNGV AND HAGV VEF.
CC -----
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CC EMBL; D14871; BAA03587.1; ..
KW Glycoprotein; Late protein.
FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 349 349 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 540 540 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 595 595 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 642 642 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 683 683 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 698 698 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 901 AA; 104252 MW; 5D0E542A858FE5FB CRC64;

Query Match 53.5%; Score 38; DB 1; Length 901;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQOWFWL 10
DB 353 PYQIWSWL 361

RESULT 36
VEF_GVTN STANDARD; PRT; 901 AA.
AC P29998:
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE VIRAL ENHANCING FACTOR (VEF) (ENHANCIN) (104 KDA GLYCOPROTEIN)
GN (SYNERGISTIC FACTOR).
DE VEF.

OS Trichoplusia ni granulosis virus (TnGV) (Trichoplusia ni
OS granulovirus).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX NCBI_TaxID=10462;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=92044434; PubMed=1940861;
RA Hashimoto Y., Corsaro B.G., Granados R.R.;
RT "Location and nucleotide sequence of the gene encoding the viral
RT enhancing factor of the Trichoplusia ni granulosis virus.";
RL J. Gen. Virol. 72:2645-2651(1991).

CC -I- FUNCTION: INVOLVED IN DISRUPTION OF THE PERITROPHIC MEMBRANE AND
CC FUSION OF NUCLEOCAPSIDS WITH MIDGUT CELLS.
CC -I- SIMILARITY: TO PUGV AND HAGV VEF.

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CC EMBL; D12617; BAA02141.1; ..
DR PIR; J01328; WNVN.
KW Glycoprotein; Late protein.
FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 349 349 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 540 540 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 595 595 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 642 642 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 683 683 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 698 698 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 901 AA; 104322 MW; 74DB822E0A11CD6A CRC64;

Query Match 53.5%; Score 38; DB 1; Length 901;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQOWFWL 10
DB 353 PYQIWSWL 361

RESULT 37
Y812_ARCFU STANDARD; PRT; 298 AA.
ID Y812_ARCFU
AC Q29446;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN AF0812.
GN AF0812.

OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodak A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;

RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).

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CC EMBL; AE001048; AAB90432.1; ..
DR TIGR; AF0812; ..
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 298 AA; 34385 MW; ED59E86A07AC5A30 CRC64;

Query Match 52.8%; Score 37.5; DB 1; Length 298;
Best Local Similarity 66.7%; Pred. No. 97;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 2 PKPQOWFW 9
DB 62 PKPEYFWR 70

RESULT 38
DNBI_HSV1 STANDARD; PRT; 375 AA.
ID DNBI_HSV1
AC Q03444;

DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MAJOR DNA-BINDING PROTEIN (FRAGMENT).
GN 31.
OS Equine herpesvirus type 1 (isolate HVS25A) (EHV-1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10327;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=94106109; PubMed=8279122;
RA Bell C.W., Whalley J.M.;
RT "Herpesvirus ICP18.5 and DNA-binding protein genes are conserved in
equine herpesvirus-1";
RL Virus Genes 7:219-228(1993).
CC -!- FUNCTION: SINGLE-STRAND DNA-BINDING PROTEIN REQUIRED FOR DNA
REPLICATION.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE HERPESVIRUSES DNA-BINDING PROTEIN
FAMILY.
CC -----
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CC -----
DR EMBL; D13930; BAA03033.1; -;
DR PIR; JQ0846; JQ0846.
KW DNA-binding; DNA replication; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 375 AA; 40309 MW; ECF327925EBF999B CRC64;

Query Match 52.8%; Score 37.5; DB 1; Length 375;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 2 PRPQOWFWLM 11
Db 10 PNP-QWFWTL 18
: | | | | |
P N P Q O W F W T L 1 8

RESULT 39
ID DNBI_HSV11 STANDARD; PRT; 1196 AA.
AC P04296;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MAJOR DNA-BINDING PROTEIN (INFECTED CELL PROTEIN 8) (ICP 8 PROTEIN).
GN DBP OR UL29 OR ICP8.
OS Herpes simplex virus (type 1 / strain 17).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10299;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=88274327; PubMed=2839594;
RA McGeoch D.J., Dairymple M.A., Davison A.J., Dolan A., Frame M.C.,
RA McNab D., Perry L.J., Scott J.E., Taylor P.;
RT "The complete DNA sequence of the long unique region in the genome of
herpes simplex virus type 1";
RL J. Gen. Virol. 69:1531-1574(1988).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=86067223; PubMed=2999714;
RA Quinn J.P., McGeoch D.J.;
RT "DNA sequence of the region in the genome of herpes simplex virus
type 1 containing the genes for DNA polymerase and the major DNA

binding protein";
RL Nucleic Acids Res. 13:8143-8163(1985).
[3]
RN SEQUENCE OF 1062-1196 FROM N.A.
RX MEDLINE=88306232; PubMed=2457278;
RA Hammerschmidt W., Conraths F., Mankertz J., Buhk H.-J., Pauli G.,
RA Ludwig H.;
RT "Common epitopes of glycoprotein B map within the major DNA-binding
proteins of bovine herpesvirus type 2 (BHV-2) and herpes simplex
virus type 1 (HSV-1).";
RL Virology 165:406-418(1988).
CC -!- FUNCTION: SINGLE-STRAND DNA-BINDING PROTEIN REQUIRED FOR DNA
REPLICATION.
CC -!- SUBCELLULAR LOCATION: NUCLEAR. IN THE ABSENCE OF DNA REPLICATION,
CC FOUND IN THE NUCLEAR FRAMEWORK-ASSOCIATED STRUCTURES
CC (PERIPHERAL SITES); AS VIRAL DNA REPLICATION PROCEEDS, IT
CC MIGRATES TO GLOBULAR INTRANUCLEAR STRUCTURES (REPLICATION
CC COMPARTMENTS).
CC -!- SIMILARITY: BELONGS TO THE HERPESVIRUSES DNA-BINDING PROTEIN
FAMILY.
CC -----
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CC -----
DR EMBL; D10879; BAA01675.1; -;
DR EMBL; X14112; CAA32322.1; -;
DR EMBL; X03181; CAA26940.1; -;
DR EMBL; M21631; AAA45787.1; -;
DR PIR; A03790; DNBV1.
DR PIR; B30085; B30085.
DR InterPro; IPR000635; Viral_DNA_bind.
DR Pfam; PF00747; viral_DNA_bp.1.
KW DNA-binding; DNA replication; Zinc-finger; Nuclear protein.
FT ZN_FING 499 512 C2HC-TYPE
SQ SEQUENCE 1196 AA; 128349 MW; 4537991625B99E9 CRC64;

Query Match 52.8%; Score 37.5; DB 1; Length 1196;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 RPKPQOWFW 9
Db 837 QPNP-QWFW 844
: | | | | |
R P K P Q O W F W 9

RESULT 40
ID DNBI_HSV1F STANDARD; PRT; 1196 AA.
AC P17469;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MAJOR DNA-BINDING PROTEIN (INFECTED CELL PROTEIN 8) (ICP 8 PROTEIN).
GN DBP OR UL29 OR ICP8.
OS Herpes simplex virus (type 1 / strain F).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10304;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=88306231; PubMed=2841793;
RA Hammerschmidt W., Conraths F., Mankertz J., Pauli G., Ludwig H.,
RA Buhk H.-J.;
RT "Conservation of a gene cluster including glycoprotein B in bovine
herpesvirus type 2 (BHV-2) and herpes simplex virus type 1 (HSV-1).";
RL Virology 165:388-405(1988).
CC -!- FUNCTION: SINGLE-STRAND DNA-BINDING PROTEIN REQUIRED FOR DNA

RA Toh Y., Liu Y., Tanaka S., Mori R.;
RT "Nucleotide sequence of the major DNA-binding protein gene of herpes
RL Arch. Virol. 129:183-196(1993).
CC -!- FUNCTION: SINGLE-STRAND DNA-BINDING PROTEIN REQUIRED FOR DNA
CC REPLICATION.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE HERPESVIRUSES DNA-BINDING PROTEIN
CC FAMILY.
DR PIR; A48350; A48350.
DR InterPro; IPR000635; Viral_DNA_bind.
DR Pfam; PF00747; Viral_DNA_bp; 1.
KW DNA-binding; DNA replication; Zinc-finger; Nuclear protein.
FT ZN_FING 499 512 C2HC-TYPE.
FT DOMAIN 1169 1197 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ SEQUENCE 1197 AA; 128412 MW; C1576B5B865BFB CRC64;

Query Match 52.8%; Score 37.5; DB 1; Length 1197;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

OY 1 RPKPOQWFLM 9
DB 837 QPNP-QWFWL 844
: | | | | |

RESULT 44
DNBI_VZVD STANDARD; PRT; 1204 AA.
AC P09246;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MAJOR DNA-BINDING PROTEIN.
GN 29.
OS Varicella-zoster virus (strain Dumas) (VZV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10338;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86306657; PubMed=3018124;
RA Davison A.J., Scott J.E.;
RT "The complete DNA sequence of varicella-zoster virus.";
RL J. Gen. Virol. 67:1759-1816(1986).
CC -!- FUNCTION: SINGLE-STRAND DNA-BINDING PROTEIN REQUIRED FOR DNA
CC REPLICATION.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE HERPESVIRUSES DNA-BINDING PROTEIN
CC FAMILY.
CC -----
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CC -----
CC EMBL; X04370; CAA27912.1; -.
DR PIR; C27214; DNBE29.
DR InterPro; IPR000635; Viral_DNA_bind.
DR Pfam; PF00747; Viral_DNA_bp; 1.
KW DNA-binding; DNA replication; Zinc-finger; Nuclear protein.
FT ZN_FING 497 510 C2HC-TYPE.
SQ SEQUENCE 1204 AA; 132139 MW; D2FEE65DC0CC674 CRC64;

Query Match 52.8%; Score 37.5; DB 1; Length 1204;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 2 PKPOQWFLM 11
DB 836 PNP-QWFWL 844
: | | | | |

RESULT 45
DNBI_HSVB STANDARD; PRT; 1209 AA.
AC P28932;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MAJOR DNA-BINDING PROTEIN.
GN 31.
OS Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=31520;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92295566; PubMed=1318606;
RA Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-1.";
RL Virology 189:304-316(1992).
CC -!- FUNCTION: SINGLE-STRAND DNA-BINDING PROTEIN REQUIRED FOR DNA
CC REPLICATION.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE HERPESVIRUSES DNA-BINDING PROTEIN
CC FAMILY.
CC -----
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CC -----
CC EMBL; M86664; AAB02466.1; -.
DR PIR; E36798; DNBE64.
DR InterPro; IPR000635; Viral_DNA_bind.
DR Pfam; PF00747; Viral_DNA_bp; 1.
KW DNA-binding; DNA replication; Zinc-finger; Nuclear protein.
FT ZN_FING 503 516 C2HC-TYPE.
SQ SEQUENCE 1209 AA; 129982 MW; 1A728FB04484FE95 CRC64;

Query Match 52.8%; Score 37.5; DB 1; Length 1209;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 2 PKPOQWFLM 11
DB 844 PNP-QWFWL 852
: | | | | |

RESULT 46
TKNA_ONCMY STANDARD; PRT; 11 AA.
AC P28499;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92298992; PubMed=1376687;

RA Jensen J., Conlon J.M.;
RT "Substance-P-related and neurokinin-A-related peptides from the brain
RL of the cod and trout.";
CC Eur. J. Biochem. 206:659-664(1992).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: S23307; S23307.
DR PIR: S23308; S23308.
DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART: SM00203; TK; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
DR Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
KW Tachykinin; 11
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 11;
Best Local Similarity 54.5%; Pred. No. 5.8; Indels 2; Gaps 0;
Matches 6; Conservative 3; Mismatches 0;

QY 1 RPKPQOWFWLM 11
:|:|:|:|
DB 1 KPRPHQFFGLM 11

RESULT 47
HOBB_ECOLI
ID HOBB_ECOLI STANDARD; PRT; 175 AA.
AC P36558;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VERY HYPOTHETICAL HOBB PROTEIN.
GN HOBB.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-K12 / W3110.
RC MEDLINE=95009972; PubMed=7925311;
RA Herrick J., Kern R., Guha S., Landoulsi A., Fayet O., Malki A.,
RA Kohiyama M.;
RT "Parental strand recognition of the DNA replication origin by the
RT outer membrane in Escherichia coli.";
RL EMBO J. 13:4695-4703(1994).
RN [2]
RP COMMENT ABOUT THIS PROTEIN.
RA Balroch A.;
RL Unpublished observations (NOV-1994).
CC -1- FUNCTION: DNA-BINDING PROTEIN SPECIFIC OF THE E.COLI ORIGIN OF
CC REPLICATION (ORIC).
CC -1- CAUTION: THIS PROTEIN MAY NOT BE THE "REAL" HOBB BECAUSE IT IS ON
CC THE OPPOSITE FRAME OF AN ORF (APHA) WHICH HAS BEEN SHOWN, BY
CC MICROSEQUENCING, TO EXIST. FURTHERMORE THE REAL HOBB IS PROBABLY
CC SEQA.
CC
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CC
CC EMBL; Z26592; CAA81346.1; ALT_SEQ.
DR PIR: S37475; S37475.

KW Hypothetical protein; DNA-binding.
SQ SEQUENCE 175 AA; 20876 MW; 3E8119754B0ADEB4 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 175;
Best Local Similarity 71.4%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOOW 7
|:|:|:|
DB 160 RPKPNEW 166

RESULT 48
HRB3_XANCV
ID HRB3_XANCV STANDARD; PRT; 253 AA.
AC P80152;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE HRPB3 PROTEIN PRECURSOR.
GN HRPB3.
OS Xanthomonas campestris (pv. vesicatoria).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xanthomonas.
OX NCBI_TaxID=341;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-ISOLATE 75-3;
RC MEDLINE=93113007; PubMed=1472717;
RX Fenselau S., Balbo I., Bonas U.;
RT "Determinants of pathogenicity in Xanthomonas campestris pv.
RT vesicatoria are related to proteins involved in secretion in
RT bacterial pathogens of animals.";
RL Mol. Plant Microbe Interact. 5:390-396(1992).
CC -1- FUNCTION: NECESSARY FOR BOTH BASIC PATHOGENICITY AND THE INDUCTION
CC OF THE HYPERSENSITIVE RESPONSE IN RESISTANT PLANTS. COULD BE A
CC PART OF A SPECIFIC TRANSPORT APPARATUS OR A SECRETION APPARATUS
CC THAT IS REQUIRED FOR PATHOGENICITY. HRP PROTEINS MAY FORM A
CC COMPLEX (TUNNEL/PORE) THAT ENABLES THE EXPORT OF MOLECULES SUCH AS
CC VIRULENCE AND AVIRULENCE FACTORS.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPID
CC ANCHOR (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE YSCJ FAMILY OF LIPOPROTEINS.
CC
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CC
CC EMBL; U33548; AAB08458.1;
DR EMBL; M99175; AAA27604.1;
DR InterPro: IPR003282; SecIIOMP_K.
DR InterPro: IPR002920; YscJ_Flip.
DR Pfam: PF01514; YscJ_Flip; 1.
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW Transport; Protein transport; Outer membrane; Signal; Lipoprotein;
KW Hypersensitive response.
FT CHAIN 1 18
FT SIGNAL 19 253
FT LIPID 19 19
FT N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 253 AA; 27263 MW; 35A80820C2D3555A CRC64;

Query Match 52.1%; Score 37; DB 1; Length 253;
Best Local Similarity 55.6%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOOWFWL 10
|:|:|:|

DR 204 PRPSPWNL 212

RESULT 49

FUT7_HUMAN

AC Q11130; STANDARD; PRT; 342 AA.

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE ALPHA-1,3-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 7) (FUCT-VII) (SELECTIN-LIGAND SYNTHASE).

DE LIGAND SYNTHASE).

GN FUT7.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94266898; PubMed=8207002;

RA Natsuka S., Gersten K.M., Zenita K., Kannagi R., Lowe J.B.; "Molecular cloning of a cDNA encoding a novel human leukocyte alpha-1,3-fucosyltransferase capable of synthesizing the sialyl Lewis x determinant.";

RT Lewis x determinant.";

RL J. Biol. Chem. 269:16789-16794(1994).

RN [2]

RP REVISIONS.

RX MEDLINE=94327669; PubMed=8051184;

RA Natsuka S., Gersten K.M., Zenita K., Kannagi R., Lowe J.B.; "Molecular cloning of a cDNA encoding a novel human leukocyte alpha-1,3-fucosyltransferase capable of synthesizing the sialyl Lewis x determinant.";

RT Lewis x determinant.";

RL J. Biol. Chem. 269:20806-20806(1994).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=94237894; PubMed=8182079;

RA Sasaki K., Kurata K., Funayama K., Nagata M., Watanabe E., Ohta S., Hanai N., Nishi T.; "Expression cloning of a novel alpha 1,3-fucosyltransferase that is involved in biosynthesis of the sialyl Lewis x carbohydrate determinants in leukocytes.";

RT Lewis x determinant.";

RL J. Biol. Chem. 269:14730-14737(1994).

RN [4]

RP SEQUENCE FROM N.A.

RA Hiraiwa N., Hiraiwa M., Kannagi R.; "The human selectin-ligand synthase (hPuc-T VII) gene structure and characterization of the promoter.";

RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN THE EXPRESSION OF SIALYL LEWIS X ANTIGENS.

CC -!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + ALPHA-2,3-NEU-N-ACETYL-1,4-BETA-D-GALACTOSYL-N-ACETYL-D-GLUCOSAMINYL-R = GDP + ALPHA-2,3-NEU-N-ACETYL-1,4-BETA-D-GALACTOSYL-(ALPHA-1,3-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.

CC -!- PATHWAY: GLYCOSYLATION.

CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.

CC -!- TISSUE SPECIFICITY: LEUKOCYTIC/MYELOID LINEAGE CELLS.

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CC EMBL; X78031; CAA54962.1; -

CC EMBL; U11282; AAA20468.1; -

CC EMBL; U08112; AAA56869.1; -

CC EMBL; AB012668; BAA32819.1; -

CC MIM; 602030; -

DR EMBL; X78031; CAA54962.1; -

DR EMBL; U11282; AAA20468.1; -

DR EMBL; U08112; AAA56869.1; -

DR EMBL; AB012668; BAA32819.1; -

DR MIM; 602030; -

DR InterPro; IPR001503; Glyco_transf_10.

DR Pfam; PF00852; Glyco_transf_10; 1.

KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;

KW Signal-anchor; Golgi stack.

FT DOMAIN 1 14 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 15 36 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).

FT DOMAIN 37 342 LUMENAL, CATALYTIC (POTENTIAL).

FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 161 162 GP -> A (IN REF. 1; AAA56869).

FT CONFLICT 304 305 RL -> SV (IN REF. 1; AAA56869).

SQ SEQUENCE 342 AA; 39238 MW; D31BFF90DD64DFAB CRC64;

Query Match 52.1%; Score 37; DB 1; Length 342;

Best Local Similarity 55.6%; Pred. No. 1.3e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQWFW 9

DB 110 RPRGQWFW 118

II: I I I I

RESULT 50

YCGF_ECOLI

ID YCGF_ECOLI STANDARD; PRT; 403 AA.

AC P75990;

DT 20-AUG-2001 (Rel. 40, Created)

DT 20-AUG-2001 (Rel. 40, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE HYPOTHETICAL PROTEIN YCGF.

GN YCGF OR B1163.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12.";

RT Science 277:1453-1474(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=K12.

RX MEDLINE=97061202; PubMed=8905232;

RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikenoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.; "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";

RT DNA Res. 3:1137-1155(1996).

CC -!- SIMILARITY: CONTAINS 1 DUF2 DOMAIN.

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CC EMBL; AE000215; AAC74247.1; -

CC EMBL; D90750; BAA35998.1; -

CC EMBL; D90751; BAA36002.1; -

DR EcoGene; EGI3887; ycgF.
DR InterPro: IPR001633; DUF2.
DR Pfam: PF00563; DUF2; 1.
DR SMART; SM00052; DUF2; 1.
KW Hypothetical protein; Complete proteome.
FT DOMAIN 159 394 DUF2.
SQ SEQUENCE 403 AA; 45295 MW; 57B662BEC10957DA CRC64;

Query Match 52.1%; Score 37; DB 1; Length 403;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQOWFWL 10
I::I I I
DB 367 PEEHWWL 373

RESULT 51
CYB_MARPO
ID CYB_MARPO STANDARD; PRT; 404 AA.
AC P26852;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOCHROME B.
GN COB OR CVTB.
OS Marchantia polymorpha (Liverwort).
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
OC Marchantiales; Marchantiaceae; Marchantia.
OX NCBI_TaxID=3197;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92114051; PubMed=1731062;
RA Oda K., Yamato K., Ohta E., Nakamura Y., Takemura M., Nozato N.,
RA Akashi K., Kanehara T., Ogura Y., Kohchi T., Ohyama K.;
RT "Gene organization deduced from the complete sequence of liverwort
Marchantia polymorpha mitochondrial DNA. A primitive form of plant
mitochondrial genome.";
RT J. Mol. Biol. 223:1-7(1992).

CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS.
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN.
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
CC -----
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DR EMBL; M68929; AAC09441.1; -
DR PIR; S25953; S25953.
DR Mendel; 2054; MARPO; cob; 1.
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam; PF00032; cytochrome_b_c; 1.
DR Pfam; PF00033; cytochrome_b_n; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_OO; 1.
KW Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
KW Heme.
FT METAL 85 85 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 99 99 IRON 2 (HEME B566 AXIAL LIGAND).
FT METAL 186 186 IRON 2 (HEME B562 AXIAL LIGAND).
FT METAL 200 200 IRON 1 (HEME B566 AXIAL LIGAND).

SQ SEQUENCE 404 AA; 45188 MW; AFFCA920DD4783A2 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 404;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
I::I I I I I
DB 322 RPIHQFFWLL 332

RESULT 52
NEC3_MOUSE
ID NEC3_MOUSE STANDARD; PRT; 655 AA.
AC P29121;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE NEUROENDOCRINE CONVERTASE 3 PRECURSOR (EC 3.4.21.-) (NEC 3) (PC4)
DE (PROHORMONE CONVERTASE 3) (KEX2-LIKE ENDOPEPTIDASE 3).
GN PCSK4 OR NEC3 OR NEC-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92210552; PubMed=1372895;
RA Nakayama K., Kim W.S., Torii S., Hosaka M., Nakagawa T.,
RA Ikemizu J., Baba T., Murakami K.;
RT "Identification of the fourth member of the mammalian endoprotease
family homologous to the yeast Kex2 protease. Its testis-specific
expression.";
RT J. Biol. Chem. 267:5897-5900(1992).

CC -1- FUNCTION: INVOLVED IN THE PROCESSING OF HORMONE AND OTHER PROTEIN
CC PRECURSORS AT SITES COMPRISED OF PAIRS OF BASIC AMINO ACID
CC RESIDUES.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
CC SUBTILASE FAMILY. FURIN SUBFAMILY.
CC -----
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DR EMBL; D01093; BAA00877.1; -
DR PIR; A42151; A42151.
DR HSP; Q99405; IMPT.
DR MEROPS; S08.074; -
DR MGD; MGI:97514; Pcsk4.
DR InterPro: IPR002884; P_domain.
DR InterPro: IPR000209; Peptidase_S8.
DR Pfam; PF01483; P; 1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; P00723; SUBTILISIN.
DR ProDom; PD000717; P_domain; 1.
DR PROSITE; PS00136; SUBTILASE_ASP; 1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal.
FT SIGNAL 1 26 BY SIMILARITY.
FT PROPEP 27 110 POTENTIAL.
FT CHAIN 111 655 NEUROENDOCRINE CONVERTASE 3.
FT DOMAIN 121 414 CATALYTIC.
FT ACT_SITE 155 155 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 196 196 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 370 370 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 472 472 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 655 AA; 73213 MW; 4E4E32CEDECB59 CRC64;

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Query Match          52.1%; Score 37; DB 1; Length 655;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 QOWFWL 10
DB 625 QOWFWL 630

RESULT 53
TRA_BPMU          STANDARD;          PRT;          663 AA.
AC P07636; P06021;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TRANSPOSASE.
GN A OR 3.
OS Bacteriophage Mu.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae.
OX NCBI_TaxID=10677;
RN [1]
RP MEDLINE=86067968; PubMed=2999776;
RA Harshey R.M., Getzoff E.D., Baldwin D.L., Miller J.L., Chaconas G.;
RT "Primary structure of phage mu transposase: homology to mu repressor.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7676-7680(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA Priess H., Brauer B., Schmidt C., Kamp D.;
RT "Sequence of the left end of Mu.";
RL (In) Symonds N., Toussaint A., van de Putte P., Howe M.M. (eds.);
RL Phage Mu, pp.277-296, Cold Spring Harbor Laboratory Press, New York (1987).
RN [3]
RP SEQUENCE FROM N.A.
RA Morgan G., Hatfull G., Hendrix R.;
RT "Genome of bacteriophage Mu and comparison with the Haemophilus influenzae Mu-like prophage Flumu.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-88 FROM N.A.
RX MEDLINE=83012203; PubMed=6214696;
RA Priess H., Kamp D., Kahmann R., Braeuer B., Delius H.;
RT "Nucleotide sequence of the immunity region of bacteriophage Mu.";
RL Mol. Gen. Genet. 186:315-321(1982).
RN [5]
RP SEQUENCE OF 1-84 FROM N.A.
RX MEDLINE=83218562; PubMed=6222246;
RA Toussaint A., Faelen M., Desmet L., Allet B.;
RT "The products of gene A of the related phages Mu and D108 differ in their specificities.";
RL Mol. Gen. Genet. 190:70-79(1983).
RN [6]
RP STRUCTURE BY NMR OF 1-76.
RX MEDLINE=95187707; PubMed=7881904;
RA Clubb R.T., Omichinski J.G., Savilahti H., Mizuuchi K., Gronenborn A.M., Clore G.M.;
RT "A novel class of winged helix-turn-helix protein: the DNA-binding domain of Mu transposase.";
RL Structure 2:1041-1048(1994).
RN [7]
RP STRUCTURE BY NMR OF 76-174.
RX MEDLINE=98070329; PubMed=9405381;
RA Schumacher S., Clubb R.T., Cai M., Mizuuchi K., Clore G.M., Gronenborn A.M.;
RT "Solution structure of the Mu end DNA-binding beta subdomain of phage Mu transposase: modular DNA recognition by two tethered domains.";
RL EMBO J. 16:7532-7541(1997).

[8]
RN RP STRUCTURE BY NMR OF 173-247.
RX MEDLINE=98035037; PubMed=9367742;
RA Clubb R.T., Schumacher S., Mizuuchi K., Gronenborn A.M., Clore G.M.;
RT "Solution structure of the I gamma subdomain of the Mu end DNA-binding domain of phage Mu transposase.";
RL J. Mol. Biol. 273:19-25(1997).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 248-574.
RX MEDLINE=95354202; PubMed=7628012;
RA Rice P., Mizuuchi K.;
RT "Structure of the bacteriophage Mu transposase core: a common structural motif for DNA transposition and retroviral integration.";
RL Cell 82:209-220(1995).
CC 1- FUNCTION: THIS TRANSPOSASE IS ESSENTIAL FOR INTEGRATION, REPLICATION-TRANSDUCTION, AND EXCISION OF MU DNA.
CC 2- MISCELLANEOUS: MU CAN TRANSDUCE ITS DNA INTO MULTIPLE SITES IN MANY BACTERIAL GENOMES AND MEDIATE A VARIETY OF DNA REARRANGEMENTS. TRANSDUCTION REQUIRES BOTH TRANSPOSASE (ENCODED BY GENE A) AND TRANSDUCTION ENHANCER (ENCODED BY GENE B).
CC 3- MISCELLANEOUS: UNLIKE OTHER TRANSPOSONS MU HAS DISSIMILAR SEQUENCES AT ITS LEFT AND RIGHT ENDS. TRANSPOSASE APPARENTLY BINDS 3 SPECIFIC BLOCKS OF SEQUENCES AT EACH END OF MU DNA.
CC 4- MISCELLANEOUS: THE A GENE IS REGULATED BY THE REPRESSOR C, WHICH BINDS TO AN OPERATOR SEQUENCE & TURNS OFF TRANSCRIPTION. REPRESSOR C CAN, AT HIGH CONCENTRATIONS, OCCUPY ALMOST THE EXACT SAME SITES ON MU ENDS AS THE TRANSPOSASE, AND TRANSPOSASE CAN BIND TO FRAGMENTS CONTAINING THE MU OPERATOR SEQUENCE.
CC 5- SIMILARITY: STRONG, TO H.INFLUENZAE H11478.
CC
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CC
DR EMBL; M11195; AAA32369.1; -
DR EMBL; M64097; AAA32379.1; -
DR EMBL; AF083977; AAF01083.1; -
DR EMBL; V01464; CAA24713.1; -
DR EMBL; V00868; CAA24236.1; -
DR PIR; A24746; TOBPU.
DR PDB; 1TNS; 14-FEB-95.
DR PDB; 1TNT; 14-FEB-95.
DR PDB; 1BCM; 15-OCT-95.
DR PDB; 1BCO; 15-OCT-95.
DR PDB; 2EZH; 03-DEC-97.
DR PDB; 2EZI; 03-DEC-97.
DR PDB; 2EJK; 14-JAN-98.
DR PDB; 2EKL; 14-JAN-98.
DR InterPro; IPR003314; Mu_DNA_bind.
DR Pfam; PF02316; Mu_DNA_bind; 1.
KW Transposition; Transposable element; DNA-binding; DNA excision;
KW DNA integration; DNA recombination; 3D-structure.
FT DNA_BIND 35 55 H-T-H MOTIF (POTENTIAL).
FT DNA_BIND 390 409 H-T-H MOTIF (POTENTIAL).
FT CONFLICT 66 66 G -> R (IN REF. 5).
FT CONFLICT 408 408 P -> S (IN REF. 2).
SQ SEQUENCE 663 AA; 75003 MW; B882CFDCBFC0B2E3 CRC64;

Query Match          52.1%; Score 37; DB 1; Length 663;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQWFW 9
DB 286 RPKTWF 292

RESULT 54
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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DT T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56).
GN TBR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=95344783; PubMed=7619531;
RA Bulfone A., Smiga S.M., Shimamura K., Peterson A., Puelles L.,
RA Rubinstein J.L.R.;
RT "T-brain-1: a homolog of Brachyury whose expression defines
RT molecularly distinct domains within the cerebral cortex.";
RL Neuron 15:63-78(1995).
CC -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC DEVELOPMENTAL PROCESSES. TBR1 IS REQUIRED FOR NORMAL BRAIN
CC DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -!- TISSUE SPECIFICITY: BRAIN.
CC -!- SIMILARITY: CONTAINS A T-BOX DOMAIN.
CC -----
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CC -----
DR EMBL; U49250; AAA92010.1; -.
DR HSP; P24781; 1XBR.
DR MIM; 604616; -.
DR InterPro; IPR001699; T-box.
DR Pfam; PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR SMART; SM00425; TBOX; 1.
DR PROSITE; PS01283; TBOX_1; 1.
DR PROSITE; PS01264; TBOX_2; 1.
DR PROSITE; PS0252; TBOX_3; 1.
DR Transcription regulation; DNA-binding; Nuclear protein.
KW DNA_BIND 213 393
FT DOMAIN 569 573 POLY-ALA.
FT SEQUENCE 682 AA; 74053 MW; E1C8D84206EFFFFB5 CRC64;
SQ
Query Match 52.1%; Score 37; DB 1; Length 682;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 PKPQQWF 8
Dd 479 PSPQRF 485
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| |||

RESULT 56
AMDI_HUMAN
ID AMDI_HUMAN STANDARD; PRT; 747 AA.
AC P23109;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE AMP DEAMINASE 1 (EC 3.5.4.6) (MYOADENYLATE DEAMINASE) (AMP DEAMINASE
DE ISOFORM M).
DE AMPD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; HMO.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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TBR1_MOUSE STANDARD; PRT; 681 AA.
ID TBR1_MOUSE
AC Q64336;
AD 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56).
GN TBR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Fetal brain;
RX MEDLINE=95344783; PubMed=7619531;
RA Bulfone A., Smiga S.M., Shinamura K., Peterson A., Puelles L.,
RA Rubenstein J.L.R.;
RT "T-brain-1: a homolog of Brachyury whose expression defines
RT molecularly distinct domains within the cerebral cortex.";
RL Neuron 15:63-78(1995).
CC -1- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC DEVELOPMENTAL PROCESSES. TBR1 IS REQUIRED FOR NORMAL BRAIN
CC DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN SPECIFIC LAMINA IN THE DEVELOPING
CC AND ADULT BRAIN.
CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED AROUND DAY 10 OF EMBRYONIC
CC DEVELOPMENT IN THE PREPLATE, AT DAY 12.5, IN THE CORTICAL PLATE
CC AND INTERMEDIATE ZONE, AND FROM DAY 16.5 TO 18.5, IN A ROSTRO-
CC CAUDAL GRADIENT IN THE SUBPLATE. IN THE THALAMUS, EXPRESSION IS
CC FIRST OBSERVED AT POSTNATAL STAGE, P7, AND WEAK EXPRESSION
CC CONTINUES IN LATER POSTNATAL AND ADULT STAGES.
CC -1- SIMILARITY: CONTAINS A T-BOX DOMAIN.
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EMBL; U49251; AAA92011.1; -
DR HSSP; P24781; 1XBR
DR MGD; MGI:107404; Tbr1.
DR InterPro; IPR001699; T-box.
DR Pfam; PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR SMART; SM00425; TBOX; 1.
DR PROSITE; PS01283; TBOX_1; 1.
DR PROSITE; PS01284; TBOX_2; 1.
DR PROSITE; PS50252; TBOX_3; 1.
DR Transcription regulation; DNA-binding; Nuclear protein.
KW DNA_BIND 213 393
FT DOMAIN 569 573 T-BOX.
FT POLY-ALA.
SQ SEQUENCE 681 AA; 73941 MW; 8732EF250EFD009 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 681;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKQQQWF 8
| ||||
DB 479 PSPQWF 485

RESULT 55
TBR1_HUMAN STANDARD; PRT; 682 AA.
ID TBR1_HUMAN
AC Q16650;
AD 01-NOV-1997 (Rel. 35, Created)

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RX MEDLINE=90264442; PubMed=2345176;
RA Sabina R.L., Morisaki T., Clarke P., Eddy R., Shows T.B., Morton C.C.,
RA Holmes E.W.;
RT "Characterization of the human and rat myoadenylate deaminase
RT genes";
RL J. Biol. Chem. 265:9423-9433(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92131279; PubMed=1370861;
RA Sabina R.L., Fishbein W.N., Pezeshkpour G., Clarke P.R., Holmes E.W.;
RT "Molecular analysis of the myoadenylate deaminase deficiencies";
RL Neurology 42:170-179(1992).
CC -!- FUNCTION: AMP DEAMINASE PLAYS A CRITICAL ROLE IN ENERGY
CC METABOLISM.
CC -!- CATALYTIC ACTIVITY: AMP + H(2)O = IMP + NH(3).
CC -!- PATHWAY: PURINE NUCLEOTIDE CYCLE.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- TISSUE SPECIFICITY: THREE ISOFORMS ARE PRESENT IN MAMMALS: AMP
CC DEAMINASE 1 IS THE PREDOMINANT FORM IN SKELETAL MUSCLE; AMP
CC DEAMINASE 2 PREDOMINATES IN SMOOTH MUSCLE, NON-MUSCLE TISSUE,
CC EMBRYONIC MUSCLE AND UNDIFFERENTIATED MYOBLASTS; AMP DEAMINASE 3
CC IS FOUND IN ERYTHROCYTES.
CC -!- SIMILARITY: BELONGS TO THE ADENOSINE AND AMP DEAMINASES FAMILY.

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DR EMBL; M37931; AAG24258.1; JOINED.
DR EMBL; M37920; AAG24258.1; JOINED.
DR EMBL; M37921; AAG24258.1; JOINED.
DR EMBL; M37922; AAG24258.1; JOINED.
DR EMBL; M37923; AAG24258.1; JOINED.
DR EMBL; M37924; AAG24258.1; JOINED.
DR EMBL; M37927; AAG24258.1; JOINED.
DR EMBL; M37928; AAG24258.1; JOINED.
DR EMBL; M37929; AAG24258.1; JOINED.
DR EMBL; M37930; AAG24258.1; JOINED.
DR EMBL; M60092; AAA57281.1; JOINED.
DR MIM; 102770; -.
DR InterPro: IPR001365; A.deaminase.
DR Pfam: PF00962; A.deaminase; 1.
DR PROSITE: PS00485; A.DEAMINASE; 1.
KW Hydrolase; Nucleotide metabolism; Multigene family.
FT ACT_SITE 363 363 BY SIMILARITY.
FT ACT_SITE 573 573 BY SIMILARITY.
FT ACT_SITE 649 649 BY SIMILARITY.
FT ACT_SITE 650 650 BY SIMILARITY.
SQ SEQUENCE 747 AA; 86489 MW; 1E15EBEE98B95763 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 747;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 PRKQOW 7
Db 528 PRKQOW 533
|||||

RESULT 57
METE_SOLSC
ID METE_SOLSC STANDARD; PRT; 764 AA.
AC Q42662;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE 5-METHYLTHETRAHYDROPTEROYLTRIGUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE
(EC 2.1.1.14) (VITAMIN-B12-INDEPENDENT METHIONINE SYNTHASE ISOZYME)

DE (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE ISOZYME).
GN MET.
OS Solenostemon scutellarioides (Coleus blumei).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Lamiaceae; Solenostemon.
OX NCBI_TaxID=4142;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RA Petersen M., Van der Straeten D., Bauw G.;
RT "Full-length cDNA clone from Coleus blumei with high similarity to
RT cobalamin-independent methionine synthase";
RL (In) Plant Gene Register PGR95-049.
CC -!- FUNCTION: CATALYZES THE TRANSFER OF A METHYL GROUP FROM 5-
CC METHYLTHETRAHYDROPTEROL TO HOMOCYSTEINE RESULTING IN METHIONINE
CC FORMATION (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: 5-METHYLTHETRAHYDROPTEROYL-L-GLUTAMATE + L-
CC HOMOCYSTEINE = TETRAHYDROPTEROYL-L-GLUTAMATE + L-METHIONINE.
CC -!- COFACTOR: ZINC (BY SIMILARITY).
CC -!- PATHWAY: TERMINAL STEP IN THE DE NOVO BIOSYNTHESIS OF METHIONINE.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE VITAMIN-B12 INDEPENDENT METHIONINE
CC SYNTHASE FAMILY.

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DR EMBL; Z49150; CAA89019.1; ALT INIT.
DR Mendel; 11673; Colbl:1331:11673.
DR InterPro: IPR002829; Methionine_synth.
DR Pfam; PF01717; Methionine_synth; 2.
KW Transferase; Methyltransferase; Methionine biosynthesis; Zinc.
FT METAL 646 646 ZINC (BY SIMILARITY).
FT METAL 648 648 ZINC (BY SIMILARITY).
FT METAL 732 732 ZINC (BY SIMILARITY).
SQ SEQUENCE 764 AA; 84589 MW; 43D65134C253602F CRC64;

Query Match 52.1%; Score 37; DB 1; Length 764;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPQPQWFW 9
Db 533 RPQPQWFW 541
|||||

RESULT 58
NUTL_MAGGR
ID NUTL_MAGGR STANDARD; PRT; 956 AA.
AC Q04168;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE NITROGEN REGULATORY PROTEIN NUTL.
GN NUTL.
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes; Incertae sedis; Magnaportheaceae; Magnaporthe.
OX NCBI_TaxID=148305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CUYANE 11;
RX MEDLINE=96335139; PubMed=8757395;
RA Froeliger E.H., Carpenter B.E.;
RT "NUT1, a major nitrogen regulatory gene in Magnaporthe grisea, is
RT dispensable for pathogenicity".
RL Mol. Gen. Genet. 251:647-656(1996).

CC -1- FUNCTION: MAJOR NITROGEN REGULATORY PROTEIN; ACTIVATES EXPRESSION
CC OF NITROGEN-REGULATED GENES.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: CONTAINS 1 GATA-TYPE ZINC FINGER.

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CC -----
CC EMBL: U60290; AAB03415.1; -
CC HSSP: P17429; 5GAT.
CC InterPro: IPR000679; Znf_GATA.
CC Pfam: PF00320; GATA; 1.
CC PRINTS: PR00619; GATAZNFINGER.
CC SMART: SM00401; Znf_GATA; 1.
CC PROSITE: PS00344; GATA_ZN_FINGER_1; 1.
CC PROSITE: PS01114; GATA_ZN_FINGER_2; 1.
CC Transcription regulation; Activator; DNA-binding; Zinc-finger;
CC Nuclear protein; Nitrate assimilation.
CC ZN_FING 663 687 GATA-TYPE.
CC SEQUENCE 956 AA; 100874 MW; 40ABDA5A07A7D7AB CRC64;

Query Match 52.1%; Score 37; DB 1; Length 956;
Best Local Similarity 71.4%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQOWFWL 10
||:|:|
DB 946 PQEWDL 952

RESULT 59
AREA_GIBFU STANDARD; PRT; 971 AA.
AC P78688;
DT 15-JUL-1998 (Rel. 36, Created)
DT 18-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE NITROGEN REGULATORY PROTEIN AREA.
GN AREA.
OS Gibberella fujikuroi (Bakanae and foot rot disease fungus) (Fusarium
OS moniliforme).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5127;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M567;
RA Tudzynski B., Feng B., Marzluf G.A.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAJOR NITROGEN REGULATORY PROTEIN. POSITIVELY ACTING
CC REGULATORY GENE OF NITROGEN METABOLITE REPRESSION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: CONTAINS 1 GATA-TYPE ZINC FINGER.

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CC -----
CC EMBL: Y11006; CAA71897.1; -
CC HSSP: P17429; 5GAT.
CC InterPro: IPR000679; Znf_GATA.
CC Pfam: PF00320; GATA; 1.
CC PRINTS: PR00619; GATAZNFINGER.

DR SMART; SM00401; Znf_GATA; 1.
DR PROSITE; PS00344; GATA_ZN_FINGER_1; 1.
DR PROSITE; PS01114; GATA_ZN_FINGER_2; 1.
KW Transcription regulation; Activator; DNA-binding; Zinc-finger;
KW Nuclear protein; Nitrate assimilation.
FT ZN_FING 694 718 GATA-TYPE.
SQ SEQUENCE 971 AA; 103580 MW; 887DD882141C7453 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 971;
Best Local Similarity 71.4%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQOWFWL 10
||:|:|
DB 961 PQEWEL 967

RESULT 60

DOR_DROME STANDARD; PRT; 1002 AA.
AC Q24314;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE DEEP ORANGE PROTEIN.
GN DOR OR EG171E4.1.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97218037; PubMed=9065698;
RA Shostopal S.A., Makulin I.V., Belyaeva E.S., Ashburner N.;
RT "Molecular characterization of the deep orange (dor) gene of
RT Drosophila melanogaster."
RL Mol. Gen. Genet. 253:642-648(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RX MEDLINE=20196011; PubMed=10731137;
RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demallies J., Cadieu E.,
RA Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
RA Modolell J., Peter A., Schoettler P., Werner M., Mourikoti F.,
RA Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the X chromosome of D.
RT melanogaster."
RL Science 287:2220-2222(2000).
CC -1- SIMILARITY: SOME, TO YEAST PEP3.

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CC -----
CC EMBL: X86683; CAA60382.1; -
CC EMBL: AL021726; CAA16809.1; -
CC FlyBase; FBgn0000482; dor.
CC InterPro: IPR000547; Clathrin_repeat.
CC InterPro: IPR001841; Znf_ring.
CC SMART; SM00299; CUH; 1.
CC SMART; SM00184; RING; 1.

KW Zinc-finger; Transmembrane.
FT ZN_FING 885 910 C3H2C-TYPE.
FT TRANSMEM 971 991 POTENTIAL.
FT CONFLICT 169 169 A -> P (IN REF. 1).
FT CONFLICT 581 581 Q -> H (IN REF. 1).
FT CONFLICT 865 865 A -> V (IN REF. 1).
SQ SEQUENCE 1002 AA; 115305 MW; D59690A0FC95182F CRC64;

Query Match 52.1%; Score 37; DB 1; Length 1002;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQFWL 10
I:|I|I|
Db 301 PKQAWL 307

RESULT 61
DPOG_HUMAN
ID DPOG_HUMAN STANDARD; PRT; 1239 AA.
AC P54098; O92515;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DNA POLYMERASE GAMMA (EC 2.7.7.7) (MITOCHONDRIAL DNA POLYMERASE
DE CATALYTIC SUBUNIT).
GN POLG OR MDPI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97038687; PubMed-8884268;
RA Ropp P.A., Copeland W.C.;
RT "Cloning and characterization of the human mitochondrial DNA
RT polymerase, DNA polymerase gamma.";
RL Genomics 36:449-458(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-97186710; PubMed-9034326;
RA Lecrenier N.L., van der Bruggen P., Foury F.;
RT "Mitochondrial DNA polymerases from yeast to man: a new family of
RT polymerases.";
RL Gene 185:147-152(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Watanabe T.K., Shimizu F., Nishino N., Fujiwara T., Kanemoto N.,
RA Suzuki M., Nakamura Y., Hirai Y., Maekawa H., Takahashi E.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN THE REPLICATION OF MITOCHONDRIAL DNA.
CC -!- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =
CC N PYROPHOSPHATE + DNA(N).
CC -!- COFACTOR: MAGNESIUM.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -!- MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:
CC ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR
CC DIFFERENT REACTIONS OF DNA SYNTHESIS.
CC -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-A FAMILY.
CC -----
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CC -----
DR EMBL; U60325; AAC50712.1; -.
DR EMBL; X98093; CAA66719.1; -.

DR EMBL; D84103; BAA12223.1; -.
DR MIM; 174763; -.
DR InterPro; IPR002297; DNA_polg.
DR InterPro; IPR001098; DNA_pol_A.
DR Pfam; PF00476; DNA_pol_A; 1.
DR PRINTS; PR00867; DNAPOLG.
DR SMART; SM00482; POLAC; 1.
DR PROSITE; PS00447; DNA_POLYMERASE_A; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; Mitochondrion; Magnesium.
FT DOMAIN 43 60 POLY-GLN.
FT DOMAIN 535 538 POLY-GLU.
FT CONFLICT 55 55 Q -> QQQ (IN REF. 3).
SQ SEQUENCE 1239 AA; 139562 MW; 2D9ECCD75AD6E01E CRC64;

Query Match 52.1%; Score 37; DB 1; Length 1239;
Best Local Similarity 62.5%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOQFW 9
| | | | |
Db 164 PKPPANAW 171

RESULT 62
ATS9_HUMAN
ID ATS9_HUMAN STANDARD; PRT; 1629 AA.
AC Q9P2N4; Q9NR29;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADAM-TS 9 PRECURSOR (EC 3.4.24.-) (A DISINTEGRIN AND METALLOPROTEINASE
DE WITH THROMBOSPONDIN MOTIFS 9) (ADAMTS-9) (ADAM-TS9).
GN ADAMTS9 OR KIAA1312.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RC TISSUE=Fetal;
RX MEDLINE-20396138; PubMed-10936055;
RA Clark M.E., Kelnner G.S., Turbeville L.A., Boyer A., Arden K.A.,
RA Maki R.A.;
RT "ADAMTS 9, a novel member of the ADAM-TS/Metallospondin gene
RT family.";
RL Genomics 67:343-350(2000).
RN [2]
RP SEQUENCE OF 159-1629 FROM N.A. (LONG ISOFORM).
RC TISSUE=Brain;
RX MEDLINE-20181126; PubMed-10718198;
RA Nagase T., Kikuno R., Ishikawa K.-I., Hirose M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVI.
RT The complete sequences of 150 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:65-73(2000).
CC -!- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED. ASSOCIATED WITH THE EXTRACELLULAR
CC MATRIX (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ALL FETAL TISSUES.
CC EXPRESSED SLIGHTLY IN ADULT OVARY, PANCREAS, HEART, KIDNEY, LUNG,
CC PLACENTA. ALSO DETECTED IN SPINAL CORD AND BRAIN. NOT DETECTED IN
CC COLON, SMALL INTESTINE, TESTIS, LIVER, SKELETAL MUSCLE, SPLEEN OR
CC THYMUS.
CC -!- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT
CC FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
CC SIMILARITY).
CC -!- PTM: THE PRECURSOR IS CLEAVED BY A URIN ENDOPEPTIDASE (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B (ZINC

METALLOPROTEASE); ALSO KNOWN AS THE REPOLYSIN SUBFAMILY.
-1- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-1- SIMILARITY: CONTAINS 11 TSP TYPE-1 DOMAINS.

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EMBL; AF261918; AAF89106.1; -
EMBL; AB037733; BAA92550.1; -
MIM; 605421; -
InterPro: IPR001590; Reprolysin.
InterPro: IPR000884; TSPL.
InterPro: IPR000130; Zn_MTPptdse.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF00090; tsp_1; 11.
SMART; SM00209; TSPL; 13.
PROSITE; PS00215; ADAM_MEPRO; 1.
PROSITE; PS00427; DISINTEGRINS; FALSE_NEG.
PROSITE; PS00092; TSPL; 9.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
Repeat; Extracellular matrix; Alternative splicing.

FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 287 BY SIMILARITY.
FT CHAIN 288 1629 ADAM-TS 9.
FT DOMAIN 509 587 DISINTEGRIN-LIKE.
FT DOMAIN 589 642 TSP TYPE 1 1.
FT DOMAIN 645 752 CYS-RICH.
FT DOMAIN 753 880 SPACER.
FT DOMAIN 999 1053 TSP TYPE 1 2.
FT DOMAIN 1056 1108 TSP TYPE 1 3.
FT DOMAIN 1111 1156 TSP TYPE 1 4.
FT DOMAIN 1184 1239 TSP TYPE 1 5.
FT DOMAIN 1240 1295 TSP TYPE 1 6.
FT DOMAIN 1332 1383 TSP TYPE 1 7.
FT DOMAIN 1386 1439 TSP TYPE 1 8.
FT DOMAIN 1445 1498 TSP TYPE 1 9.
FT DOMAIN 1501 1554 TSP TYPE 1 10.
FT DOMAIN 1562 1612 TSP TYPE 1 11.
FT DOMAIN 88 96 POLY-SER.
FT SITE 223 223 CYSTEINE SWITCH (POTENTIAL).
FT METAL 434 434 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 435 435 BY SIMILARITY.
FT METAL 438 438 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 444 444 ZINC (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 749 749 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 840 840 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1213 1213 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1267 1267 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 1064 1072 CLVTCCKGH -> VRWEGCYFP (IN SHORT ISOFORM).
FT VARSPLIC 1073 1629 MISSING (IN SHORT ISOFORM).
FT CONFLICT 367 367 F -> L (IN REF. 1).
SQ SEQUENCE 1629 AA; 182649 MW; C1C4CEFF58B8941F CRC64;

Query Match 52.1%; Score 37; DB 1; Length 1629;
Best Local Similarity 71.4%; Pred. NO. 5.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 KPQOWFW 9
DB 875 KPQOWFW 881
||||:|

RESULT 63
CPFF6_RAT STANDARD; PRT; 537 AA.
AC P51871.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOCHROME P450 4F6 (EC 1.14.14.1) (CYP11B1)
GN CYP4F6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RA MEDLINE=96125358; PubMed=8554568;
RX Kawashima H., Strobel H.W.;
RT "cDNA cloning of three new forms of rat brain cytochrome P450
belonging to the CYP4F subfamily";
RL Biochem. Biophys. Res. Commun. 217:1137-1144(1995).
CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) -> ROH +
OXIDIZED FLAVOPROTEIN + H(2)O.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN LIVER AND KIDNEY. LOWER
EXPRESSION IN BRAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

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EMBL; U39208; AAC52360.1; -
DR InterPro: IPR001128; Cyt_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PRINTS; PR00464; EP450II.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT BINDING 468 468 HEME (BY SIMILARITY).
FT SEQUENCE 537 AA; 61541 MW; 4D96D761A2BEA7E9 CRC64;

Query Match 51.4%; Score 36.5; DB 1; Length 537;
Best Local Similarity 75.0%; Pred. NO. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 2 KPQOWFW 9
DB 55 KPQOWFW 61
|||||

RESULT 64
NOX1_HUMAN STANDARD; PRT; 564 AA.
AC Q9Y5S8; O95691;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE NADPH OXIDASE HOMOLOG 1 (NOX-1) (NADH/NADPH MITOGENIC
OXIDASE SUBUNIT P65-MOX) (MITOGENIC OXIDASE 1) (MOX1).
GN NOX1 OR NOH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM NOH-1L).

RC TISSUE-Colon epithelium;
RX MEDLINE=99413719; PubMed=10485709;
RA Suh Y.-A., Arnold R.S., Lassegue B., Shi J., Xu X., Sorescu D.,
RA Chung A.B., Griendling K.K., Lambeth J.D.;
RT "Cell transformation by the superoxide-generating oxidase Mox1.";
RL Nature 401:79-82(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS NOH-1L; NOH-1LV AND NOH-1S).
RX MEDLINE=20082959; PubMed=10615049;
RA Banfi B., Maturana A., Jaconi S., Arnaudeau S., Laforge T., Sinha B.,
RA Ligeti E., Denaurex N., Krause K.-H.;
RT "A mammalian H+ channel, generated through alternative splicing of the
RT NADPH oxidase homolog NOH-1.";
RL Science 287:138-142(2000).
RN [3]
RP SEQUENCE OF 16-564 FROM N.A. (ISOFORM NOH-1L).
RA Lloyd D.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: NOH-1S IS A VOLTAGE-GATED PROTON CHANNEL THAT MEDIATES
CC THE H+ CURRENTS OF RESTING PHAGOCYTES AND OTHER TISSUES. IT
CC PARTICIPATES IN THE REGULATION OF CELLULAR PH AND IS BLOCKED BY
CC ZINC. NOH-1L IS A PYRIDINE NUCLEOTIDE-DEPENDENT OXIDOREDUCTASE
CC THAT GENERATES SUPEROXIDE AND MIGHT CONDUCT H+ IONS AS PART OF ITS
CC ELECTRON TRANSPORT MECHANISM, WHEREAS NOH-1S DOES NOT CONTAIN AN
CC ELECTRON TRANSPORT CHAIN.
CC -!- COFACTOR: NADP AND FAD (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; NOH-1L (SHOWN HERE), NOH-1S AND
CC NOH-1LV; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: NOH-1L IS DETECTED IN COLON, UTERUS, PROSTATE,
CC AND COLON CARCINOMA, BUT NOT IN PERIPHERAL BLOOD LEUKOCYTES. NOH-
CC 1S IS DETECTED ONLY IN COLON AND COLON CARCINOMA CELLS.
CC -!- SIMILARITY: BELONGS TO THE FRE / CYBB FAMILY.
CC
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CC
CC EMBL; AF127763; AAD38133.1; -
DR EMBL; AF166326; AAF23232.1; -
DR EMBL; AF166327; AAF23233.1; -
DR EMBL; AF166328; AAF23234.1; -
DR EMBL; Z83819; CAB06073.1; ALT_SEQ.
DR MIM; 300225; -
DR InterPro; IPR002916; Ferric_reduct.
DR InterPro; IPR000778; GP91Phox.
DR Pfam; PF01794; Ferric_reduct; 1.
DR PRINTS; PR00466; GP91PHOX.
DR OXidoreductase; NADP; Electron transport; Transmembrane; FAD; Heme;
KW Glycoprotein; Voltage-gated channel; Ionic channel;
KW Alternative splicing.
FT DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 10 30 POTENTIAL.
FT DOMAIN 31 44 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 45 72 POTENTIAL.
FT DOMAIN 73 102 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 103 123 POTENTIAL.
FT DOMAIN 124 168 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 169 189 POTENTIAL.
FT DOMAIN 190 206 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 207 227 POTENTIAL.
FT DOMAIN 228 396 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 397 417 POTENTIAL.
FT DOMAIN 418 564 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 338 344 FAD (POTENTIAL).
FT BINDING 101 101 HEME (PROBABLE).
FT BINDING 115 115 HEME (PROBABLE).
FT BINDING 209 209 HEME (PROBABLE).
FT BINDING 221 221 HEME (PROBABLE).

FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 159 190 QSRNTVEYVTFSTAGTGVIMTIALIMVT -> HPHIT
FT PTVMFTVTFDMLSSVNSNLLFLIK (IN ISOFORM
FT NOH-1S).
FT VARSPLIC 191 564 MISSING (IN ISOFORM NOH-1S).
FT VARSPLIC 433 481 MISSING (IN ISOFORM NOH-1LV).
FT CONFLICT 173 173 I -> V (IN REF. 2).
SQ SEQUENCE 564 AA; 64870 MW; C3BE290FAE6DBC9A CRC64;

Query Match 51.4%; Score 36.5; DB 1; Length 564;
Best Local Similarity 37.5%; Pred. No. 2.4e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 5; Gaps 1;

Qy 1 RPK-----PQOWFWLM 11
||| | : | : :
Db 259 RPKFEGHPPEMKWIL 274

RESULT 65
Y102_MYCLE
ID Y102_MYCLE STANDARD; PRT: 659 AA.
AC P53525;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 71.2 KDA PROTEIN ML1998.
GN ML1998 OR O659.
OS Mycobacterium leprae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96059637; PubMed=7476188;
RA Fsihi H., Cole S.T.;
RT "The Mycobacterium leprae genome: systematic sequence analysis
RT identifies key catabolic enzymes, ATP-dependent transport systems and
RT a novel *polA* locus associated with genomic variability.";
RL Mol. Microbiol. 16:909-919(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-TN:
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Elgimeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.-A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- SIMILARITY: STRONG, TO M.TUBERCULOSIS RV0102.
CC
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CC
CC EMBL; Z46257; CAA86362.1; -
DR EMBL; AL583924; CAC30953.1; -
DR Leproma; ML1998; -
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 24 44 POTENTIAL.
FT TRANSMEM 71 91 POTENTIAL.

```
FT TRANSEM 115 135 POTENTIAL.
FT TRANSEM 157 177 POTENTIAL.
FT TRANSEM 183 203 POTENTIAL.
FT TRANSEM 214 234 POTENTIAL.
FT TRANSEM 242 262 POTENTIAL.
FT TRANSEM 279 299 POTENTIAL.
FT TRANSEM 311 331 POTENTIAL.
FT TRANSEM 365 385 POTENTIAL.
FT TRANSEM 393 413 POTENTIAL.
FT TRANSEM 433 453 POTENTIAL.
FT TRANSEM 490 510 POTENTIAL.
FT TRANSEM 517 537 POTENTIAL.
FT TRANSEM 550 570 POTENTIAL.
FT TRANSEM 596 616 POTENTIAL.
SQ SEQUENCE 659 AA; 71246 MW; 2C1D90C6BF720E39 CRC64;

Query Match 51.4%; Score 36.5; DB 1; Length 659;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 RPKPOQWF-WLM 11
   :|:|:|
Db 464 QPGPRLTWLM 475

RESULT 66
DNBL_HSVB2
ID DNBL_HSVB2 STANDARD; PRT; 1186 AA.
AC P12639;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MAJOR DNA-BINDING PROTEIN.
GN DBP OR UL29.
OS Bovine herpesvirus type 2 (strain BWV) (Bovine mammillitis virus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OC NCBI_TaxID=10296;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88306231; PubMed=2841793;
RA Hammerschmidt W., Conraths F., Mankertz J., Pauli G., Ludwig H.,
RA Buhk H.-J.;
RT "Conservation of a gene cluster including glycoprotein B in bovine
RT herpesvirus type 2 (BHV-2) and herpes simplex virus type 1 (HSV-1).";
RL Virology 165:388-405(1988).
RN [2]
RP SEQUENCE OF 1058-1186 FROM N.A.
RX MEDLINE=88306232; PubMed=2457278;
RA Hammerschmidt W., Conraths F., Mankertz J., Buhk H.-J., Pauli G.,
RA Ludwig H.;
RT "Common epitopes of glycoprotein B map within the major DNA-binding
RT proteins of bovine herpesvirus type 2 (BHV-2) and herpes simplex
RT virus type 1 (HSV-1).";
RL Virology 165:406-418(1988).
CC -1- FUNCTION: SINGLE-STRAND DNA-BINDING PROTEIN REQUIRED FOR DNA
CC REPLICATION.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES DNA-BINDING PROTEIN
CC FAMILY.
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EMBL; M21630; AAA46051.1;
PIR; A29242; DNBEBG.
HSSP; P25816; ICQA.
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DR InterPro: IPR000635; Viral_DNA_bind.
DR Pfam: PF00747; Viral_DNA_bp; 1.
KW DNA-binding; DNA replication; Zinc-finger; Nuclear protein.
FT ZN_FING 495 508 C2HC-TYPE.
SQ SEQUENCE 1186 AA; 127286 MW; A586ECC1479FBD2C CRC64;

Query Match 51.4%; Score 36.5; DB 1; Length 1186;
Best Local Similarity 75.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 RPKPOQWF 9
   :|:|:|
Db 834 PNP-QMFW 840

RESULT 67
TKNA_GADMO
ID TKNA_GADMO STANDARD; PRT; 11 AA.
AC P28498;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P.
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidae; Gadidae;
OC Gadus.
OX NCBI_TaxID=8049;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
RT "Substance P-related and neurokinin-A-related peptides from the brain
RT of the cod and trout.";
RL Eur. J. Biochem. 206:659-664(1992).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART: SM00203; TK; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 50.7%; Score 36; DB 1; Length 11;
Best Local Similarity 54.5%; Pred. No. 8;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQWFWM 11
   :|:|:|
Db 1 KRPQOQFGLM 11

RESULT 68
ATP8_DICLA
ID ATP8_DICLA STANDARD; PRT; 55 AA.
AC Q36362;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (ATPASE SUBUNIT 8) (A6L).
GN ATP8 OR ATP8.
OS Dicertrachus labrax (European sea bass).
OG Mitochondrion.
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RESULT 71
MSBB_HAEIN STANDARD; PRT; 318 AA.
AC P44567.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update).
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE LIPID A BIOSYNTHESIS (KDO)2-(LAUROYL)-LIPID IVA ACYLTRANSFERASE
DE (EC 2.3.1.-).
GN MSBB OR HI0199.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
ON NCBI_TaxID=727;
RX [1]
SEQUENCE FROM N.A.
STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fieleschmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd."
RL Science 269:496-512(1995).
CC -1- FUNCTION: TRANSFERS MYRISTATE OR LAURATE, ACTIVATED ON ACP, TO
CC (KDO)2-(LAUROYL)-LIPID IVA (BY SIMILARITY).
CC -1- PATHWAY: LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
CC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE HTRB/MSBB FAMILY.
CC -----
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CC -----
DR EMBL; U32705; AAC21868.1; -
DR TIGR; HI0199; -
KW Lipopolysaccharide biosynthesis; Transferase; Acyltransferase;
KW Transmembrane; Inner membrane; Complete proteome.
FT TRANSMEM 27 47 POTENTIAL.
FT TRANSMEM 91 111 POTENTIAL.
FT TRANSMEM 138 158 POTENTIAL.
FT SEQUENCE 318 AA; 36882 MW; DE59952D78719445 CRC64;
SQ

Query Match 50.7%; Score 36; DB 1; Length 318;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPQOWFLWM 11
| | | | |
DB 295 PAPEQVWIL 304

RESULT 72
Y355_SYN3
ID Y355_SYN3 STANDARD; PRT; 330 AA.
AC P74366;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)

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genes.";
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RL -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
CC MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX.
CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AY009399; AAC38659.1; .
DR InterPro; IPR000970; Wnt1.
DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
KW Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 359 WNT-5B PROTEIN.
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 359 AA; 40476 MW; AD1E8D395609E1C2 CRC64;

Query Match 50.7%; Score 36; DB 1; Length 359;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 RPK--PQOWFW 9
||| |:
Db 148 RPKDLPDRLW 158

RESULT 74
WN5B_MOUSE STANDARD; PRT; 359 AA.
AC P22726;
DT 01-AUG-1991 (Rel. 19, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE WNT-5B PROTEIN PRECURSOR.
GN WNT5B OR WNT-5B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91122634; PubMed-2279700;
RA Gavin B.J., McMahon J.A., McMahon A.P.;
RT "Expression of multiple novel Wnt-1/int-1-related genes during fetal
RT and adult mouse development.";
RL Genes Dev. 4:2319-2332(1990).
CC -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
CC MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.
CC -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX.
CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC -----
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CC -----
CC EMBL; M89799; AAA40568.1; ALT_INT.
DR PIR; E36470; E36470.
DR MGD; MGI:98959; Wnt5b.
DR InterPro; IPR000970; Wnt1.
DR Pfam; PF00110; wnt; 1.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 359 WNT-5B PROTEIN.
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 359 AA; 40343 MW; 308ED393D3020DEB CRC64;

Query Match 50.7%; Score 36; DB 1; Length 359;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 RPK--PQOWFW 9
||| |:
Db 148 RPKDLPDRLW 158

RESULT 75
WN5C_XENLA STANDARD; PRT; 360 AA.
AC P33945; Q91928;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE WNT-5C PROTEIN PRECURSOR (XWNT-5C).
GN WNT-5C.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Koster J.G., Kuiken G.A., Stegeman B., Peterson J., Eizema K.,
RA Stabel L., Dekker E.J., Destree O.H.J.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-27 FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE-94261437; PubMed-8202371;
RA Kuiken G.A., Bertens P.J.A., Peterson-Maduro J., Veenstra G.J.C.,
RA Koster J.G., Destree O.H.J.;
RT "The promoter of the Wnt-5C gene contains octamer and AP-2 motifs
RT functional in Xenopus embryos".
RL Nucleic Acids Res. 22:1675-1680(1994).
CC -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
CC MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.
CC -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX.
CC -!- DEVELOPMENTAL STAGE: EXPRESSION IN THE EARLY GASTRULA STAGE
CC ONWARDS.
CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC -----
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CC EMBL: X73510; CAA51916.1; -.
DR EMBL: X76190; CAA53784.1; -.
DR PIR: S34173; S34173; Wnt1.
DR InterPro: IPR000970; Wnt1.
DR Pfam: PF00110; wnt; 1.
DR SMART: SM00097; WNT1; 1.
DR PROSITE: PS00246; WNT1; 1.
KW Developmental protein; Glycoprotein; Signal; Extracellular matrix.
FT SIGNAL 1 16
FT CHAIN 17 360
FT CARBOHYD 94 94
FT CARBOHYD 100 100
FT CARBOHYD 292 292
FT CARBOHYD 306 306
FT CARBOHYD 306 306
FT CONFLICT 15 15
FT SEQUENCE 360 AA; 40714 MW; 93CBD15D7A92779E CRC64;

Query Match 50.7%; Score 36; DB 1; Length 360;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 RPK--PQQWF 9
   ||| | | |
DB 149 RPKDPLDPLW 159

RESULT 76
FUT3_BOVIN
ID FUT3_BOVIN STANDARD; PRT; 365 AA.
AC Q11126;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE GALACTOSIDE 3(4)-L-FUCOSYLTRANSFERASE (EC 2.4.1.65) (BLOOD GROUP LEWIS
DE ALPHA-4-FUCOSYLTRANSFERASE) (LEWIS FT) (FUCOSYLTRANSFERASE 3) (FUCT-
DE III) (FUTB).
GN FUT3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP MEDLINE=97236840; PubMed=9079712;
RA Oulmoudene A., Wierinckx A., Petit J.-M., Costache M., Palcic M.M.,
RA Mollicon R., Oriol R., Julien R.;
RT "Molecular cloning and expression of a bovine alpha(1,3)-
RT fucosyltransferase gene homologous to a putative ancestor gene of the
RT human FUT3-FUT5-FUT6 cluster."
RL J. Biol. Chem. 272:8764-8773(1997).
CC -!- FUNCTION: MAY CATALYSE ALPHA-1,3 AND ALPHA-1,4 GLYCOSIDIC LINKAGES
CC INVOLVED IN THE EXPRESSION OF SIALYL LEWIS X AND LEWIS X/SSA-1
CC ANTIGENS. IT MAY BE INVOLVED IN BLOOD GROUP LEWIS DETERMINATION.
CC -!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-
CC N-ACETYL-D-GLUCOSAMINYL-R = GDP + 1,3-BETA-D-GALACTOSYL-
CC (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
CC -!- PATHWAY: GLYCOSYLATION
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC FORM IN TRANS CISTERNAE OF GOLGI.
CC -!- TISSUE SPECIFICITY: LIVER, KIDNEY, LUNG AND BRAIN.
CC -!- MISCELLANEOUS: ALSO ACTS ON THE CORRESPONDING 1,4-GALACTOSYL
CC DERIVATIVE, FORMING 1,3-L-FUCOSYL LINKS.
CC -!- SIMILARITY: STRUCTURAL SIMILARITY WITH THE OTHER MAMMALIAN
CC GLYCOSYLTRANSFERASES.
CC -----
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CC -----
DR EMBL: X87810; CAA61079.1; -.
DR InterPro: IPR001503; Glyco_transf_10.
DR Pfam: PF00852; Glyco_transf_10; 1.
DR Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
KW Signal-anchor; Golgi stack.
FT DOMAIN 1 14
FT TRANSMEM 15 34
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 35 365
FT LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 100 100
FT CARBOHYD 158 158
FT CARBOHYD 189 189
FT CARBOHYD 189 189
FT N-LINKED (GLCNAC. . .) (PROBABLE).
FT N-LINKED (GLCNAC. . .) (PROBABLE).
FT SEQUENCE 365 AA; 42654 MW; 18715A361B0025D3 CRC64;

Query Match 50.7%; Score 36; DB 1; Length 365;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
   || | | |
DB 130 RPPQQRWV 138

RESULT 77
WNT5A_HUMAN
ID WNT5A_HUMAN STANDARD; PRT; 365 AA.
AC P41221;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE WNT-5A PROTEIN PRECURSOR.
GN WNT5A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94116991; PubMed=8288227;
RA Clark C.C., Cohen I.R., Eichstetter I., Cannizzaro L.A.,
RA McPherson J.D., Wasmuth J.J., Iozzo R.V.;
RT "Molecular cloning of the human proto-oncogene Wnt-5A and mapping of
RT the gene (WNT5A) to chromosome 3p14-p21."
RL Genomics 18:249-260(1993).
CC -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
CC MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.
CC -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX.
CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC -----
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CC EMBL: L20861; AAA16842.1; -.
DR MIM: 164975;
DR InterPro: IPR000970; Wnt1.
DR Pfam: PF00110; Wnt; 1.
DR SMART: SM00097; WNT1; 1.
DR PROSITE: PS00246; WNT1; 1.
KW Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 365
FT CARBOHYD 99 99
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 311 311 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 365 AA; 40886 MW; 1B869F60D53D583B CRC64;

Query Match 50.7%; Score 36; DB 1; Length 365;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 RPK--PQQWF 9
   ||| | : | |
Db 154 RPKDLPRDLWL 164

RESULT 78
CYB_ASTPE STANDARD; PRT; 379 AA.
AC Q33818;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOCHROME B.
GN COB OR CYTB.
OS Asterina pectinifera (Starfish).
OG Mitochondrion.
CC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
CC Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
CC NCBI_TaxID=7594;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Ovary;
RX MEDLINE=95402698; PubMed=7672576;
RA Asakawa S., Himeno H., Miura K.-I., Watanabe K.;
RT "Nucleotide sequence and gene organization of the starfish Asterina
RT pectinifera mitochondrial genome.";
RL Genetics 140:1047-1060(1995).
CC -!- FUNCTION: COMPONENT OF THE UBIQUITINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS.
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN.
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
CC -----
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CC -----
DR EMBL; D16387; BAA03877.1; ALT_INIT.
DR InterPro; IPR000179; Cyt_b_b6.
DR Pfam; PF00032; cytochrome_b_c; 1.
DR Pfam; PF00033; cytochrome_b_n; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_OO; 1.
KW Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
KW Heme.
FT METAL 84 84 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 98 98 IRON 2 (HEME B566 AXIAL LIGAND).
FT METAL 183 183 IRON 2 (HEME B562 AXIAL LIGAND).
FT METAL 197 197 IRON 1 (HEME B566 AXIAL LIGAND).
SQ SEQUENCE 379 AA; 42646 MW; 33A96455922F929E CRC64;

Query Match 50.7%; Score 36; DB 1; Length 379;
Best Local Similarity 54.5%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 RPKPQQWF 11
   || | |||
Db 319 RPKSQSLFWLL 329
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RESULT 79
WN5A_MOUSE STANDARD; PRT; 379 AA.
ID WN5A_MOUSE
AC P22725;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE WNT-5A PROTEIN PRECURSOR.
GN WNT5A OR WNT-5A.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91122634; PubMed=2279700;
RA Gavin B.J., McMahon J.A., McMahon A.P.;
RT "Expression of multiple novel Wnt-1/int-1-related genes during fetal
RT and adult mouse development.";
RL Genes Dev. 4:2319-2332(1990).
CC -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
CC MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.
CC -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX.
CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC -----
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CC -----
DR EMBL; M89798; AAA40567.1; -.
DR PIR; D36470; D36470.
DR MGD; MGI:98958; Wnt5a.
DR InterPro; IPR000970; Wnt1.
DR Pfam; PF00110; wnt; 1.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 379 WNT-5A PROTEIN.
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 311 311 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 379 AA; 42153 MW; E26266F47E169B50 CRC64;
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Query Match 50.7%; Score 36; DB 1; Length 379;
Best Local Similarity 54.5%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 RPK--PQQWF 9
   ||| | : | |
Db 168 RPKDLPRDLWL 178

RESULT 80
WN5A_RAT STANDARD; PRT; 379 AA.
ID WN5A_RAT
AC Q90XQ7;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
```


CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN.
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
CC
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CC
CC EMBL: Y16474; CAA76246.1; -
CC EMBL: Y09849; CAA70979.1; -
CC InterPro: IPR000179; Cyt_b_b6.
CC Pfam: PF00032; cytochrome_b_c; 1.
CC Pfam: PF00033; cytochrome_b_n; 1.
CC PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
CC PROSITE: PS00193; CYTOCHROME_B_OO; 1.
CC Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
CC
CC Heme.
CC METAL 84 84 IRON 1 (HEME B562 AXIAL LIGAND).
CC METAL 98 98 IRON 2 (HEME B566 AXIAL LIGAND).
CC METAL 183 183 IRON 2 (HEME B562 AXIAL LIGAND).
CC METAL 197 197 IRON 1 (HEME B566 AXIAL LIGAND).
CC CONFLICT 247 247 S -> C (IN REF. 2).
CC SEQUENCE 380 AA; 42639 MW; 514EA8E40537E814 CRC64;

Query Match 50.7%; Score 36; DB 1; Length 380;
Best Local Similarity 63.6%; Pred. NO. 2e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 RPKQQQWFLM 11
||| |
Db 319 RPLAQVLFWM 329

RESULT 83
WNSA_XENLA STANDARD; PRT; 380 AA.
ID WNSA_XENLA
AC P31286;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE WNT-5A PROTEIN PRECURSOR (XWNT-5A).
GN WNT-5A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RX MEDLINE=94102052; PubMed=8275867;
RA Moon R.T., Campbell R.M., Christian J.L., McGrew L.L., Shih J.,
RA Fraser S.;
RT "Wnt-5A: a maternal Wnt that affects morphogenetic movements after
RT overexpression in embryos of Xenopus laevis.";
RL Development 119:97-111(1993).
RN [2]
RP SEQUENCE OF 238-363 FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=91122437; PubMed=1991549;
RA Christian J.L., Gavin B.J., McMahon A.P., Moon R.T.;
RA "Isolation of cDNAs partially encoding four Xenopus
RT Wnt-1/int-1-related proteins and characterization of their transient
RT expression during embryonic development.";
RL Dev. Biol. 143:230-234(1991).
CC -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING

CC MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.
CC AFFECTS MORPHOGENETIC MOVEMENT.
CC -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX.
CC -!- TISSUE SPECIFICITY: FOUND PRIMARILY IN ECTODERM WITH LOWER LEVELS
CC OF EXPRESSION IN MESODERM. DETECTED IN THE HEAD AND TAIL WITH
CC LOWER EXPRESSION IN THE MIDDLE OF THE EMBRYO. NO EXPRESSION WAS
CC FOUND IN THE NOTOCHORD.
CC -!- DEVELOPMENTAL STAGE: PRESENT IN OOCYTES. LEVELS DECREASE DURING
CC EARLY EMBRYO DEVELOPMENT AND THEN INCREASE CONSIDERABLY IN
CC NEURULA AND TADPOLE STAGES.
CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC
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CC
CC EMBL: L19716; AAA16628.1; -
CC EMBL: M55056; AAA50011.1; -
CC InterPro: IPR000970; Wnt1.
CC Pfam: PF00110; wnt1; 1.
CC SMART: SM00097; Wnt1; 1.
CC PROSITE: PS00246; WNT1; 1.
CC Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 40
FT CHAIN 41 380
FT CARBOHYD 114 114 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 312 312 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 261 261 MISSING (IN REF. 2).
FT CONFLICT 265 265 H -> L (IN REF. 2).
FT CONFLICT 274 274 G -> A (IN REF. 2).
SQ SEQUENCE 380 AA; 42519 MW; 822E2259739EB15D CRC64;

Query Match 50.7%; Score 36; DB 1; Length 380;
Best Local Similarity 54.5%; Pred. NO. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
Qy 1 RPK--PQQRFW 9
||| |
Db 169 RPKDLPDRLW 179

RESULT 84
CYB_CARPL STANDARD; PRT; 381 AA.
ID CYB_CARPL
AC P34866;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOCHROME B.
GN MTCYB OR COB OR CYTB.
OS Carcharhinus plumbeus (Sandbar shark).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Carcharhinidae; Carcharhinus.
OX NCBI_TaxID=7808;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92252907; PubMed=1579163;
RA Martin A.P., Naylor G.J.P., Palumbi S.R.;
RA "Rates of mitochondrial DNA evolution in sharks are slow compared
RT with mammals.";
RL Nature 357:153-155(1992).
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE

CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS.
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN.
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
CC -----
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CC -----
CC EMBL: L08032; AAA31703.1; -
CC InterPro: IPR000179; Cyt_b_b6.
CC Pfam: PF00032; cytochrome_b_c1; 1.
CC PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
CC PROSITE: PS00193; CYTOCHROME_B_QO; 1.
CC Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
CC Heme.
CC METAL 84 84 IRON 1 (HEME B562 AXIAL LIGAND).
CC METAL 98 98 IRON 2 (HEME B566 AXIAL LIGAND).
CC METAL 183 183 IRON 2 (HEME B562 AXIAL LIGAND).
CC METAL 197 197 IRON 1 (HEME B566 AXIAL LIGAND).
CC SEQUENCE 381 AA; 43366 MW; 8A429923A8F17A11 CRC64;
CC
CC Query Match 50.7%; Score 36; DB 1; Length 381;
CC Best Local Similarity 54.5%; Pred. No. 2e+02;
CC Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
CC
CC QY 1 RPKPQQWFWM 11
CC || | :|||
CC Db 319 RPKPQQWFWM 329
CC
CC RESULT 85
CC CYB_CHOCR STANDARD; PRT; 381 AA.
CC AC P48875;
CC DT 01-FEB-1996 (Rel. 33, Created)
CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC DE CYTOCHROME B.
CC GN COB OR CYTB.
CC OS Chondrus crispus (Carragheen).
CC OG Mitochondrion.
CC OC Eukaryota; Rhodophyta; Florideophyceae; Gigartinales; Gigartiniaceae;
CC OC Chondrus.
CC OX NCBI_TaxID=2769;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=Apices;
CC RX MEDLINE=95341681; PubMed=7616569;
CC RA Leblanc C., Boyen C., Richard O., Bonnard G., Grienemberger J.M.,
CC RA Kloeareg B.;
CC RT "Complete sequence of the mitochondrial DNA of the rhodophyte
CC Chondrus crispus (Gigartinales). Gene content and genome
CC organization.";
CC RL J. Mol. Biol. 250:484-495 (1995).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS.
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN.
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
CC -----
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CC -----
CC EMBL: L08032; AAA31703.1; -
CC InterPro: IPR000179; Cyt_b_b6.
CC Pfam: PF00032; cytochrome_b_c1; 1.
CC PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
CC PROSITE: PS00193; CYTOCHROME_B_QO; 1.
CC Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
CC Heme.
CC METAL 84 84 IRON 1 (HEME B562 AXIAL LIGAND).
CC METAL 98 98 IRON 2 (HEME B566 AXIAL LIGAND).
CC METAL 183 183 IRON 2 (HEME B562 AXIAL LIGAND).
CC METAL 197 197 IRON 1 (HEME B566 AXIAL LIGAND).
CC SEQUENCE 381 AA; 43366 MW; 8A429923A8F17A11 CRC64;
CC
CC Query Match 50.7%; Score 36; DB 1; Length 381;
CC Best Local Similarity 54.5%; Pred. No. 2e+02;
CC Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
CC
CC QY 1 RPKPQQWFWM 11
CC || | :|||
CC Db 319 RPKPQQWFWM 329
CC
CC RESULT 85
CC CYB_CHOCR STANDARD; PRT; 381 AA.
CC AC P48875;
CC DT 01-FEB-1996 (Rel. 33, Created)
CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC DE CYTOCHROME B.
CC GN COB OR CYTB.
CC OS Chondrus crispus (Carragheen).
CC OG Mitochondrion.
CC OC Eukaryota; Rhodophyta; Florideophyceae; Gigartinales; Gigartiniaceae;
CC OC Chondrus.
CC OX NCBI_TaxID=2769;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=Apices;
CC RX MEDLINE=95341681; PubMed=7616569;
CC RA Leblanc C., Boyen C., Richard O., Bonnard G., Grienemberger J.M.,
CC RA Kloeareg B.;
CC RT "Complete sequence of the mitochondrial DNA of the rhodophyte
CC Chondrus crispus (Gigartinales). Gene content and genome
CC organization.";
CC RL J. Mol. Biol. 250:484-495 (1995).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS.
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN.
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L08032; AAA31703.1; -
CC InterPro: IPR000179; Cyt_b_b6.
CC Pfam: PF00032; cytochrome_b_c1; 1.
CC PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
CC PROSITE: PS00193; CYTOCHROME_B_QO; 1.
CC Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
CC Heme.
CC METAL 84 84 IRON 1 (HEME B562 AXIAL LIGAND).
CC METAL 98 98 IRON 2 (HEME B566 AXIAL LIGAND).
CC METAL 183 183 IRON 2 (HEME B562 AXIAL LIGAND).
CC METAL 197 197 IRON 1 (HEME B566 AXIAL LIGAND).
CC SEQUENCE 381 AA; 43366 MW; 8A429923A8F17A11 CRC64;
CC
CC Query Match 50.7%; Score 36; DB 1; Length 381;
CC Best Local Similarity 54.4%; Pred. No. 2e+02;
CC Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
CC
CC QY 3 KPOQWFWM 11
CC || | :|||
CC Db 107 KPRHWVWVI 115
CC
CC RESULT 86
CC CYB_PRIGL STANDARD; PRT; 381 AA.
CC AC P34873;
CC DT 01-FEB-1994 (Rel. 28, Created)
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC DE CYTOCHROME B.
CC GN MTCYB OR COB OR CYTB.
CC OS Prionace glauca (Blue shark).
CC OG Mitochondrion.
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
CC OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
CC OC Carcharhinidae; Prionace.
CC OX NCBI_TaxID=7815;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=9252907; PubMed=1579163;
CC RA Martin A.P., Naylor G.J.P., Palumbi S.R.;
CC RT "Rates of mitochondrial DNA evolution in sharks are slow compared
CC with mammals.";
CC RL Nature 357:153-155 (1992).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS.
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN.
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: 247547; CAA87609.1; -
CC Mendel: 7723; CHOCr: cob.1.
CC InterPro: IPR000179; Cyt_b_b6.
CC Pfam: PF00032; cytochrome_b_c1; 1.
CC PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
CC PROSITE: PS00193; CYTOCHROME_B_QO; 1.
CC Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
CC Heme.
CC METAL 81 81 IRON 1 (HEME B562 AXIAL LIGAND).
CC METAL 95 95 IRON 2 (HEME B566 AXIAL LIGAND).
CC METAL 182 182 IRON 2 (HEME B562 AXIAL LIGAND).
CC METAL 196 196 IRON 1 (HEME B566 AXIAL LIGAND).
CC SEQUENCE 381 AA; 43765 MW; 945E974B0918EF65 CRC64;
CC
CC Query Match 50.7%; Score 36; DB 1; Length 381;
CC Best Local Similarity 44.4%; Pred. No. 2e+02;
CC Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
CC
CC QY 3 KPOQWFWM 11
CC || | :|||
CC Db 107 KPRHWVWVI 115

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: 247547; CAA87609.1; -
CC Mendel: 7723; CHOCr: cob.1.
CC InterPro: IPR000179; Cyt_b_b6.
CC Pfam: PF00032; cytochrome_b_c1; 1.
CC PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
CC PROSITE: PS00193; CYTOCHROME_B_QO; 1.
CC Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
CC Heme.
CC METAL 81 81 IRON 1 (HEME B562 AXIAL LIGAND).
CC METAL 95 95 IRON 2 (HEME B566 AXIAL LIGAND).
CC METAL 182 182 IRON 2 (HEME B562 AXIAL LIGAND).
CC METAL 196 196 IRON 1 (HEME B566 AXIAL LIGAND).
CC SEQUENCE 381 AA; 43765 MW; 945E974B0918EF65 CRC64;
CC
CC Query Match 50.7%; Score 36; DB 1; Length 381;
CC Best Local Similarity 44.4%; Pred. No. 2e+02;
CC Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
CC
CC QY 3 KPOQWFWM 11
CC || | :|||
CC Db 107 KPRHWVWVI 115
CC
CC RESULT 86
CC CYB_PRIGL STANDARD; PRT; 381 AA.
CC AC P34873;
CC DT 01-FEB-1994 (Rel. 28, Created)
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC DE CYTOCHROME B.
CC GN MTCYB OR COB OR CYTB.
CC OS Prionace glauca (Blue shark).
CC OG Mitochondrion.
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
CC OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
CC OC Carcharhinidae; Prionace.
CC OX NCBI_TaxID=7815;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=9252907; PubMed=1579163;
CC RA Martin A.P., Naylor G.J.P., Palumbi S.R.;
CC RT "Rates of mitochondrial DNA evolution in sharks are slow compared
CC with mammals.";
CC RL Nature 357:153-155 (1992).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS.
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN.
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: 247547; CAA87609.1; -
CC Mendel: 7723; CHOCr: cob.1.
CC InterPro: IPR000179; Cyt_b_b6.
CC Pfam: PF00032; cytochrome_b_c1; 1.
CC PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
CC PROSITE: PS00193; CYTOCHROME_B_QO; 1.
CC Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
CC Heme.
CC METAL 81 81 IRON 1 (HEME B562 AXIAL LIGAND).
CC METAL 95 95 IRON 2 (HEME B566 AXIAL LIGAND).
CC METAL 182 182 IRON 2 (HEME B562 AXIAL LIGAND).
CC METAL 196 196 IRON 1 (HEME B566 AXIAL LIGAND).
CC SEQUENCE 381 AA; 43765 MW; 945E974B0918EF65 CRC64;
CC
CC Query Match 50.7%; Score 36; DB 1; Length 381;
CC Best Local Similarity 44.4%; Pred. No. 2e+02;
CC Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
CC
CC QY 3 KPOQWFWM 11
CC || | :|||
CC Db 107 KPRHWVWVI 115

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L08040; AAA32042.1; -.
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00032; cytochrome_b_c; 1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE: PS00193; CYTOCHROME_B_OO; 1.
DR Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
KW Heme.
FT METAL 84 84 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 98 98 IRON 2 (HEME B566 AXIAL LIGAND).
FT METAL 183 183 IRON 2 (HEME B562 AXIAL LIGAND).
FT METAL 197 197 IRON 1 (HEME B566 AXIAL LIGAND).
SQ SEQUENCE 381 AA; 43282 MW; DAF9ELB516B97C4B CRC64;

Query Match 50.7%; Score 36; DB 1; Length 381;
Best Local Similarity 54.5%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKQWFWLM 11
||| |:::
Db 319 RPMTQIFFWLL 329

RESULT 87
CIW4_HUMAN STANDARD; PRT; 393 AA.
AC Q9NYG8;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 4 (TWIK-RELATED ARACHIDONIC ACID-
DE STIMULATED POTASSIUM CHANNEL PROTEIN) (TRAAK).
GN KCNK4 OR TRAAK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20499203; PubMed=11042359;
RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,
RA Kelsell R.E., Murdoch P.R., Randall A.D., Rennie G.I., Gloger I.S.;
RT "Cloning, localisation and functional expression of a novel human,
RL cerebellum specific, two pore domain potassium channel.";
RL Brain Res. Mol. Brain Res. 82:74-83(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Frontal cortex;
RA Gray A.T.;
RT "Assignment of KCNK4 encoding the human potassium channel TRAAK to
RL chromosome 11.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231699; PubMed=10767409;
RA Lesage F., Maignret F., Lazdunski M.;
RT "Cloning and expression of human TRAAK, a polyunsaturated fatty
RL acids-activated and mechano-sensitive K(+) channel.";
RL FEBS Lett. 471:137-140(2000).
CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
CC EXTERNAL K+ CONCENTRATIONS (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF248242; AAG31731.1; -.
DR EMBL: AF247042; AAF64062.1; ALT_INIT.
DR InterPro: IPR003280; 2poreK channel.
DR InterPro: IPR002025; CNG_membrane.
DR InterPro: IPR001622; Channel_pore_K.
DR InterPro: IPR002958; Occludin.
DR InterPro: IPR002965; P-rich_extensn.
DR InterPro: IPR000099; TWIK_channel.
DR Pfam: PF00914; CNG_membrane; 1.
DR Pfam: PF02168; Occludin; 1.
DR Pfam: PF02034; TWIK_channel; 1.
DR PRINTS: PR01333; 2POREKCHANNEL.
DR Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 4 24 POTENTIAL.
FT DOMAIN 89 113 PORE-FORMING (POTENTIAL).
FT TRANSMEM 118 138 POTENTIAL.
FT DOMAIN 140 171 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 172 192 POTENTIAL.
FT DOMAIN 197 221 PORE-FORMING (POTENTIAL).
FT TRANSMEM 234 254 POTENTIAL.
FT DOMAIN 255 393 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 78 78 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 82 82 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 328 328 P -> L (IN REF. 2).
SQ SEQUENCE 393 AA; 42704 MW; 7F18E53A0A9AD57D CRC64;

Query Match 50.7%; Score 36; DB 1; Length 393;
Best Local Similarity 44.4%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 RPKQWFWLM 11
||| |:::
Db 232 QPLVWFIL 240

RESULT 88
CIW4_MOUSE STANDARD; PRT; 398 AA.
ID CIW4_MOUSE
AC O88454;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 4 (TWIK-RELATED ARACHIDONIC ACID-
DE STIMULATED POTASSIUM CHANNEL PROTEIN) (TRAAK).
GN KCNK4 OR TRAAK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98292450; PubMed=9628867;
RA Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M.,
RA Lazdunski M.;
RT "A neuronal two P domain K+ channel stimulated by arachidonic acid and
RL polyunsaturated fatty acids.";
RL EMBO J. 17:3297-3308(1998).
RN [2]
RP ACTIVATION
RX MEDLINE=99254548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+
RT channels.";
```

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RL  Nat. Neurosci. 2:422-426(1999).
CC  -|- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
CC  POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
CC  EXTERNAL K+ CONCENTRATIONS.
CC  -|- SUBUNIT: HOMODIMER (POTENTIAL).
CC  -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC  -|- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND
CC  2/TRAAT/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC  -|- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE. NOT
CC  DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND
CC  TESTIS.
CC  -|- MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED
CC  FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANAESTHETICS SUCH AS
CC  CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLURANE.
CC  -|- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC  CHANNELS.
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CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; AF056492; AAC40181.1; -.
CC  DR  MGD; MGI:1298234; Kcnk4.
CC  DR  InterPro: IPR003280; 2porek_channel.
CC  DR  InterPro: IPR001622; Channel_pore_K.
CC  DR  Pfam; PF02034; TWIK_channel; 1.
CC  DR  PRINTS; PR01333; 2POREKCHANNEL.
CC  KW  Ionic channel; Transmembrane; Ion transport; Potassium transport;
CC  Glycoprotein; Alternative splicing.
CC  FT  DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).
CC  TRANSMEM 4 24 POTENTIAL.
CC  FT  DOMAIN 89 113 PORE-FORMING (POTENTIAL).
CC  TRANSMEM 119 139 POTENTIAL.
CC  FT  DOMAIN 140 171 CYTOPLASMIC (POTENTIAL).
CC  TRANSMEM 172 192 POTENTIAL.
CC  FT  DOMAIN 198 222 PORE-FORMING (POTENTIAL).
CC  TRANSMEM 235 255 POTENTIAL.
CC  FT  DOMAIN 256 398 CYTOPLASMIC (POTENTIAL).
CC  CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC  CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC  VARSPLIC 63 67 KLIVE -> KAWAI (IN ISOFORM 2).
CC  VARSPLIC 68 398 MISSING (IN ISOFORM 2).
CC  SEQUENCE 398 AA; 43051 MW; 478A834B7B/AEC92 CRC64;

Query Match 50.7%; Score 36; DB 1; Length 398;
Best Local Similarity 44.4%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFWM 11
   :| :| :| :|
DB 233 QPLVWFWM 241

RESULT 89
CIST_SCHPO STANDARD; PRT; 473 AA.
AC Q10306;
DT 01-OCT-1996 (Rel. 34, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROBABLE CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
GN SPAC6C3.03.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OC NCBI_TaxID=4896;

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RN SEQUENCE FROM N.A.
RP STRAIN=972;
RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: CITRATE + COA -> ACETYL-COA + H(2)O +
CC OXALOACETATE.
CC -|- PATHWAY: TRICARBOXYLIC ACID CYCLE.
CC -|- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
CC -|- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
CC CAPABLE OF OXIDATIVE METABOLISM.
CC -|- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; Z69731; CA93617.2; -.
CC  DR  HSSP; P23007; 5CSC.
CC  DR  InterPro: IPR002020; Citrate_synt.
CC  DR  Pfam; PF00285; citrate_synt; 1.
CC  DR  PRINTS; PR00143; CITRATESYNTHASE.
CC  DR  PROSITE; PS00480; CITRATE_SYNTHASE; 1.
CC  KW  Hypothetical protein; Lyase; Tricarboxylic acid cycle; Mitochondrion;
CC  Transit peptide.
CC  FT  TRANSIT 1 35 MITOCHONDRION (BY SIMILARITY).
CC  CHAIN 36 473 PROBABLE CITRATE SYNTHASE.
CC  ACT_SITE 310 310 BY SIMILARITY.
CC  ACT_SITE 356 356 BY SIMILARITY.
CC  ACT_SITE 411 411 BY SIMILARITY.
CC  SEQUENCE 473 AA; 52973 MW; 86E35E34ADC3E060 CRC64;

Query Match 50.7%; Score 36; DB 1; Length 473;
Best Local Similarity 45.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRPQQWFWM 11
   :| :| :| :|
DB 122 QPLPESLFWLL 132

RESULT 90
CPF4_RAT
ID GPF4_RAT STANDARD; PRT; 522 AA.
AC P51869;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOCHROME P450 4F4 (EC 1.14.14.1) (CYP11B4).
GN CYP4F4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN SEQUENCE FROM N.A.
RP STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=96125358; PubMed=8554568;
RA Kawashima H., Strobel H.W.;
RT "cDNA cloning of three new forms of rat brain cytochrome P450
RT belonging to the Cyp4f subfamily.";
RL Biochem. Biophys. Res. Commun. 217:1137-1144(1995).
CC -|- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) -> ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -|- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -|- TISSUE SPECIFICITY: HIGH EXPRESSION IN LIVER AND KIDNEY. LOWER
CC EXPRESSION IN BRAIN.
CC -|- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

```


Search completed: April 1, 2002, 16:20:19
Job time: 165 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2002, 16:20:04 ; Search time 35.93 Seconds
(without alignments)
44.781 Million cell updates/sec

Title: US-09-988-792-2

Perfect score: 71

Sequence: 1 RKPOQWFWM 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 14627329 residues

Total number of hits satisfying chosen parameters: 244

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 50%

Maximum Match 100%

Listing first 1000 summaries

Database :

SPTREMBL_17:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp Vertebrate:*

14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	67.6	72	4	Q9Y494
2	48	67.6	114	6	Q97947
3	48	67.6	128	4	Q9Y6V5
4	48	67.6	129	6	Q97948
5	45	63.4	453	2	Q9PL30
6	45	63.4	455	2	Q84013
7	44	62.0	97	11	Q9Z0K2
8	44	62.0	115	11	Q9Z0K1
9	44	62.0	130	11	Q9Z0K0
10	43	60.6	314	2	Q9A645
11	43	60.6	365	2	Q9JY60
12	43	60.6	365	2	Q9JY60
13	43	60.6	818	12	Q9PWS3
14	43	60.6	898	12	Q9PYP2
15	41	57.7	158	2	Q34889
16	41	57.7	159	2	Q84560
17	41	57.7	209	11	Q9DAS6
18	41	57.7	261	2	Q9HXA6
19	41	57.7	286	2	Q9PAV0

20	41	57.7	290	2	Q9AKK5
21	41	57.7	291	2	Q55507
22	41	57.7	304	1	Q9HNN1
23	41	57.7	392	2	Q9F849
24	41	57.7	529	2	P74332
25	40	56.3	45	5	Q9V6W6
26	40	56.3	154	11	Q9R129
27	40	56.3	155	11	Q9R132
28	40	56.3	155	11	Q9R131
29	40	56.3	155	11	Q9R127
30	40	56.3	155	11	Q9JKI6
31	40	56.3	273	2	Q9KQ09
32	40	56.3	289	2	Q9JYV2
33	40	56.3	289	2	Q9JTU4
34	40	56.3	290	2	Q9ZCL1
35	40	56.3	290	2	Q9AKF0
36	40	56.3	290	2	Q9AKA6
37	40	56.3	318	2	Q9KVD3
38	40	56.3	332	2	Q82937
39	40	56.3	343	2	Q9ZGU3
40	40	56.3	363	2	P73727
41	40	56.3	367	10	Q9C5G0
42	40	56.3	381	10	Q9FYI5
43	40	56.3	411	4	Q9NRT2
44	40	56.3	639	4	Q9H8K3
45	40	56.3	665	5	Q9V7L5
46	40	56.3	774	4	Q9NWT0
47	40	56.3	797	10	Q9CAX2
48	40	56.3	937	3	Q9HE57
49	39.5	55.6	548	2	Q9RV51
50	39	54.9	55	8	Q79563
51	39	54.9	99	12	Q69572
52	39	54.9	208	2	Q55572
53	39	54.9	341	2	Q9JSJ3
54	39	54.9	361	4	Q9PLW6
55	39	54.9	383	2	Q9F669
56	39	54.9	412	2	Q9ZJ55
57	39	54.9	416	2	Q9HU99
58	39	54.9	452	2	Q9PIU6
59	39	54.9	462	2	Q9K217
60	39	54.9	467	2	Q9Z983
61	39	54.9	480	1	Q9YDN6
62	39	54.9	499	5	Q9VJ81
63	39	54.9	524	4	Q9HB16
64	39	54.9	525	2	Q83145
65	39	54.9	778	13	Q9PDA3
66	39	54.9	825	13	Q9I906
67	39	54.9	827	5	Q9U6M1
68	39	54.9	852	13	Q9IAI1
69	39	54.9	853	13	Q9W6Q2
70	39	54.9	854	13	Q93244
71	39	54.9	854	13	Q91953
72	39	54.9	862	11	Q9WVS9
73	39	54.9	875	13	Q9W7C3
74	39	54.9	893	13	Q9W6J4
75	39	54.9	1023	5	Q9VSB0
76	39	54.9	1219	2	Q53785
77	38.5	54.2	673	10	Q9FVG4
78	38	53.5	105	2	Q9HZ24
79	38	53.5	122	11	Q62024
80	38	53.5	124	11	Q62023
81	38	53.5	175	8	Q9T6A9
82	38	53.5	188	11	Q9DI21
83	38	53.5	220	2	Q07878
84	38	53.5	253	2	Q9ANC0
85	38	53.5	260	5	Q9GUP1
86	38	53.5	270	6	P79391
87	38	53.5	273	4	P78380
88	38	53.5	274	6	Q9TTK7
89	38	53.5	322	11	Q99L65
90	38	53.5	330	11	Q62022
91	38	53.5	356	13	Q98952
92	38	53.5	363	11	Q9EQ09

Q9akk5	rickettsia
Q55507	synecocyst
Q9hnn1	halobacteri
Q9f849	streptomyce
P74332	synecocyst
Q9v6w6	dirosophila
Q9r129	rattus norv
Q9r132	rattus norv
Q9r131	rattus norv
Q9r127	rattus norv
Q9jki6	mus saxicol
Q9krq9	vibrio chol
Q9jyv2	neisseria m
Q9jtu4	neisseria m
Q9zcl1	rickettsia
Q9akf0	rickettsia
Q9aka6	rickettsia
Q9kvd3	vibrio chol
Q82937	escherichia
Q9zgu3	escherichia
P73727	synecocyst
Q9c5g0	arabidopsis
Q9fyi5	arabidopsis
Q9nrt2	homo sapien
Q9h8k3	homo sapien
Q9v7l5	dirosophila
Q9nwy0	homo sapien
Q9cax2	arabidopsis
Q9he57	neurospora
Q9rv51	deinococcus
Q79563	mustelus ma
Q69572	human herpe
Q55572	synecocyst
Q9jsj3	chlamydia p
Q9plw6	homo sapien
Q9f669	pseudomonas
Q9zj55	helicobacte
Q9hu99	pseudomonas
Q9piu6	campylobact
Q9k217	chlamydia p
Q9z983	chlamydia p
Q9ydn6	aeropyrum p
Q9vj81	dirosophila
Q9hb16	homo sapien
Q83145	treponema p
Q9pu43	xenopus lae
Q9i906	xenopus lae
Q9u6m1	leishmania
Q9iai1	gallus gall
Q9w6q2	gallus gall
Q93244	oncorhynch
Q9i953	cuturnix co
Q9wvs9	rattus norv
Q9w7c3	gallus gall
Q9w6j4	brachydanio
Q9vzb0	dirosophila
Q53785	streptomyce
Q9fvq4	zea mays (m
Q9hz24	pseudomonas
Q62024	mus muscucu
Q62023	mus muscucu
Q9t6a9	culicoides
Q9dlz1	mus muscucu
Q07878	sphingomona
Q9anc0	bradyrhizob
Q9gup1	caenorhabdi
P79391	bos taurus
P78380	homo sapien
Q9ttk7	homo scrofa
Q99l65	mus muscucu
Q62022	mus muscucu
Q98952	gallus gall
Q9eq09	mus muscucu

93	38	53.5	364	11	070156	070156 rattus norv	166	37	52.1	1589	13	Q91588	Q91588 xenopus lae
94	38	53.5	368	2	Q9A8W6	Q9A8W6 xyllobacter	167	37	52.1	1635	5	O17368	O17368 caenorhabdi
95	38	53.5	373	3	Q9PDR6	Q9PDR6 xylella fas	168	37	52.1	2458	2	O51827	O51827 pseudomonas
96	38	53.5	392	10	Q9FHER	Q9FHER arabidopsis	169	36.5	51.4	523	11	Q99N19	Q99N19 mus musculu
97	38	53.5	401	11	Q9JIK2	Q9JIK2 cricetulus	170	36.5	51.4	523	11	Q99KY6	Q99KY6 mus musculu
98	38	53.5	412	2	O26064	O26064 helicobacte	171	36	50.7	93	10	Q9SDN8	Q9SDN8 phytophthor
99	38	53.5	421	10	Q9CAP2	Q9CAP2 arabidopsis	172	36	50.7	103	2	P73564	P73564 synecocyst
100	38	53.5	433	11	Q99N88	Q99N88 rattus norv	173	36	50.7	104	5	O76548	O76548 dictyostell
101	38	53.5	455	10	O65524	O65524 arabidopsis	174	36	50.7	105	2	Q9AFZ7	Q9AFZ7 shigella fi
102	38	53.5	458	5	Q9WLD1	Q9WLD1 drosophila	175	36	50.7	125	11	Q9DCS0	Q9DCS0 mus musculu
103	38	53.5	635	5	Q9VUK7	Q9VUK7 drosophila	176	36	50.7	135	8	Q36742	Q36742 cottus kess
104	38	53.5	684	5	Q9UAC1	Q9UAC1 leishmania	177	36	50.7	154	2	Q9RVC1	Q9RVC1 deinococcus
105	38	53.5	691	5	Q9UAB7	Q9UAB7 leishmania	178	36	50.7	171	2	Q9HWX8	Q9HWX8 pseudomonas
106	38	53.5	697	10	Q9LUQ4	Q9LUQ4 arabidopsis	179	36	50.7	241	10	Q9FRE0	Q9FRE0 oryza sativ
107	38	53.5	698	5	Q9UAC0	Q9UAC0 leishmania	180	36	50.7	250	8	Q9TAK3	Q9TAK3 cafeteria r
108	38	53.5	700	5	Q9UAB9	Q9UAB9 leishmania	181	36	50.7	254	6	O19110	O19110 bos taurus
109	38	53.5	722	10	Q9W7X1	Q9W7X1 arabidopsis	182	36	50.7	268	5	O21187	Q21187 caenorhabdi
110	38	53.5	901	12	Q9DXA2	Q9DXA2 choristoneu	183	36	50.7	280	2	Q9KRT5	Q9KRT5 vibrio chol
111	38	53.5	909	2	P74693	P74693 synecocyst	184	36	50.7	287	2	Q9KX15	Q9KX15 deinococcus
112	38	53.5	956	5	O00908	O00908 cryptospori	185	36	50.7	302	2	O53945	O53945 streptomyce
113	38	53.5	1184	4	O75339	O75339 homo sapien	186	36	50.7	320	11	Q9CYX6	Q9CYX6 mus musculu
114	38	53.5	1216	11	Q9QYV8	Q9QYV8 rattus norv	187	36	50.7	343	8	Q9B4H0	Q9B4H0 callisaurus
115	38	53.5	1216	11	Q9QYV7	Q9QYV7 rattus norv	188	36	50.7	347	2	O47471	O47471 erwinia car
116	38	53.5	1528	5	P81137	P81137 manduca sex	189	36	50.7	359	8	Q9MW76	Q9MW76 gallotia ga
117	38	53.5	1717	5	Q9GPJ9	Q9GPJ9 manduca sex	190	36	50.7	359	4	Q9BV04	Q9BV04 homo sapien
118	38	53.5	1832	5	O96503	O96503 cryptospori	191	36	50.7	360	6	Q9XT34	Q9XT34 sus scrofa
119	38	53.5	2237	5	Q9V122	Q9V122 drosophila	192	36	50.7	362	11	O35886	O35886 cricetulus
120	37.5	52.8	100	14	Q99IT0	Q99IT0 uncultured	193	36	50.7	362	11	Q9R220	Q9R220 cricetulus
121	37.5	52.8	213	2	Q99ZD5	Q99ZD5 streptococ	194	36	50.7	362	11	Q9R219	Q9R219 cricetulus
122	37.5	52.8	300	11	Q9CY68	Q9CY68 mus musculu	195	36	50.7	369	2	P73843	P73843 synecocyst
123	37.5	52.8	473	11	Q9Z1X2	Q9Z1X2 mus musculu	196	36	50.7	380	8	Q9XPE2	Q9XPE2 eumeces egr
124	37.5	52.8	474	11	O08888	O08888 cricetulus	197	36	50.7	385	13	Q9YXG6	Q9YXG6 gallus gall
125	37.5	52.8	487	4	Q9BVG9	Q9BVG9 homo sapien	198	36	50.7	454	5	Q9VNP0	Q9VNP0 drosophila
126	37.5	52.8	1177	12	Q92611	Q92611 pseudorabie	199	36	50.7	482	8	Q9MGA9	Q9MGA9 chrysodidym
127	37.5	52.8	1194	12	Q9E1V7	Q9E1V7 cercopithe	200	36	50.7	534	11	Q9N18	Q9N18 mus musculu
128	37.5	52.8	1203	12	Q99101	Q99101 herpes simp	201	36	50.7	603	2	Q9L217	Q9L217 streptomyce
129	37.5	52.8	1203	12	Q99549	Q99549 bovine herp	202	36	50.7	605	2	O86684	O86684 streptomyce
130	37.5	52.8	1208	12	O39273	O39273 equine herp	203	36	50.7	611	11	O60850	O60850 mus musculu
131	37	52.1	53	8	Q9YTB3	Q9YTB3 tadorna var	204	36	50.7	633	5	Q9VT54	Q9VT54 drosophila
132	37	52.1	53	8	Q9YTB2	Q9YTB2 escherichia	205	36	50.7	643	1	O29580	O29580 archaeoglob
133	37	52.1	116	2	Q9RM36	Q9RM36 streptomyce	206	36	50.7	656	10	O65001	O65001 zea mays (m
134	37	52.1	181	2	Q9ADB8	Q9ADB8 streptomyce	207	36	50.7	670	2	Q9RXQ7	Q9RXQ7 deinococcus
135	37	52.1	220	3	O14264	O14264 schizosacch	208	36	50.7	704	2	Q9KX19	Q9KX19 vibrio chol
136	37	52.1	226	5	Q9V424	Q9V424 drosophila	209	36	50.7	729	4	Q9JY93	Q9JY93 homo sapien
137	37	52.1	273	11	Q9D3C8	Q9D3C8 mus musculu	210	36	50.7	774	2	Q9K2S2	Q9K2S2 bacillus su
138	37	52.1	292	2	Q9AP18	Q9AP18 methylobact	211	36	50.7	804	2	P70811	P70811 bacillus ha
139	37	52.1	314	5	Q9VHB7	Q9VHB7 drosophila	212	36	50.7	805	2	Q9RGZ5	Q9RGZ5 bacillus fi
140	37	52.1	331	3	O00893	O00893 collettotric	213	36	50.7	817	4	Q9H814	Q9H814 homo sapien
141	37	52.1	359	4	Q9Y231	Q9Y231 homo sapien	214	36	50.7	823	4	O15033	O15033 homo sapien
142	37	52.1	359	11	O88819	O88819 mus musculu	215	36	50.7	829	2	O55414	O55414 synecocyst
143	37	52.1	359	11	Q9JIG1	Q9JIG1 cricetulus	216	36	50.7	861	2	O06944	O06944 synecocyst
144	37	52.1	359	11	Q95JB3	Q95JB3 rattus norv	217	36	50.7	886	5	Q9VZV1	Q9VZV1 drosophila
145	37	52.1	365	6	Q9TQ03	Q9TQ03 bos taurus	218	36	50.7	894	4	Q9C096	Q9C096 homo sapien
146	37	52.1	406	2	Q9KQW4	Q9KQW4 vibrio chol	219	36	50.7	894	4	Q9C096	Q9C096 homo sapien
147	37	52.1	421	2	Q9EX44	Q9EX44 streptomyce	220	36	50.7	959	4	Q9UFZ7	Q9UFZ7 homo sapien
148	37	52.1	467	2	Q9CK08	Q9CK08 pasteurella	221	36	50.7	1038	5	O01261	O01261 caenorhabdi
149	37	52.1	529	2	Q9FDI3	Q9FDI3 brevibacter	222	36	50.7	1039	5	Q23567	Q23567 caenorhabdi
150	37	52.1	536	2	Q9KLT3	Q9KLT3 vibrio chol	223	36	50.7	1043	5	Q9VL84	Q9VL84 drosophila
151	37	52.1	555	2	Q9RPG1	Q9RPG1 myxococcus	224	36	50.7	1148	4	Q9H6W7	Q9H6W7 homo sapien
152	37	52.1	595	2	Q9RJ38	Q9RJ38 streptomyce	225	36	50.7	1236	4	Q9C012	Q9C012 homo sapien
153	37	52.1	604	8	Q9XMR9	Q9XMR9 tetrahymena	226	36	50.7	1239	11	Q9J128	Q9J128 mus musculu
154	37	52.1	645	11	Q62094	Q62094 mus musculu	227	36	50.7	1243	5	O9NGT8	O9NGT8 leishmania
155	37	52.1	656	12	Q9QU36	Q9QU36 ttv-like mi	228	36	50.7	1377	5	P91854	P91854 caenorhabdi
156	37	52.1	669	13	Q9PVX6	Q9PVX6 cynops pyrr	229	36	50.7	1493	5	Q9GPA0	Q9GPA0 caenorhabdi
157	37	52.1	765	10	Q9SRV5	Q9SRV5 arabidopsis	230	36	50.7	1527	11	Q9JLA3	Q9JLA3 rattus norv
158	37	52.1	765	10	Q9LM03	Q9LM03 solanum tub	231	36	50.7	1555	4	Q9NYU2	Q9NYU2 homo sapien
159	37	52.1	806	10	Q9EFF2	Q9EFF2 arabidopsis	232	36	50.7	1620	4	Q9UT8	Q9UT8 homo sapien
160	37	52.1	918	3	Q9HEW7	Q9HEW7 cladosporiu	233	36	50.7	1674	10	Q9FV08	Q9FV08 arabidopsis
161	37	52.1	944	3	O60043	O60043 metarhizium	234	36	50.7	1952	4	Q9UJ92	Q9UJ92 homo sapien
162	37	52.1	1002	5	Q9W570	Q9W570 drosophila	235	36	50.7	2135	4	O43157	O43157 homo sapien
163	37	52.1	1081	4	Q9H8F3	Q9H8F3 homo sapien	236	36	50.7	2135	4	Q9UIV7	Q9UIV7 homo sapien
164	37	52.1	1301	4	O94987	O94987 homo sapien	237	36	50.7	2396	5	O77291	O77291 drosophila
165	37	52.1	1418	13	O93457	O93457 scophthalmu	238	36	50.7	5201	5	Q9U479	Q9U479 drosophila

239 36 50.7 5385 5 Q9V6V3 Q9v6v3 drosophila
240 36 50.7 5496 5 Q9V6V2 Q9v6v2 drosophila
241 36 50.7 8805 5 Q9V6V4 Q9v6v4 drosophila
242 35.5 50.0 383 2 Q56675 Q56675 vibrio chol
243 35.5 50.0 842 13 Q9W6K7 Q9w6k7 brachydanio
244 35.5 50.0 4861 4 Q15751 Q15751 homo sapien

ALIGNMENTS

RESULT 1
Q9Y494 ID Q9Y494 PRELIMINARY; PRT; 72 AA.
AC Q9Y494
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE GAMMA PREPROTACHYKININ (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD, AND BRAIN;
RA Lai J.P., Douglas S.D., Rappaport E., Wu J.M., Ho W.Z.;
RT "Identification of a Delta Isoform of preprotachykinin mRNA in Human
RT Mononuclear Phagocytes and Lymphocytes";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF050657; AAC15703.1; -;
DR InterPro; IPR002040; Tachykinin.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.
DR SMART; SM00203; TK; 2.
FT NON_TER 1
FT NON_TER 72
SQ SEQUENCE 72 AA; 8274 MW; 2C02B2BA41EAD16 CRC64;

Query Match 67.6%; Score 48; DB 4; Length 72;
Best Local Similarity 81.8%; Pred. No. 1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQQFWLM 11
|||||: ||
Db 23 RPKPQQQFFGLM 33

RESULT 2
Q97947 ID Q97947 PRELIMINARY; PRT; 114 AA.
AC Q97947
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE GAMMA PREPROTACHYKININ I.
OS Tupia belangeri (northern tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupia.
OX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Heitland A., Maegert H.J., Kruhoffer M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50785; CAA90648.1; -;
DR InterPro; IPR002040; Tachykinin.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR ProDom; PD005598; Protachykinin; 1.

DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.
DR SMART; SM00203; TK; 2.
FT CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 92 NEUROPEPTIDE GAMMA.
FT CHAIN 83 92 NEUROKININ A.
SQ SEQUENCE 114 AA; 13281 MW; B439C3D27FDA7CAB CRC64;

Query Match 67.6%; Score 48; DB 6; Length 114;
Best Local Similarity 81.8%; Pred. No. 1.6;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQQFWLM 11
|||||: ||
Db 58 RPKPQQQFFGLM 68

RESULT 3
Q9Y6V5 ID Q9Y6V5 PRELIMINARY; PRT; 128 AA.
AC Q9Y6V5
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE WUGSC:H-DJ0841B21.1 PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kalicki J., Angell S.;
RT "The sequence of Homo sapiens PAC clone DJ0841B21";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004140; AAC02754.1; -;
DR InterPro; IPR002040; Tachykinin.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.
DR SMART; SM00203; TK; 1.
SQ SEQUENCE 128 AA; 14770 MW; 0F8D61774AFEC1CA CRC64;

Query Match 67.6%; Score 48; DB 4; Length 128;
Best Local Similarity 81.8%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQQFWLM 11
|||||: ||
Db 58 RPKPQQQFFGLM 68

RESULT 4
Q97948 ID Q97948 PRELIMINARY; PRT; 129 AA.
AC Q97948
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE BETA PREPROTACHYKININ I.
OS Tupia belangeri (northern tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupia.
OX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Heitland A., Maegert H.J., Kruhoffer M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";

RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; Z50786; CAA90649.1; -
DR InterPro: IPR002040; Tachykinin.
DR InterPro: IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR ProDom; PD005598; Protachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.
DR SMART; SM00203; TK; 2.
FT CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 107 NEUROPEPTIDE K.
FT CHAIN 98 107 NEUROKININ A.
SQ SEQUENCE 129 AA; 14941 MW; 5855E7ADC2D8674E CRC64;

Query Match 67.6%; Score 48; DB 6; Length 129;

Best Local Similarity 81.8%; Pred. No. 1.8; Mismatches 1; Indels 0; Gaps 0;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPQPQWFWM 11

|||||:|

Db 58 RPQPQWFGLM 68

RESULT 5

Q9PL30 PRELIMINARY; PRT; 453 AA.

AC Q9PL30; 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE LIPID A BIOSYNTHESIS LAUROYL ACYLTRANSFERASE, PUTATIVE.

GN TC0278.

OS Chlamydia muridarum.

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI_TaxID=83560;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MOPN / NIGG;

RX MEDLINE=20150255; PubMed=10684935;

RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,

RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,

RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,

RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,

RA Eisen J., Fraser C.M.;

RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia

RT pneumoniae AR39.";

RL Nucleic Acids Res. 28:1397-1406(2000).

DR EMBL; AE002295; AAF39146.1; -

DR TIGR; TC0278; -

KW Complete proteome.

SQ SEQUENCE 453 AA; 51463 MW; 6221515A00A093FF CRC64;

Query Match 63.4%; Score 45; DB 2; Length 453;

Best Local Similarity 75.0%; Pred. No. 18; Mismatches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPQWFWM 10

|||||

Db 303 KPQWLM 310

RESULT 6

O84013 PRELIMINARY; PRT; 455 AA.

AC O84013; 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE ACYLTRANSFERASE.

GN HTRB OR CT010.

OS Chlamydia trachomatis.

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI_TaxID=813;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=D/UW-3/CX;

RX MEDLINE=99000809; PubMed=9784136;

RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe F., Aravind L.,

RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,

RA Davis R.W.;

RT "Genome sequence of an obligate intracellular pathogen of humans:

RT Chlamydia trachomatis";

RL Science 282:754-759(1998).

DR EMBL; AE001275; AAC67600.1; -

KW Transferase; Acyltransferase; Complete proteome.

SQ SEQUENCE 455 AA; 52058 MW; 0404B6326C67ACCF CRC64;

Query Match 63.4%; Score 45; DB 2; Length 455;

Best Local Similarity 75.0%; Pred. No. 18;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPQWFWM 10

|||||

Db 303 KPQWLM 310

RESULT 7

Q9Z0K2 PRELIMINARY; PRT; 97 AA.

AC Q9Z0K2; 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE DELTA PREPROTACHYKININ I.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.

OX NCBI_TaxID=10141;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PIRBRIDGE WHITE; TISSUE=BRAIN;

RA Heitland A., Maegert H.J., Kruehoffer M., Forssmann W.G.;

RA "Tachykinin precursors are highly conserved among different mammals.";

RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; Z50782; CAA90645.1; -

DR InterPro; IPR003580; Protachykinin.

DR ProDom; PD005598; Protachykinin; 1.

FT CHAIN 58 68 SUBSTANCE P.

SQ SEQUENCE 97 AA; 11222 MW; FFD50C3297E3F7E3 CRC64;

Query Match 62.0%; Score 44; DB 11; Length 97;

Best Local Similarity 81.8%; Pred. No. 5.7;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPQPQWFWM 11

|||||

Db 58 RPQPQWFGLM 68

RESULT 8

Q9Z0K1 PRELIMINARY; PRT; 115 AA.

AC Q9Z0K1; 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE GAMMA PREPROTACHYKININ I.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.

OX NCBI_TaxID=10141;

RN [1]

RP SEQUENCE FROM N.A.

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RC STRAIN=PIRBRIDGE WHITE; TISSUE=BRAIN;
RA Heitland A., Maegert H.J., Kruhoefter M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50783; CAA90647.1; -.
DR InterPro; IPR002040; Tachykinin.
DR ProDom; PD003580; Protachykinin.
DR PROSITE; PS005598; Protachykinin; 1.
DR CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 92 NEUROPEPTIDE GAMMA.
FT CHAIN 83 92 NEUROKININ A.
SQ SEQUENCE 115 AA; 13190 MW; 39EFFB8CBB47174 CRC64;

Query Match 62.0%; Score 44; DB 11; Length 115;
Best Local Similarity 81.8%; Pred. No. 6.7;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
||||| |||
Db 58 RPKPQQSFGLM 68

RESULT 9
Q9Z0K0 PRELIMINARY; PRT; 130 AA.
AC Q9Z0K0;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE BETA PREPROTACHYKININ I.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PIRBRIDGE WHITE; TISSUE=BRAIN;
RA Heitland A., Maegert H.J., Kruhoefter M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50784; CAA90647.1; -.
DR InterPro; IPR002040; Tachykinin.
DR ProDom; PD003598; Protachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_1.
FT CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 107 NEUROPEPTIDE K.
FT CHAIN 98 107 NEUROKININ A.
SQ SEQUENCE 130 AA; 14850 MW; C4B2F55B6A60A7C0 CRC64;

Query Match 62.0%; Score 44; DB 11; Length 130;
Best Local Similarity 81.8%; Pred. No. 7.6;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
||||| |||
Db 58 RPKPQQSFGLM 68

RESULT 10
Q9A645 PRELIMINARY; PRT; 314 AA.
AC Q9A645;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL PROTEIN CC2250.
GN CC2250.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;

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OC Caulobacter.
OX NCBI_TaxID=69394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005895; AAK24221.1; -.
DR TIGR; CC2250; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 314 AA; 35316 MW; 59825ADEF764362A CRC64;

Query Match 60.6%; Score 43; DB 2; Length 314;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 10
|:|:|:|:|
Db 282 RERPAENFWV 291

RESULT 11
Q9JY60 PRELIMINARY; PRT; 365 AA.
ID Q9JY60;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE, SUBUNIT III.
GN NMB1723.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
RA Cotton M.D., Uterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Pizza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.";
RL Science 287:1809-1815(2000).
DR EMBL; AE002522; AAF42068.1; -.
DR TIGR; NMB1723; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR003088; Cyt_C1.
DR InterPro; IPR002329; Cyt_C1C.
DR Pfam; PF00034; cytochrome.c.2.
DR PRINTS; PR00605; CYTOCHROME_C1C.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 365 AA; 40039 MW; AF344435A51EB4A2 CRC64;

Query Match 60.6%; Score 43; DB 2; Length 365;
Best Local Similarity 56.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RPKPQQWFWM 10

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Db 62 PLPRWFWL 70
| | | | |

RESULT 12

Q9JUT44 PRELIMINARY; PRT; 365 AA.
AC Q9JUT44;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PUTATIVE CYTOCHROME C.
GN NMA1977.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491";
RL Nature 404:502-506(2000).
RL EMBL; AL162757; CAB85197.1; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR003088; Cyt.C1.
DR InterPro; IPR002329; Cyt.C1C.
DR Pfam; PF00034; cytochrome_c; 2.
DR PRINTS; P00605; CYTOCHROME_C.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 365 AA; 40011 MW; AF223552A51EB4A2 CRC64;

Query Match 60.6%; Score 43; DB 2; Length 365;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPQWFWL 10
| | | | |

Db 62 PLPRWFWL 70

RESULT 13

Q9PWS3 PRELIMINARY; PRT; 818 AA.
AC Q9PWS3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE GAG-ABL PROTEIN (FRAGMENT).
OS Abelson murine leukemia virus.
OC Viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses.
OX NCBI_TaxID=11788;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee R., Paskind M., Wang J.Y.J., Baltimore D.;
RT "Abelson (P160) murine leukemia virus (Ab-MLV) abl gene."; (In) Weiss R., Teich N., Varmus H., Coffin J. (eds.);
RL RNA tumor viruses, pp.861-868, Cold Spring Harbor Laboratory Press, New York (1985).
RL EMBL; X02963; CAB56204.1; -.
DR HSP; P00519; 2ABL.
DR InterPro; IPR00719; Euk_pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001245; Tyr_kin.
DR Pfam; PF00069; pkinase; 1.

Pfam; PF00017; SH2; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_APP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00001; SH2; 1.
KW ATP-binding; Transferase; Tyrosine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 818 AA; 90973 MW; C2F5F417D0A9FE0C CRC64;

Query Match 60.6%; Score 43; DB 12; Length 818;
Best Local Similarity 77.8%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPQWFWL 10
| | | | |

Db 545 PKQQWGWL 553

RESULT 14

Q9PYP2 PRELIMINARY; PRT; 898 AA.
AC Q9PYP2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ORF154.
GN ORF154.
OS Xestia c-nigrum granulosis virus (XnGV) (Xestia c-nigrum granulovirus).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX NCBI_TaxID=51677;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99434230; PubMed=10502508;
RA Hayakawa T., Ko R., Okano K., Seong S.I., Goto C., Maeda S.;
RT "Sequence analysis of the Xestia c-nigrum granulovirus genome."; Virology 262:277-297(1999).
RL EMBL; AF162221; AAF05268.1; -.
DR EMBL; AF162221; AAF05268.1; -.
SQ SEQUENCE 898 AA; 104261 MW; DDE9900AEE146834 CRC64;

Query Match 60.6%; Score 43; DB 12; Length 898;
Best Local Similarity 70.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQWFWL 11
| | | | |

Db 353 PYQIWAFLM 362

RESULT 15

O34889 PRELIMINARY; PRT; 158 AA.
AC O34889;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE HYPOTHEICAL 18.7 KDA PROTEIN YVAV (OREA).
GN YVAV.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JH642;
RA Nakamura A., Grau R., Perego M., Hoch J.A.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

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[2]
RN  SEQUENCE FROM N.A.
RP  STRAIN=168;
RX  MEDLINE=98044033; PubMed=9384377;
RA  Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA  Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA  Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA  Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA  Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA  Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA  Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA  Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA  Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA  Guisepi G., Guy B.J., Haga K., Haech J., Harwood C.R., Henaut A.,
RA  Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA  Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA  Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA  Kurita K., Lapidus A., Lardinis S., Lauber J., Lazarevic V.,
RA  Lee S.M., Levine A., Liu H., Masuda S., Mauei C., Medigue C.,
RA  Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA  Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA  Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA  Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA  Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadale Y.,
RA  Sato T., Scaulan E., Schleich S., Schroeter R., Scoffone F.,
RA  Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA  Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA  Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA  Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA  Visari A., Wambutt R., Wedler H., Wedler H., Weitzenecker T.,
RA  Winters K., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA  Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT  "The complete genome sequence of the gram-positive bacterium Bacillus
RT  subtilis."
RL  Nature 390:249-256(1997).
DR  EMBL; AB006738; BAA21900.1; -.
DR  EMBL; 299121; CAB15380.1; -.
KW  Hypothetical protein; Complete proteome.
SQ  SEQUENCE 158 AA; 18650 MW; C495D20D39CF46C7 CRC64;

Query Match 57.7%; Score 41; DB 2; Length 158;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKQOWFWL 10
DB 131 ROKPLSWYI 140

RESULT 16
OB4560 PRELIMINARY; PRT; 159 AA.
ID OB4560;
AC OB4560;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE HYPOTHETICAL 17.8 KDA PROTEIN.
GN CT556.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=D/UW-3/CX;
RA MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
DR EMBL; AE001326; AAC68158.1; -.

KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 159 AA; 17755 MW; 16CC06BAECAFA6CBB CRC64;

Query Match 57.7%; Score 41; DB 2; Length 159;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOQWFWL 10
DB 89 PAPSQWDL 97

RESULT 17
Q9DAS6 PRELIMINARY; PRT; 209 AA.
ID Q9DAS6;
AC Q9DAS6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ADULT FEMALE PLACENTA CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:1600029015, FULL INSERT SEQUENCE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=PLACENTA;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojorori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK005564; BAB24124.1; -.
DR InterPro; IPR001063; Ribosomal_L22.
DR Pfam; PF00237; Ribosomal_L22; 1.
DR ProDom; PD001032; Ribosomal_L22; 1.
DR PROSITE; PS00464; RIBOSOMAL_L22; 1.
SQ SEQUENCE 209 AA; 24121 MW; AEFEDB4286CD0C3 CRC64;

Query Match 57.7%; Score 41; DB 11; Length 209;
Best Local Similarity 62.5%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPOQWFW 9
DB 66 PRPKQWGW 73

RESULT 18
Q9HXA6 PRELIMINARY; PRT; 261 AA.
ID Q9HXA6;
AC Q9HXA6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
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DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE HYPOTHETICAL PROTEIN PA3907.
GN PA3907.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01.
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.F., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Huynh W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL: AE004808; AG07294.1; --
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 261 AA; 29879 MW; 65556F1E9C330449 CRC64;

Query Match 57.7%; Score 41; DB 2; Length 261;
Best Local Similarity 62.5%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPQWFW 9
| | : | | |
Db 126 PFPHEWFW 133

RESULT 19
Q9PAVO PRELIMINARY; PRT; 286 AA.
AC Q9PAVO;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ACETYLXYLIAN ESTERASE.
GN XF2395.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Arya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frome M., Furian L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Marzocca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Paixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quagdo R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,

RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL: AE004048; AAF85194.1; --
DR InterPro: IPR002509; Polysac_deacet.
DR Pfam: PF01522; Polysac_deacet; 1.
KW Complete proteome.
SQ SEQUENCE 286 AA; 32166 MW; 013067BBEBEC173F CRC64;

Query Match 57.7%; Score 41; DB 2; Length 286;
Best Local Similarity 62.5%; Pred. No. 48;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQQWFW 11
| | | | :
Db 165 PQQWFWAL 172

RESULT 20
Q9AKK5 PRELIMINARY; PRT; 290 AA.
AC Q9AKK5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HTRB PROTEIN.
GN HTRB.
OS Rickettsia montana.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=33991;
RN [1]
RP SEQUENCE FROM N.A.
RA Andersson J.O., Andersson S.G.E.;
RT "Pseudogenes, junk DNA and the Dynamics of Rickettsia genomes.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ293330; CAC33650.1; --
SQ SEQUENCE 290 AA; 33635 MW; 9599E3C0C3C076F9 CRC64;

Query Match 57.7%; Score 41; DB 2; Length 290;
Best Local Similarity 55.6%; Pred. No. 48;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQWFW 9
: | | | |
Db 275 KQNPQWFW 283

RESULT 21
Q55507 PRELIMINARY; PRT; 291 AA.
AC Q55507;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE AMMONIUM TRANSPORT PROTEIN.
GN CYSQ OR SLL0895.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC6803;
RA Tabata S.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;

RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugitani M., Tabata S.,
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RL region from map positions 64% to 92% of the genome.",
RL DNA Res. 2:153-166(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugitani M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpō S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.,
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.",
RL DNA Res. 3:109-136(1996).
DR EMBL; D64006; BAA10862.1; -
DR InterPro; IPR000760; Inositol_P.
DR Pfam; PF00459; Inositol_P; 1.
DR PROSITE; PS00630; IMP_2; 1.
KW Complete proteome.
SQ SEQUENCE 291 AA; 32197 MW; F045980AA033E0E3 CRC64;

Query Match 57.7%; Score 41; DB 2; Length 291;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 RPKPQWFWL 11
DB 88 PLPQDQWVWII 97

RESULT 22

ID Q9HNN1 PRELIMINARY; PRT; 304 AA.
AC Q9HNN1;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE ACETYLTRANSFERASE HOMOLOG.
GN YVAI OR VNG2025G.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Balliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Madlocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1.",
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005096; AAG20189.1; -
DR InterPro; IPR001451; Hexapep_transf.
DR Pfam; PF00132; hexapep; 4.
KW Transferase; Complete proteome.
SQ SEQUENCE 304 AA; 32960 MW; 89EFA2E9A32A921 CRC64;

Query Match 57.7%; Score 41; DB 1; Length 304;
Best Local Similarity 56.7%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQWFW 9

Db 96 RSKPLOWLW 104
RESULT 23
Q9F849
ID Q9F849 PRELIMINARY; PRT; 392 AA.
AC Q9F849;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE CMIG.
OS Streptomyces venezuelae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=54571;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ISP5230;
RA He J., Magarvey M.A., Pirae M., Vining L.C.;
RT "Chloramphenicol Biosynthesis in Streptomyces venezuelae ISP5230:
RT Functions of Genes Upstream of pabAB.",
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF262220; AAG21974.1; -
SQ SEQUENCE 392 AA; 43167 MW; 75213EA4FA432CC4 CRC64;

Query Match 57.7%; Score 41; DB 2; Length 392;
Best Local Similarity 50.0%; Pred. No. 65;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQWFWL 10
DB 326 RPEPDRRWV 335

RESULT 24

ID P74332 PRELIMINARY; PRT; 529 AA.
AC P74332;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE HYPOTHETICAL 58.0 KDA PROTEIN.
GN SLR0959.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugitani M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpō S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.,
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.",
RL DNA Res. 3:109-136(1996).
DR EMBL; D90914; BAA18426.1; -
DR InterPro; IPR003675; Abi.
DR Pfam; PF02517; Abi; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 529 AA; 57992 MW; D2A1B702784AC6B7 CRC64;

Query Match 57.7%; Score 41; DB 2; Length 529;
Best Local Similarity 70.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQWFWL 10
DB 1111111111


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Db 368 RPLPQDWFLL 377
RESULT 25
Q9V6W6 PRELIMINARY; PRT; 45 AA.
AC Q9V6W6;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DE CG13352 PROTEIN.
GN CG13352.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler G., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003816; AAF58301.1; -.
DR FlyBase; FBgn0033894; CG13352.
SQ SEQUENCE 45 AA; 5134 MW; AAAAA100A982418DC CRC64;
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Query Match 56.3%; Score 40; DB 5; Length 45;
Best Local Similarity 62.5%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PKPQWFW 9
1:1:1:1
Db 14 PSPQWQW 21
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RESULT 26
Q9R129 PRELIMINARY; PRT; 154 AA.
AC Q9R129;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE RIBONUCLEASE 8 PRECURSOR (FRAGMENT).
GN R8.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Singhanian N.A., Dyer K.D., Zhang J., Deming M.S., Bonville C.A.,
RA Domachowski J.B., Rosenberg H.F.;
RT "Rapid evolution of the Ribonuclease A superfamily: adaptive expansion
of independent gene clusters in rats and mice.";
RL J. Mol. Evol. 0:0-0(1999).
DR EMBL; AF171646; AAD51666.1; -.
DR HSSP; P00656; ILSD.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnsaeA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
KW Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 >154 RIBONUCLEASE 8.
FT NON_TER 154 154
SQ SEQUENCE 154 AA; 17215 MW; F841AF2931FB2B67 CRC64;

Query Match 56.3%; Score 40; DB 11; Length 154;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RPKPQWFW 8
1:1:1:1
Db 27 RPTPSQWF 34

RESULT 27
Q9R132 PRELIMINARY; PRT; 155 AA.
AC Q9R132;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE RIBONUCLEASE 4 PRECURSOR (FRAGMENT).
GN R4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Singhanian N.A., Dyer K.D., Zhang J., Deming M.S., Bonville C.A.,
RA Domachowski J.B., Rosenberg H.F.;
RT "Rapid evolution of the Ribonuclease A superfamily: adaptive expansion
of independent gene clusters in rats and mice.";
RL J. Mol. Evol. 0:0-0(1999).
DR EMBL; AF171643; AAD51663.1; -.
DR HSSP; P00656; 1RBD.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnsaeA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 25 POTENTIAL.
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```
FT CHAIN 26 >155 RIBONUCLEASE 4.
FT NON_TER 155 155
SQ SEQUENCE 155 AA; 17223 MW; 5FDF6ECE0A15263C CRC64;

Query Match 56.3%; Score 40; DB 11; Length 155;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQWF 8
Db 27 RPTPSQWF 34

RESULT 28
Q9R131 ID Q9R131 PRELIMINARY; PRT; 155 AA.
AC Q9R131;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE RIBONUCLEASE 5 PRECURSOR (FRAGMENT).
GN R5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Singhanian N.A., Dyer K.D., Zhang J., Deming M.S., Bonville C.A.,
RA Domachowski J.B., Rosenberg H.F.;
RT "Rapid evolution of the Ribonuclease A superfamily: adaptive expansion
of independent gene clusters in rats and mice.";
RL J. Mol. Evol. 0:0-0(1999).
DR EMBL; AF171644; AAD51664.1; -.
DR HSSP; P00656; 1RBD.
DR InterPro; IPR001427; RNaseA.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 >155 RIBONUCLEASE 14.
FT NON_TER 155 155
SQ SEQUENCE 155 AA; 17332 MW; 4F7B83380AA0C6A8 CRC64;

Query Match 56.3%; Score 40; DB 11; Length 155;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQWF 8
Db 27 RPTPSQWF 34

RESULT 30
Q9JKI6 ID Q9JKI6 PRELIMINARY; PRT; 155 AA.
AC Q9JKI6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE EOSINOPHIL-ASSOCIATED RIBONUCLEASE 6 PRECURSOR.
GN EAR6.
OS Mus saxicola (Spiny mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10094;
RN [1]
RP SEQUENCE FROM N.A.
RA Singhanian N.A., Dyer K.D., Zhang J., Deming M.S., Bonville C.A.,
RA Domachowski J.B., Rosenberg H.F.;
RT "Rapid evolution of the Ribonuclease A superfamily: adaptive expansion
of independent gene clusters in rats and mice.";
RL J. Mol. Evol. 0:0-0(1999).
DR EMBL; AF171644; AAD51664.1; -.
DR HSSP; P00656; 1RBD.
DR InterPro; IPR001427; RNaseA.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 >155 RIBONUCLEASE 5.
FT NON_TER 155 155
SQ SEQUENCE 155 AA; 17189 MW; 36C6F3381DB92787 CRC64;

Query Match 56.3%; Score 40; DB 11; Length 155;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQWF 8
Db 27 RPTPSQWF 34

RESULT 29
Q9R127 ID Q9R127 PRELIMINARY; PRT; 155 AA.
AC Q9R127;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE RIBONUCLEASE 14 PRECURSOR (FRAGMENT).
GN R14.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
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RA Singhanian N.A., Dyer K.D., Zhang J., Deming M.S., Bonville C.A.,
RA Domachowski J.B., Rosenberg H.F.;
RT "Rapid evolution of the Ribonuclease A superfamily: adaptive expansion
of independent gene clusters in rats and mice.";
RL J. Mol. Evol. 0:0-0(1999).
DR EMBL; AF171644; AAD51664.1; -.
DR HSSP; P00656; 1RBD.
DR InterPro; IPR001427; RNaseA.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 >155 RIBONUCLEASE 14.
FT NON_TER 155 155
SQ SEQUENCE 155 AA; 17332 MW; 4F7B83380AA0C6A8 CRC64;

Query Match 56.3%; Score 40; DB 11; Length 155;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQWF 8
Db 27 RPTPSQWF 34

RESULT 30
Q9JKI6 ID Q9JKI6 PRELIMINARY; PRT; 155 AA.
AC Q9JKI6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE EOSINOPHIL-ASSOCIATED RIBONUCLEASE 6 PRECURSOR.
GN EAR6.
OS Mus saxicola (Spiny mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10094;
RN [1]
RP SEQUENCE FROM N.A.
RA Singhanian N.A., Dyer K.D., Zhang J., Deming M.S., Bonville C.A.,
RA Domachowski J.B., Rosenberg H.F.;
RT "Rapid evolution of the rodent eosinophil-associated ribonuclease gene
family by rapid gene sorting and positive selection.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR EMBL; AF238397; AAF67697.1; -.
DR InterPro; IPR001427; RNaseA.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
SQ SEQUENCE 155 AA; 17363 MW; 8B5401F0C26CA1EF CRC64;

Query Match 56.3%; Score 40; DB 11; Length 155;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQWF 8
Db 27 RPTPSQWF 34

RESULT 31
Q9KRQ9 ID Q9KRQ9 PRELIMINARY; PRT; 273 AA.
AC Q9KRQ9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
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DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HYPOTHETICAL PROTEIN VC1577.
GN VC1577.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Uitterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
DR EMBL: AE004235; AAF94731.1; -.
DR TIGR: VC1577; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 273 AA; 31087 MW; 9A21040F4DBA773E CRC64;

Query Match 56.3%; Score 40; DB 2; Length 273;
Best Local Similarity 71.4%; Pred. No. 65;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQFWL 10
Db 262 PEQWIL 268
|:|:|

RESULT 32
Q9JYV2 PRELIMINARY; PRT; 289 AA.
AC Q9JYV2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HTRB/MSBB FAMILY PROTEIN.
GN NMB1418.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Cittoni H., Clark E.B.,
RA Cotton M.D., Uitterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
DR EMBL: AE002491; AAF41779.1; -.
DR TIGR: NMB1418; -.
KW Complete proteome.
SQ SEQUENCE 289 AA; 33843 MW; 3BF100F050576512 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 289;
Best Local Similarity 60.0%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY 1 RPKPQQFWL 10
Db 265 REHQEQFWL 274
|:|:|

RESULT 33
Q9JUT4 PRELIMINARY; PRT; 289 AA.
AC Q9JUT4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE PUTATIVE ACETYLTRANSFERASE.
GN NMA1630.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491."
RL Nature 404:502-506(2000).
DR EMBL: AL162756; CAB84858.1; -.
KW Transferase; Complete proteome.
SQ SEQUENCE 289 AA; 33867 MW; 4FAE453B5A632C1D CRC64;

Query Match 56.3%; Score 40; DB 2; Length 289;
Best Local Similarity 60.0%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQFWL 10
Db 265 REHQEQFWL 274
|:|:|

RESULT 34
Q9ZCL1 PRELIMINARY; PRT; 290 AA.
AC Q9ZCL1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE LIPID A BIOSYNTHESIS LAUROYL ACYLTRANSFERASE (HTRB).
GN RP718.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria."
RL Nature 396:133-140(1998).
DR EMBL: AJ235273; CAA15149.1; -.
KW Complete proteome.
SQ SEQUENCE 290 AA; 33809 MW; 991FF50AB841D5B3 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 290;
```

Best Local Similarity 55.6%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKPQOWFW 9
Db 275 KONPAQWFW 283

RESULT 35

O9AKF0 PRELIMINARY; PRT; 290 AA.
AC O9AKF0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE HTRB PROTEIN.
GN HTRB.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=84-21C;
RA Andersson J.O., Andersson S.G.E.;
RT "Pseudogenes, junk DNA and the dynamics of Rickettsia genomes."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ293329; CAC33715.1; -.
SQ SEQUENCE 290 AA; 33550 MW; 9FC5D73E5CBE89A CRC64;

RESULT 36

O9AKA6 PRELIMINARY; PRT; 290 AA.
AC O9AKA6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE HTRB PROTEIN.
GN HTRB.
OS Rickettsia typhi.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=785;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WILMINGTON;
RA Andersson J.O., Andersson S.G.E.;
RT "Pseudogenes, junk DNA and the dynamics of Rickettsia genomes."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ293328; CAC33762.1; -.
SQ SEQUENCE 290 AA; 33814 MW; 2E9B2D3193B70EDD CRC64;

Query Match 56.3%; Score 40; DB 2; Length 290;
Best Local Similarity 55.6%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKPQOWFW 9
Db 275 KONPAQWFW 283

RESULT 37

O9AKA6 PRELIMINARY; PRT; 318 AA.
AC O9AKA6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE LIPID A BIOSYNTHESIS LAUROYL ACYLTRANSFERASE.
GN VC0213.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
EX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hick E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischman R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.W.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
cholerae."
RL Nature 406:477-483(2000).
DR EMBL; AE004111; AAF93389.1; -.
DR TIGR; VC0213; -.
KW Transferrase; Acyltransferase; Complete proteome.
SQ SEQUENCE 318 AA; 36542 MW; FE95D7A4C83106E1 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 290;
Best Local Similarity 55.6%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKPQOWFW 9
Db 275 KONPAQWFW 283

RESULT 38

O9AKA6 PRELIMINARY; PRT; 332 AA.
AC O9AKA6;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE LIPID A BIOSYNTHESIS (KDO)2-(LAUROYL)-LIPID IVA ACYLTRANSFERASE.
GN ECF4 OR MSBB.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98290540; PubMed=9628576;
RA Makino K., Ishii K., Yasunaga T., Hattori M., Yokoyama K.,
RA Yatsudo H.C., Kubota Y., Yamauchi Y., Iida T., Yamamoto K., Honda T.,
RA Han C., Ohtsubo A., Kasamatsu M., Hayashi T., Kuhara S., Shinagawa H.,
RT "Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an
enterohemorrhagic Escherichia coli O157:H7 derived from Sakai
outbreak."
RT DNA Res. 5:1-9(1998).
RN [2]
RP SEQUENCE OF 1-235 FROM N.A.
RC STRAIN=4304-PT14;
RA MEDLINE=98261495; PubMed=9596716;
RA Boerlin P., Chen S., Colbourne J.K., Johnson R., De Grandis S.,
RA Gyles C.;
RT "Evolution of enterohemorrhagic Escherichia coli hemolysin plasmids
and the locus for enterocyte effacement in shiga toxin-producing E.
coli."

RL Infect. Immun. 66:2553-2561(1998).

RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=EDL933;
RA Brundler W.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011549; BAA31840.1; -;
DR EMBL; AF043470; AAC24348.1; -;
DR EMBL; Y11275; CAA72141.1; -;
KW Transferase; Acyltransferase; Plasmid.
SQ SEQUENCE 332 AA; 37858 MW; 0D49F6B93E29E9A6 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 332;

Best Local Similarity 45.5%; Pred. No. 79;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11

||| |:: |::

Db 308 RPHPEQYTWIL 318

RESULT 39

ID Q9ZGU3 PRELIMINARY; PRT; 343 AA.
AC Q9ZGU3;

DT 01-MAY-1999 (T-EMBLrel. 10, Created)

DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)

DT 01-MAY-1999 (T-EMBLrel. 10, Last annotation update)

DE PUTATIVE ACYLTRANSFERASE.

GN L7029.

OS Escherichia coli O157:H7.

OC Plasmid pO157.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=83334;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EDL933;

RX MEDLINE=98391744; PubMed=9722640;

RA Burland V., Shao Y., Perna N.T., Plunkett G., Sofia H.J.,

Blattner F.R.;

RT "The complete DNA sequence and analysis of the large virulence plasmid

of Escherichia coli O157:H7.";

Nucleic Acids Res. 26:4196-4204(1998).

RL EMBL; AF074613; AAC70097.1; -;

KW Transferase; Acyltransferase; Plasmid.

SQ SEQUENCE 343 AA; 39074 MW; EB869F0D3D30DB6A CRC64;

Query Match 56.3%; Score 40; DB 2; Length 343;

Best Local Similarity 45.5%; Pred. No. 81;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11

||| |:: |::

Db 319 RPHPEQYTWIL 329

RESULT 40

ID P73727 PRELIMINARY; PRT; 363 AA.
AC P73727;

DT 01-FEB-1997 (T-EMBLrel. 02, Created)

DT 01-FEB-1997 (T-EMBLrel. 02, Last sequence update)

DT 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)

DE HYPOTHETICAL 41.5 KDA PROTEIN.

GN SLR1737.

OS Synechocystis sp. (strain PCC 6803).

OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.

OX NCBI_TaxID=1148;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97061201; PubMed=8905231;

RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

Miyajima N., Hirose M., Sugiyama M., Sasamoto S., Kimura T.,

Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,

Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,

Tabata S.;

RT "Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";

RL DNA Res. 3:109-136(1996).

DR EMBL; D90909; BAA17775.1; -;

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 363 AA; 41479 MW; 992646CFD9296D35 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 363;

Best Local Similarity 71.4%; Pred. No. 86;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQWFWM 10

|||||

Db 211 PSRWFWM 217

RESULT 41

ID Q9C5G0 PRELIMINARY; PRT; 367 AA.

AC Q9C5G0;

DT 01-JUN-2001 (T-EMBLrel. 17, Created)

DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)

DE PUTATIVE 11-ZINC FINGER PROTEIN.

GN F17F8.14.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,

Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,

Carinci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,

Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,

Theologis A.;

RT "Full length cDNA of gene F17F8.14 (GI:9755379).";

Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF360277; AAK25987.1; -;

DR InterPro; IPR003656; BED_finger.

DR InterPro; IPR002965; P-rich_extensn.

DR InterPro; IPR000822; Znf-C2H2.

DR Pfam; PF00096; zf-C2H2; 2.

DR PRINTS; PR01217; PRICHEXTENS.

DR SMART; SM00355; Znf_C2H2; 2.

DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.

KW DNA-binding; Metal-binding; zinc-finger.

SQ SEQUENCE 367 AA; 39801 MW; B9B2356EC3D063EE CRC64;

Query Match 56.3%; Score 40; DB 10; Length 367;

Best Local Similarity 71.4%; Pred. No. 87;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PKQQWF 8

|||||

Db 161 PRQQWY 167

RESULT 42

Q9FYI5

ID Q9FYI5 PRELIMINARY; PRT; 381 AA.

Q9FYI5;
AC 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DT F17F8.14.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C.,
RA Shinn P., Altafi H., Bei O., Chin C., Chiou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F17F8 from chromosome
RT I.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Dunn P., Khan S., Kim C.,
RA Walker M., Altafi H., Araujo R., Conn L., Conway A., Gonzalez A.,
RA Hansen N., Huizar L., Kremetskaia I., Lenz C., Li J., Liu S.,
RA Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G.,
RA Davis R., Federspiel N., Theologis A., Ecker J.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howng B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
DR EMBL; AC000107; AAF98186.1; -;
DR InterPro; IPR003656; BED_finger.
DR InterPro; IPR002965; P_rich_extensn.
DR InterPro; IPR000822; Znf-C2H2.
DR Pfam; PF00096; zf-C2H2; 2.
DR PRINTS; PR01217; PRICHEXTENS.
DR SMART; SM00355; Znf_C2H2; 2.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
KW DNA-binding; Metal-binding; Zinc-finger.
SQ SEQUENCE 381 AA; 41208 MW; ACE3B529D0022154 CRC64;

Query Match 56.3%; Score 40; DB 10; Length 381;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 PKPQQWF 8
DB 161 PRPQQWF 167

RESULT 43
Q9NRT2
ID Q9NRT2 PRELIMINARY; PRT; 411 AA.
AC Q9NRT2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE TWO-PORE DOMAIN POTASSIUM CHANNEL TREK-1.
GN TREK-1
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Meadows H.J., Benham C.D., Cairns W., Gloger I.S., Jennings C.,
RA Meadhurst A.D., Murdock P., Chapman C.G.;
RT "Cloning, localization and functional expression of the human ortholog
RT of the TREK-1 potassium channel.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF171068; AAF89743.1; -;
DR InterPro; IPR003280; 2porek_channel.
DR InterPro; IPR001622; Channel_pore_k.
DR PRINTS; PR01333; 2PORECHANNEL.
DR PRINTS; PR01499; TREKCHANNEL.
KW Ionic channel.
SQ SEQUENCE 411 AA; 45494 MW; FDE40CAB21B42A1C CRC64;
Query Match 56.3%; Score 40; DB 4; Length 411;
Best Local Similarity 55.6%; Pred. No. 97;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 3 KPQQWFWM 11
DB 271 KPQVWFWM 279
RESULT 44
Q9H8K3
ID Q9H8K3 PRELIMINARY; PRT; 639 AA.
AC Q9H8K3;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CDNA FLJ13515 FIS, CLONE PLACE1005595.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Nakamura H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
RT "NEO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK023577; BAB14613.1; -;
SQ SEQUENCE 639 AA; 68405 MW; 739FF6209738D832 CRC64;
Query Match 56.3%; Score 40; DB 4; Length 639;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 KPQQWFWM 10
DB 506 POPHNWVWL 514

```
RESULT 45
Q9V7L5 ID Q9V7L5 PRELIMINARY; PRT; 665 AA.
AC Q9V7L5; 2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CNG PROTEIN.
GN CNG OR CG7779.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier A., Fleischmann W.,
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobery C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeter F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.N., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003807; AAF58033.1; -.
DR FlyBase; FBgn014462; Cng.
DR InterPro; IPR001622; Channel_pore_K.
DR InterPro; IPR002025; Cng_membrane.
DR InterPro; IPR000595; cNMP_binding.
DR Pfam; PF00914; CNG_membrane; 1.
DR Pfam; PF00027; cNMP_binding; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; 1.
DR PROSITE; PS00889; cNMP_BINDING_2; 1.
DR PROSITE; PS50042; cNMP_BINDING_3; 1.
SQ SEQUENCE 665 AA; 75823 MW; 6E9FC9A7CA243660 CRC64;
```

Query Match 56.3%; Score 40; DB 5; Length 665;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;

```
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 RPKPQQWF 8
   |||||
DB 52 RPKPPDWF 59

RESULT 46
Q9NWY0 ID Q9NWY0 PRELIMINARY; PRT; 774 AA.
AC Q9NWY0; 2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE CDNA FLJ20539 FIS, CLONE KAT11311.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA Suzuki Y., Ohtsubashi M., Nishitani T., Shibahara T., Tanaka T.,
RA Nakamura Y., Iwaguchi T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK00546; BAA91245.1; -.
SQ SEQUENCE 774 AA; 83181 MW; 8C09E73DF939A7ED CRC64;
```

Query Match 56.3%; Score 40; DB 4; Length 774;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
QY 2 PKPQNFWL 10
   |||||
DB 641 PQPHNWVWL 649

RESULT 47
Q9CAX2 ID Q9CAX2 PRELIMINARY; PRT; 797 AA.
AC Q9CAX2; 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE HYPOTHETICAL 89.4 KDA PROTEIN.
GN F24K9.23.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansong W., Unselid M.,
RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choise N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erffie H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bagues M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauró C., Furnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
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RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:820-822(2000).
DR EMBL; AC008153; AAG51444.1; -.
KW Hypothetical protein.
SQ SEQUENCE 797 AA; 89393 MW; 2E68459765D08B52 CRC64;

Query Match 56.3%; Score 40; DB 10; Length 797;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PKPQOWFW 9
|| :|||
Db 188 PKAYEWF 195

RESULT 48
Q9HE57 PRELIMINARY; PRT; 937 AA.
AC Q9HE57;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE RELATED TO SL52 PROTEIN.
GN B2F7.50.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL451013; CAC18157.1; -.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001230; Prenyltn.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS00181; FBOX; 1.
DR PROSITE; PS00294; PRENYLATIN; UNKNOWN 1.
SQ SEQUENCE 937 AA; 104264 MW; 2F6D7A68FA851FA7 CRC64;

Query Match 56.3%; Score 40; DB 3; Length 937;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PKPQOWFW 11
|| :|||
Db 349 PKPAEWF 358

RESULT 49
Q9RV51 PRELIMINARY; PRT; 548 AA.
ID Q9RV51;
AC Q9RV51;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 59.4 KDA PROTEIN.
GN DR1179.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI.
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans RL.";
RL Science 286:1571-1577(1999).
DR EMBL; AE001967; AAF10758.1; -.
DR TIGR; DR1179; -.
DR InterPro; IPR001736; PLD.
DR Pfam; PF00614; PLDC; 2.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 548 AA; 59442 MW; AEA550EDBEE981B0 CRC64;

Query Match 55.6%; Score 39.5; DB 2; Length 548;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 RPKPOQFW 10
|| :|||
Db 521 RVPQEW-WL 529

RESULT 50
Q79563 PRELIMINARY; PRT; 55 AA.
ID Q79563
AC Q79563;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ATPASE SUBUNIT 8.
GN ATP8.
OS Mustelus manazo.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
OC Mustelus.
OX NCBI_TaxID=79736;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RA Cao Y., Waddell P.J., Okada N., Hasegawa M.;
RT "The complete mitochondrial DNA sequence of the shark (Mustelus
RT manazo): Evaluating rooting contradictions to living bony
RT vertebrates.";
RL Mol. Biol. Evol. 0:0-0(1998).
DR EMBL; AB015962; BAA33040.1; -.
DR InterPro; IPR001421; ATP-synt_8.
DR Pfam; PF00895; ATP-synt_8; 1.
KW Mitochondrion.
SQ SEQUENCE 55 AA; 6616 MW; 52DB099625A0D75D CRC64;

Query Match 54.9%; Score 39; DB 8; Length 55;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKPOQFW 9
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DB 44 KPKPNPNW 52
RESULT 51
Q69572 PRELIMINARY; PRT; 99 AA.
AC Q69572;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
DE U96 PROTEIN.
GN U96 OR HCLF1.
OS Human herpesvirus 6.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=10368;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=95266321; PubMed=7747482;
RA Compels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
RA Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
RT "The DNA sequence of human herpesvirus-6: structure, coding content,
RT and genome evolution."
RL J. Virol. 209:29-51(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=90080132; PubMed=2152817;
RA Lawrence G.L., Chee M., Craxton M.A., Compels U.A., Honess R.W.,
RA Barrell B.G.;
RT "Human herpesvirus 6 is closely related to human cytomegalovirus."
RL J. Virol. 64:287-299(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=91237802; PubMed=1851860;
RA Chang C.K., Balachandran N.;
RT "Identifying a phosphoprotein of human herpesvirus 6."
RL J. Virol. 65:2884-2894(1991).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=91333007; PubMed=1651403;
RA Teo I.A., Griffin B.E., Jones M.D.;
RT "Characterization of the DNA polymerase gene of human herpesvirus 6."
RL J. Virol. 65:4670-4680(1991).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=91226542; PubMed=1851252;
RA Thomson B.J., Efstathiou S., Honess R.W.;
RT "Acquisition of the human adeno-associated virus type-2 rep gene by
RT human herpesvirus type-6."
RL Nature 351:78-80(1991).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=91374590; PubMed=1654446;
RA Martin M.E., Nicholas J., Thomson B.J., Newman C., Honess R.W.;
RT "Identification of a transactivating function mapping to the putative
RT immediate-early locus of human herpesvirus 6."
RL J. Virol. 65:5381-5390(1991).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=92333249; PubMed=1321206;
RA Efstathiou S., Lawrence G.L., Brown C.M., Barrell B.G.;
RT "Identification of homologues to the human cytomegalovirus US22 gene
RT family in human herpesvirus 6."
RL J. Gen. Virol. 73:1661-1671(1992).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=92148942; PubMed=1310766;
RA Geng Y., Chandran B., Josephs S.F., Wood C.;
RT "Identification and characterization of a human herpesvirus 6 gene
RT segment that trans activates the human immunodeficiency virus type 1
RT promoter."
RL J. Virol. 66:1564-1570(1992).
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=93091236; PubMed=1333836;
RA Compels U.A., Carss A.L., Sun N., Arrand J.R.;
RT "Infectivity determinants encoded in a conserved gene block of human
RT herpesvirus-6."
RL DNA Seq. 3:25-39(1992).
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=92260671; PubMed=1374813;
RA Neipel F., Ellinger K., Fleckenstein B.;
RT "Gene for the major antigenic structural protein (p100) of human
RT herpesvirus 6."
RL J. Virol. 66:3918-3924(1992).
RN [11]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=92333248; PubMed=1321205;
RA Thomson B.J., Honess R.W.;
RT "The right end of the unique region of the genome of human herpesvirus
RT 6 U1102 contains a candidate immediate early gene enhancer and a
RT homologue of the human cytomegalovirus US22 gene family."
RL J. Gen. Virol. 73:1649-1660(1992).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=93187613; PubMed=8383182;
RA Ellinger K., Neipel F., Foa-Tomasi L., Campadelli-Fiume G.,
RA Fleckenstein B.;
RT "The glycoprotein B homologue of human herpesvirus 6."
RL J. Gen. Virol. 74:495-500(1993).
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=93224882; PubMed=8385692;
RA Compels U.A., Carrigan D.R., Carss A.L., Arno J.;
RT "Two groups of human herpesvirus 6 identified by sequence analyses of
RT laboratory strains and variants from Hodgkin's lymphoma and bone
RT marrow transplant patients."
RL J. Gen. Virol. 74:613-622(1993).
RN [14]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=93389439; PubMed=8397282;
RA Liu D.X., Compels U.A., Nicholas J., Lelliott C.;
RT "Identification and expression of the human herpesvirus 6 glycoprotein
RT H and interaction with an accessory 40K glycoprotein."
RL J. Gen. Virol. 74:1847-1857(1993).
RN [15]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=94025558; PubMed=7692666;
RA Liu D.X., Compels U.A., Foa-Tomasi L., Campadelli-Fiume G.;
RT "Human herpesvirus-6 glycoprotein H and L homologs are components of
RT the gp100 complex and the gH external domain is the target for
RT neutralizing monoclonal antibodies."
RL Virology 197:12-22(1993).
RN [16]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=93331710; PubMed=7687803;
RA Pellett P., Sanchez-Martinez D., Dominguez G., Black J.B., Anton E.,
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RA Greenamoyer C., Dambaugh T.R.;
RT "A strongly immunoreactive virion protein of human herpesvirus 6
RT variant B strain Z29: identification and characterization of the gene
RT and mapping of a variant-specific monoclonal antibody reactive
RT epitope.";
RL Virology 195:521-531(1993).
[17]
RN
RP SEQUENCE FROM N.A.
RX STRAIN-U1102, VARIANT A;
RX MEDLINE-93323202; PubMed=7687301;
RA Pfeiffer B., Berneman Z.N., Neipel F., Chang C.K., Tirwatnapong S.,
RA Chandran B.;
RT "Identification and mapping of the gene encoding the glycoprotein
RT complex gp82-gp105 of human herpesvirus 6 and mapping of the
RT neutralizing epitope recognized by monoclonal antibodies.";
RL J. Virol. 67:4611-4620(1993).
[18]
RN
RP SEQUENCE FROM N.A.
RX STRAIN-U1102, VARIANT A;
RX MEDLINE-95146989; PubMed=7844567;
RA Compels U.A., Macaulay H.A.;
RT "Characterization of human telomeric repeat sequences from human
RT herpesvirus 6 and relationship to replication.";
RL J. Gen. Virol. 76:451-458(1995).
[19]
RN
RP SEQUENCE FROM N.A.
RX STRAIN-U1102, VARIANT A;
RX MEDLINE-94047392; PubMed=8230490;
RA Dewhurst S., Dollard S.C., Pellett P.E., Dambaugh T.R.;
RT "Identification of a lytic-phage origin of DNA replication in human
RT herpesvirus 6B strain Z29.";
RL J. Virol. 67:7680-7683(1993).
[20]
RN
RP SEQUENCE FROM N.A.
RX STRAIN-U1102, VARIANT A;
RA Nicholas J., Martin M.;
RT "Nucleotide sequence analysis of a 38.5-kilobase-pair region of the
RT genome of human herpesvirus 6 encoding human cytomegalovirus
RT immediate-early gene homologs and transactivating functions.";
RL J. Virol. 68:597-610(1994).
[22]
RN
RP SEQUENCE FROM N.A.
RX STRAIN-U1102, VARIANT A;
RX MEDLINE-94202284; PubMed=8151768;
RA Schiwe U., Neipel F., Schreiner D., Fleckenstein B.;
RT "Structure and transcription of an immediate-early region in the human
RT herpesvirus 6 genome.";
RL J. Virol. 68:2978-2985(1994).
[23]
RN
RP SEQUENCE FROM N.A.
RX STRAIN-U1102, VARIANT A;
RX MEDLINE-94181269; PubMed=8134119;
RA Thompson J., Choudhury S., Kashanchi F., Doniger J., Berneman Z.,
RA Frenkel N., Rosenthal L.J.;
Query Match 54.9%; Score 39; DB 12; Length 99;
Best Local Similarity 50.0%; Pred. No. 35;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 4 PQQWFWM 11
Db 86 PSRWYWL 93
RESULT 52
Q55572 PRELIMINARY; PRT; 208 AA.
ID Q55572
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Q55572;
AC 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE HYPOTHETICAL 23.3 KDA PROTEIN.
GN SL0156.
OS Synchocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PCC6803;
RA Tabata S.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
[2]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE-96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugiyura M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synchocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
[3]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE-97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirose M., Sugiyura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synchocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
KW EMBL; D63999; BAA10075.1; -.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 208 AA; 23268 MW; 327BE1A8BCBBA0E CRC64;

Query Match 54.9%; Score 39; DB 2; Length 208;
Best Local Similarity 55.6%; Pred. No. 72;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 2 PKPQWFWM 10
Db 34 PSPQPMQWI 42
RESULT 53
Q55572 PRELIMINARY; PRT; 341 AA.
ID Q9JSJ3
AC Q9JSJ3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE ACYLTRANSFERASE.
GN HTRB_2.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-J138;
RX MEDLINE-20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CML029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
KW EMBL; AP002545; BAA98308.1; -.
SQ SEQUENCE 341 AA; 39044 MW; ECF7A78E1615896A CRC64;
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Query Match          54.9%   Score 39; DB 2; Length 341;
Best Local Similarity 50.0%   Pred. No. 1.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQWFNL 10
   :|:|:|
Db 180 QPEQWMI 187

RESULT 54
Q9PIW6          PRELIMINARY; PRT; 361 AA.
AC Q9PIW6
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ALPHA-(1.3/1.4)-FUCOSYLTRANSFERASE.
GN FUT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP Nishihara S.;
SEQUENCE FROM N.A.
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9190658; PubMed=10089211;
RA Nishihara S., Hiraga T., Ikehara Y., Iwasaki H., Kudo T., Yazawa S.,
RA Morozumi K., Suda Y., Narimatsu H.;
RT "Molecular behavior of mutant Lewis enzymes in vivo.";
DR EMBL; AB043998; BAA96390.1; -;
DR InterPro: IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
FT VARIANT 20 20 R->L
SQ SEQUENCE 361 AA; 42160 MW; 6157E6B63BC34E5E CRC64;

Query Match          54.9%   Score 39; DB 4; Length 361;
Best Local Similarity 55.6%   Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQWFNW 9
   ||:|:|
Db 126 RPOGQWMI 134

RESULT 55
Q9F669          PRELIMINARY; PRT; 383 AA.
AC Q9F669
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PILIN BIOGENESIS PROTEIN PILC.
GN PILC.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WCS365;
RA Camacho Carvajal M.M., de Priester W., Lugtenberg B.J.J.,
RA Bloemberg G.V.;
RT "Involvement of type 4 pili of Pseudomonas fluorescens in tomato root
RT colonization.";
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF297457; AAG18588.1; -.
DR InterPro: IPR001992; Bact_secr_systII.
DR ProPro: IPR003004; Bact_GSPF.
DR Pfam; PF00482; GSPIL_F; 1.
DR PRINTS; PR00812; BCTERIALGSPF.
DR PROSITE; PS00874; T2SP_F; 1.
SQ SEQUENCE 383 AA; 41752 MW; B0556D4ACD8FCDDF CRC64;

Query Match          54.9%   Score 39; DB 2; Length 333;
Best Local Similarity 71.4%   Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 QOWFWLM 11
   ||:|:|
Db 200 QOWWVWM 206

RESULT 56
Q9ZJ55          PRELIMINARY; PRT; 412 AA.
AC Q9ZJ55
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE UBIQUINOL CYTOCHROME C OXIDOREDUCTASE, CYTOCHROME B SUBUNIT.
GN CYTB OR PETB OR JHPL460.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RN Nature 397:176-180(1999).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
DR EMBL; AE001568; AAD07046.1; -.
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam; PF00032; cytochrome_b_c1.
DR Pfam; PF00033; cytochrome_b_n; 1.
DR PROSITE; PS00193; CYTOCHROME_B_OO; UNKNOWN_1.
KW Complete proteome; Electron transport; Heme; Respiratory chain;
KW Transmembrane.
SQ SEQUENCE 412 AA; 47631 MW; 363F3CDB3638B0BD CRC64;

Query Match          54.9%   Score 39; DB 2; Length 412;
Best Local Similarity 54.5%   Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPKPQWFNLM 11
   ||:|:|:|
Db 349 RPAFVWFLL 359

RESULT 57
Q9HU99          PRELIMINARY; PRT; 416 AA.
ID Q9HU99
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Q9HU99;
01-MAR-2001 (TReMBLrel. 16, Created)
01-MAR-2001 (TReMBLrel. 16, Last sequence update)
01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE PROBABLE OXIDOREDUCTASE.
GN PAS084.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoquchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004921; AG08469.1; -.
DR InterPro; IPR000927; DAO.
DR InterPro; IPR000205; NAD_binding.
DR InterPro; IPR000309; TrkA_Kuptake.
DR Pfam; PF01266; DAO; 1.
DR PRINTS; PR00335; KUPTAKETRA.
KW Complete proteome.
SQ SEQUENCE 416 AA; 44767 MW; 1EDE536FD784FF6F CRC64;

Query Match 54.9%; Score 39; DB 2; Length 416;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 1;
QY 1 RPK--PQWFWLM 11
II: I I I I I:
Db 80 RRLDPAQRWLL 92

RESULT 58
Q9PIU6 PRELIMINARY; PRT; 452 AA.
AC Q9PIU6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE PUTATIVE INTEGRAL MEMBRANE PROTEIN WITH HAEMOLYSIN DOMAIN.
GN CJ0183.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL; AL139074; CAB72666.1; -.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR002550; DUF21.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF01595; DUF21; 1.
DR SMART; SM00116; CBS; 2.

KW Complete proteome.
SQ SEQUENCE 452 AA; 51010 MW; E508BD021CA5C79E CRC64;

Query Match 54.9%; Score 39; DB 2; Length 452;
Best Local Similarity 44.4%; Pred. No. 1.5e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 3 KPOQWFWLM 11
II: I I I I I:
Db 160 RPLHFWFWML 168

RESULT 59
Q9K217 PRELIMINARY; PRT; 462 AA.
AC Q9K217;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE LIPID A BIOSYNTHESIS LAUROYL ACYLTRANSFERASE, PUTATIVE.
GN CP0676.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T.,
RA Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B.,
RA Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J.,
RA McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
DR EMBL; AE002225; AAF38487.1; -.
DR TIGR; CP0676; -.
DR InterPro; IPR000504; RRM.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
KW Transferase; Acyltransferase.
SQ SEQUENCE 462 AA; 52624 MW; C31CD0C9B01E13DE CRC64;

Query Match 54.9%; Score 39; DB 2; Length 462;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 KPOQWFWL 10
II: I I I I I:
Db 301 QPEQWFWL 308

RESULT 60
Q9Z983 PRELIMINARY; PRT; 467 AA.
AC Q9Z983;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ACYLTRANSFERASE.
GN HTRB OR CPN0098.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Ollinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";

RA	Nat. Genet.	21:385-389(1999).
RA	EMBL; AE001596;	AAD18251.1; -.
KW	Transferase;	Complete proteome.
SQ	SEQUENCE	467 AA; 53193 MW; D3C7C284E922DD0D CRC64;
Query Match 54.9%; Score 39; DB 2; Length 467;		
Best Local Similarity 50.0%; Pred. No. 1.6e+02;		
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;		
QY	3 KPQQWFNL 10	
DB	: :	
DB	301 QPEQMMWI 308	
RESULT 61		
Q9VJN6	PRELIMINARY; PRT; 480 AA.	
ID	Q9VDN6	
AC	Q9VDN6;	
DT	01-NOV-1999 (TrEMBLrel. 12, Created)	
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)	
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)	
DE	HYPOTHETICAL 54.4 KDA PROTEIN APE0879.	
GN	APE0879.	
OS	Aeropyrum pernix.	
OC	Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;	
OC	Aeropyrum.	
OX	NCBI_TaxID=56636;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-K1;	
RC	MEDLINE=99310339; PubMed=10382966;	
RA	Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,	
RA	Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankaï A., Kosugi H.,	
RA	Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,	
RA	Takamizaki M., Masuda S., Funanishi T., Tanaka T., Kubota Y.,	
RA	Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,	
RA	Nakamura Y., Nomura N., Sakō Y., Kikuchi H.;	
RT	"Complete genome sequence of an aerobic hyper-thermophilic	
RT	crenarchaeon, Aeropyrum pernix K1.";	
RT	DNA Res. 6:83-101(1999).	
DR	ENBL; AP00060; BAA79861.1; -.	
KW	Hypothetical protein; Complete proteome.	
SQ	SEQUENCE 480 AA; 54363 MW; C8F617CCFE11627E CRC64;	
Query Match 54.9%; Score 39; DB 1; Length 480;		
Best Local Similarity 55.6%; Pred. No. 1.6e+02;		
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;		
QY	3 KPQQWFNL 11	
DB	: :	
DB	283 KPQQWFNI 291	
RESULT 62		
Q9VJ81	PRELIMINARY; PRT; 499 AA.	
ID	Q9VJ81	
AC	Q9VJ81;	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)	
DE	CG10178 PROTEIN.	
GN	CG10178.	
OS	Drosophila melanogaster (Fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephydroidea; Drosophilidae; Drosophila.	
OX	NCBI_TaxID=7227;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-BERKELEY;	
RC	MEDLINE=20196006; PubMed=107311132;	
RT	"A novel human cytchrome p450 4F isoform (CYP4F11): cDNA cloning,	

RT expression, and genomic structural characterization.";
RL Genomics 68:161-166(2000).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL: AF236085; AAG15889.1; -;
DR InterPro: IPR001128; Cyt_P450.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 524 AA; 60209 MW; 627774C85904B918 CRC64;

Query Match 54.9%; Score 39; DB 4; Length 524;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPQPQWFW 9
: | | | |
DB 53 QPQKQWFW 61

RESULT 64
O83145 PRELIMINARY; PRT; 525 AA.
ID O83145;
AC O83145;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE LICC PROTEIN (LICC).
GN TP0107.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., Mleod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
spirochete.";
RL Science 281:375-388(1998).
DR EMBL: AE001195; AAC26555.1; -;
DR TIGR: TP0107; -;
DR InterPro: IPR001245; TYR_kin.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW Complete proteome.
SQ SEQUENCE 525 AA; 61044 MW; E46DDCACC79BAB10 CRC64;

Query Match 54.9%; Score 39; DB 2; Length 525;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPQPQWFW 9
: | | | |
DB 173 RPNRAWFW 181

RESULT 65
Q9PUA3 PRELIMINARY; PRT; 778 AA.
ID Q9PUA3;
AC Q9PUA3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CIRCADIAN RHYTHMICITY PROTEIN CLOCK.
OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim J.S., Drysdale T.A.;
RT "Sequencing of Xenopus circadian clock gene, xClock.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF203107; AAF12827.1; -;
DR HSSP: P36956; 1AM9.
DR InterPro: IPR001092; HLH_dim.
DR InterPro: IPR003015; HLH_Myc.
DR InterPro: IPR001067; Nucleinslocator.
DR InterPro: IPR001610; PAC.
DR InterPro: IPR000014; PAS.
DR Pfam: PF00010; HLH; 1.
DR Pfam: PF00785; PAC; 1.
DR Pfam: PF00989; PAS; 2.
DR PRINTS: PR00785; NCTRNLOCATR.
DR SMART: SM00353; HLH; 1.
DR SMART: SM00086; PAC; 1.
DR SMART: SM00091; PAS; 2.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
SQ SEQUENCE 778 AA; 87976 MW; A4D609E88A5F35C4 CRC64;

Query Match 54.9%; Score 39; DB 13; Length 778;
Best Local Similarity 75.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPQQWFWL 10
: | | | | |
DB 335 KQQQWIWL 342

RESULT 66
Q9I906 PRELIMINARY; PRT; 825 AA.
ID Q9I906;
AC Q9I906;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CLOCK.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RETINA;
RA Zhu H., LaRue S., Whitely A., Steeves T.D.L., Takahashi J.S.,
RA Green C.B.;
RT "The Xenopus Clock gene is constitutively expressed in retinal
photoreceptors.";
RL Brain Res. Mol. Brain Res. 0:0-0(2000).
DR EMBL: AF227985; AAF34772.1; -;
DR InterPro: IPR001092; HLH_dim.
DR InterPro: IPR003015; HLH_Myc.
DR InterPro: IPR001067; Nucleinslocator.
DR InterPro: IPR001610; PAC.
DR InterPro: IPR000014; PAS.
DR Pfam: PF00785; PAC; 1.
DR Pfam: PF00989; PAS; 2.
DR PRINTS: PR00785; NCTRNLOCATR.
DR SMART: SM00353; HLH; 1.
DR SMART: SM00086; PAC; 1.
DR SMART: SM00091; PAS; 2.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
SQ SEQUENCE 825 AA; 93269 MW; 0F657C3D9C5F24E0 CRC64;

Query Match 54.9%; Score 39; DB 13; Length 825;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFNL 10
| | | | |
Db 335 KGQQWNL 342

RESULT 67

Q9U6M1 ID Q9U6M1 PRELIMINARY; PRT; 827 AA.
AC Q9U6M1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE J-BINDING PROTEIN (FRAGMENT).
GN JBPI.
OS Leishmania tarentolae (Saurleishmania tarentolae).
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TAR IVA;
RX MEDLINE=20031668; PubMed=10562569;
RA Cross M., Kieft R., Sabatini R., Wilm M., de Kort M.,
RA van der Marel G.A., van Boom J.H., van Leeuwen F., Borst P.;
RT "The modified base J is the target for a novel DNA-binding in
RT kinetoplastid protozoans";
RL EMBO J. 18:6573-6581(1999).
DR EMBL; AF182401; AAF01743.1; -.
FT NON_TER 827
SQ SEQUENCE 827 AA; 93403 MW; 5A4B502DE70A4BFE CRC64;

Query Match 54.9%; Score 39; DB 5; Length 827;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOQWFNL 11
| | : | | | |
Db 485 PKEEQAFWM 494

RESULT 68

Q9IAI1 ID Q9IAI1 PRELIMINARY; PRT; 852 AA.
AC Q9IAI1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE BHLH/PAS TRANSCRIPTION FACTOR CLOCK.
GN CLOCK.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RT Noakes M.A., Campbell M., Van Hest B.J.;
RT "A Chicken Clock Gene Homolog";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF201076; AAF26365.1; -.
DR InterPro; IPR001092; HLH_dlm.
DR InterPro; IPR003015; HLH_Myc.
DR InterPro; IPR001067; Nucleosylator.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR PRINTS; PR00785; NCTRNLOCATR.

DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
SQ SEQUENCE 852 AA; 96072 MW; 2B4697D7DA72CDOB CRC64;

Query Match 54.9%; Score 39; DB 13; Length 852;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFNL 10
| | | | |
Db 344 KGQQWNL 351

RESULT 69

Q9W6Q2 ID Q9W6Q2 PRELIMINARY; PRT; 853 AA.
AC Q9W6Q2;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CLOCK PROTEIN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Chong N.W.S., Klein D.C.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF144425; AAD32860.1; -.
DR HSP; P36956; IAW9.
DR InterPro; IPR001092; HLH_dlm.
DR InterPro; IPR003015; HLH_Myc.
DR InterPro; IPR001067; Nucleosylator.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAC; 2.
DR PRINTS; PR00785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
SQ SEQUENCE 853 AA; 96297 MW; 5349C5C1F7293C97 CRC64;

Query Match 54.9%; Score 39; DB 13; Length 853;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFNL 10
| | | | |
Db 344 KGQQWNL 351

RESULT 70

Q93244 ID Q93244 PRELIMINARY; PRT; 854 AA.
AC Q93244;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ANDROGEN RECEPTOR ALPHA.
GN AR-ALPHA.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;

RL Brain Res. Mol. Brain Res. 0:0-0(1999).

DR EMBL; AF132531; AAD43283.1; -

DR HSSP; P36956; IAM9.

DR InterPro; IPR001092; HLH_dim.

DR InterPro; IPR003015; NucleinsLocator.

DR InterPro; IPR001067; NucleinsLocator.

DR InterPro; IPR001610; PAC.

DR InterPro; IPR000014; PAC.

DR Pfam; PF00785; PAC; 1.

DR Pfam; PF00989; PAC; 2.

DR PRINTS; PR00785; NCTNSLOCATR.

DR SMART; SM00353; HLH; 1.

DR SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAC; 2.

DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.

SQ SEQUENCE 875 AA; 98725 MW; 04DFE81D79747A4 CRC64;

Query Match 54.9%; Score 39; DB 13; Length 875;

Best Local Similarity 75.0%; Pred. No. 2.9e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQFWL 10

Db 344 KGOQWIL 351

RESULT 74

ID Q9W6J4

AC Q9W6J4 PRELIMINARY; PRT; 893 AA.

DT 01-NOV-1999 (TEMBLrel. 12, Created)

DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)

DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)

DE TRANSCRIPTION FACTOR CLOCK.

OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

OC Cypriniformes; Cyprinidae; Rasbora; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP MEDLINE-99212319; PubMed-10196586;

RA Whitmore D., Foulkes N.S., Strahle U., Sassone-Corsi P.;

RT "Zebrafish Clock rhythmic expression reveals independent peripheral

circadian oscillators";

RL Nat. Neurosci. 1:701-707(1998).

RN [2]

RP SEQUENCE FROM N.A.

RA Whitmore D., Foulkes N.S., Strahle U., Sassone-Corsi P.;

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF133306; AAD27749.1; -

DR InterPro; IPR000014; PAC.

DR InterPro; IPR001067; NucleinsLocator.

DR InterPro; IPR001092; HLH_dim.

DR InterPro; IPR001610; PAC.

DR InterPro; IPR003015; HLH_Myc.

DR Pfam; PF00010; HLH; 1.

DR Pfam; PF00785; PAC; 1.

DR Pfam; PF00989; PAC; 2.

DR PRINTS; PR00785; NCTNSLOCATR.

DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.

DR SMART; SM00353; HLH; 1.

DR SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAC; 2.

SQ SEQUENCE 893 AA; 100945 MW; B74778854457E14A CRC64;

Query Match 54.9%; Score 39; DB 13; Length 893;

Best Local Similarity 75.0%; Pred. No. 3e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQFWL 10

Db 335 KGOQWIL 342

RESULT 75

ID Q9VSB0

AC Q9VSB0 PRELIMINARY; PRT; 1023 AA.

DT 01-MAY-2000 (TEMBLrel. 13, Created)

DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)

DE CLK PROTEIN.

GN CLK OR CG7391.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY.

RA MEDLINE-20196006; PubMed-10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Adair J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,

RA Burtis K.C., Busch D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harbison M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Lilang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleab J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster";

RL Science 287:2185-2195(2000).

DR EMBL; AE003557; AAF50516.1; -

DR FlyBase; FBgn0023076; CLK.

DR InterPro; IPR001092; HLH_dim.

DR InterPro; IPR003015; HLH_Myc.

DR InterPro; IPR001067; NucleinsLocator.

DR InterPro; IPR001610; PAC.

DR InterPro; IPR000014; PAC.

DR Pfam; PF00010; HLH; 1.

DR Pfam; PF00785; PAC; 1.

DR Pfam; PF00989; PAC; 2.

DR PRINTS; PR00785; NCTNSLOCATR.

DR SMART; SM00353; HLH; 1.

DR SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAS; 2;
DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN 1;
SQ SEQUENCE 1023 AA; 115691 MW; D4D271038C0D536D CRC64;

Query Match 54.9%; Score 39; DB 5; Length 1023;
Best Local Similarity 75.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFWM 10
:|||||
DB 331 KGQOWIWL 338

RESULT 76

ID Q53785 PRELIMINARY; PRT; 1219 AA.
AC Q53785;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE TRANSMEMBRANE PROTEIN.
GN WHB2.
OS Streptomyces aureofaciens.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1894;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98234302; PubMed=9565673;
RA Homerova D., Sprusansky O., Potuckova L., Sevcikova B., Novakova R.,
RA Rezuchova B., Kormanec J.;
RT "The gene downstream of Streptomyces aureofaciens whbB encodes a large
RT protein with proposed transmembrane localization, and is induced by
RT glucose.";
RL Biochim. Biophys. Acta 1397:151-155(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Kormanec J., Gabaajova R., Homerova D., Rezuchova B.;
RA Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; L22864; AAC18892.1; -.
DR InterPro; IPR001173; Glycos_transf_2.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Transmembrane.
SQ SEQUENCE 1219 AA; 128208 MW; 0CEA4C9617ACED32 CRC64;

Query Match 54.9%; Score 39; DB 2; Length 1219;
Best Local Similarity 55.6%; Pred. No. 4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFWM 11
:|||||
DB 136 EPVOWIWL 144

RESULT 77

ID Q9FVG4 PRELIMINARY; PRT; 673 AA.
AC Q9FVG4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE TRANSPOSASE DOPA.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W22; TRANSPOSON=DOPPIA;
RA Bercury S.D., Walker E.L.;

RT "Molecular analysis of the structure and function of the Dopia
RT transposable element of maize.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187823; AAG17044.1; -.
SQ SEQUENCE 673 AA; 75138 MW; 46241159B444D59D CRC64;

Query Match 54.2%; Score 38.5; DB 10; Length 673;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 RPK-PQOWFW 9
:|||||
DB 623 RPRLPRPWF 632

RESULT 78

Q9HZ24
ID Q9HZ24 PRELIMINARY; PRT; 105 AA.
AC Q9HZ24;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE HYPOTHETICAL PROTEIN PA3216.
GN PA3216.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Miziouchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004745; AAG06604.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 105 AA; 12396 MW; D98630BC71A85177 CRC64;

Query Match 53.5%; Score 38; DB 2; Length 105;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QQFWLM 11
:|||||
DB 50 QQWLWL 56

RESULT 79

ID Q62024 PRELIMINARY; PRT; 122 AA.
AC Q62024; P97339;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PP52 (FRAGMENT).
GN LSP1 OR PP52.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=96435912; PubMed=8838798;

RA Thompson A.A., Omori S.A., Gilly M.J., May W., Gordon M.S., Wood W.J.,
RA Miyoshi E., Malone C.S., Gimble J., Kincade P.W., Denny C.T., Wall R.;
RT "Alternatively spliced exons encode the tissue-specific 5' termini of
RT leukocyte pp52 and stromal cell S37 mRNA isoforms.";
RL Genomics 32:352-357(1996).
DR EMBL; U30942; AAB37543.1; -.
DR EMBL; U30940; AAB37543.1; JOINED.
DR EMBL; U30941; AAB37543.1; JOINED.
DR MGD; MGI:96832; Lsp1.
DR InterPro; IPR002211; Lymphspecific.
DR PRINTS; PR01083; LYMPHSPECIFIC.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14237 MW; AB6AA7AF4FE7D3B1 CRC64;

Query Match 53.5%; Score 38; DB 11; Length 122;
Best Local Similarity 55.6%; Pred. No. 61;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
Db :|:|:|
90 KPEPQQFW 98

RESULT 80
Q62023 PRELIMINARY; PRT; 124 AA.
AC Q62023;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE PP52 PROTEIN (FRAGMENT).
GN LSP1 OR PP52.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=96435912; PubMed=8838798;
RA Thompson A.A., Omori S.A., Gilly M.J., May W., Gordon M.S., Wood W.J.,
RA Miyoshi E., Malone C.S., Gimble J., Kincade P.W., Denny C.T., Wall R.;
RT "Alternatively spliced exons encode the tissue-specific 5' termini of
RT leukocyte pp52 and stromal cell S37 mRNA isoforms.";
RL Genomics 32:352-357(1996).
DR EMBL; U30942; AAB37542.1; -.
DR EMBL; U30939; AAB37542.1; JOINED.
DR EMBL; U30941; AAB37542.1; JOINED.
DR MGD; MGI:96832; Lsp1.
DR InterPro; IPR002211; Lymphspecific.
DR PRINTS; PR01083; LYMPHSPECIFIC.
FT NON_TER 124 124
SQ SEQUENCE 124 AA; 14388 MW; D98E59E2EF81954F CRC64;

Query Match 53.5%; Score 38; DB 11; Length 124;
Best Local Similarity 55.6%; Pred. No. 62;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
Db :|:|:|
92 KPEPQQFW 100

RESULT 81
Q9T6A9 PRELIMINARY; PRT; 175 AA.
AC Q9T6A9;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).

GN COI.
OS Culicoides tuttifrutti.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
OC Chironomidae; Ceratopogonidae; Culicoides.
RN NCBI_TaxID=88402;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TUT 1;
RA Linton Y.-M., Meiswinkel R., Venter G.J., Mellor P.S.,
RA Mordue(Luntz) A.J., Dallas J.F.;
RT "Phylogenetic relationship between five members of the Culicoides
RT imicola species complex in South Africa based on mtDNA cytochrome
RT oxidase I sequence data.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -!- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -!- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AF069242; AAD32471.1; -.
DR InterPro; IPR002106; AA_crna_ligase_II.
DR InterPro; IPR000883; COXI.
DR InterPro; IPR001360; Glyco_hydro_1.
DR Pfam; PF00115; COXI; 1.
DR PRINTS; PR01165; CYCOXIDASEI.
DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 175 175
FT NON_TER 175 175
SQ SEQUENCE 175 AA; 18767 MW; 2D5A93BBDF049DD3 CRC64;

Query Match 53.5%; Score 38; DB 8; Length 175;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QQWF 9
Db :|:|:|
157 QQWF 161

RESULT 82
Q9D1Z1 PRELIMINARY; PRT; 188 AA.
ID Q9D1Z1
AC Q9D1Z1;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE ADULT RETINA CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:A930019G03, FULL INSERT SEQUENCE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=RETINA;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE LECTIN-LIKE OXIDIZED LDL RECEPTOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RQ SEQUENCE FROM N.A.
RP MEDLINE=97205278; PubMed=9052782;
RA Sawamura T., Kume N., Aoyama T., Moriaki H., Hoshikawa H., Aiba Y.,
Tanaka T., Miwa S., Katsura Y., Kita T., Masaki T.,
RT "An endothelial receptor for oxidized low-density lipoprotein.";
RL Nature 386:73-77(1997).
DR EMBL: D89049; BAA19005.1; -.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
DR SMART: SM00034; CLECT; 1.
KW Lectin.
SQ SEQUENCE 270 AA; 30892 MW; 6055B6881AD7053D CRC64;

Query Match 53.5%; Score 38; DB 6; Length 270;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQWF 9
DB 139 PCPDW 146

RESULT 87
P78380
ID P78380 PRELIMINARY; PRT; 273 AA.
AC P78380;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE LECTIN-LIKE OXIDIZED LDL RECEPTOR.
GN LOX-1 OR OLR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RX MEDLINE=97205278; PubMed=9052782;
RA Sawamura T., Kume N., Aoyama T., Moriaki H., Hoshikawa H., Aiba Y.,
Tanaka T., Miwa S., Katsura Y., Kita T., Masaki T.,
RT "An endothelial receptor for oxidized low-density lipoprotein.";
RL Nature 386:73-77(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Millar D.S.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Li X., Bouzyk M.M., Wang X.K.;
RT "Human oxidized low density lipoprotein receptor: characterization of
the full length cDNA sequence and assignment to human chromosome
12p13.1-12.3.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99047525; PubMed=9828121;
RA Yamanaka S., Zhang X.Y., Miura K., Kim S., Iwao H.;
RT "The human gene encoding the lectin-type oxidized LDL receptor (OLR1)
is a novel member of the natural killer gene complex with a unique
expression profile.";
RT Genomics 54:191-199(1998).

DR EMBL: AB010710; BAA24580.1; -.
DR EMBL: AJ131757; CAB36175.1; -.
DR EMBL: AF035776; AAC82329.1; -.
DR EMBL: AF079167; AAC97927.1; -.
DR EMBL: AF079164; AAC97927.1; JOINED.
DR EMBL: AF079165; AAC97927.1; JOINED.
DR EMBL: AF079166; AAC97927.1; JOINED.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
DR SMART: SM00034; CLECT; 1.
KW Lectin; Receptor; Lipoprotein.
SQ SEQUENCE 273 AA; 30959 MW; 852DE6595DC3D361 CRC64;

Query Match 53.5%; Score 38; DB 4; Length 273;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQWF 9
DB 143 PCPDW 150

RESULT 88
Q9TTK7
ID Q9TTK7 PRELIMINARY; PRT; 274 AA.
AC Q9TTK7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE LECTIN-LIKE OXIDIZED LDL RECEPTOR-1.
GN PLOX-1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Sawamura T.;
RT "Porcine lectin-like oxidized LDL receptor-1(LOX-1).";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB018668; BAA89894.1; -.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
DR SMART: SM00034; CLECT; 1.
KW Receptor; Lectin.
SQ SEQUENCE 274 AA; 31142 MW; D141776C79FB42E0 CRC64;

Query Match 53.5%; Score 38; DB 6; Length 274;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQWF 9
DB 143 PCPDW 150

RESULT 89
Q99L65
ID Q99L65 PRELIMINARY; PRT; 322 AA.
AC Q99L65;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE SIMILAR TO LYMPHOCYTE SPECIFIC 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE-MAMMARY TUMOR;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003796; AA03796.1; -.
SQ SEQUENCE 322 AA; 35763 MW; 59D77C19CDE27651 CRC64;

Query Match 53.5%; Score 38; DB 11; Length 322;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWF 9
:|:|:|
Db 90 KPEPRQWF 98

RESULT 90
O62022 PRELIMINARY; PRT; 330 AA.
AC O62022;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE P50B.
GN LSP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=THYMUS;
RA MEDLINE=95293928; PubMed=7775393;
RA Matsumoto N., Kojima S., Osawa T., Toyoshima S.;
RT "Protein kinase C phosphorylates p50 LSP1 and induces translocation of
p50 LSP1 in T lymphocytes.";
RL J. Biochem. 117:222-229(1995).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=THYMUS;
RA MEDLINE=95293928; PubMed=7775393;
RA Matsumoto N., Kojima S., Osawa T., Toyoshima S.;
RA Tsunawasa S., Toyoshima S.;
RT "Lymphocyte isoforms of mouse p50 LSP1, which are phosphorylated in
mitogen-activated T cells, are formed through alternative splicing and
phosphorylation.";
RL J. Biochem. 118:237-243(1995).
DR EMBL; D49691; BAA08541.1; -.
DR MGD; MGI:96832; Lsp1.
DR InterPro; IPR002211; Lymphspecific.
DR PRINTS; PRO1083; LYMPHSFCIFC.
SQ SEQUENCE 330 AA; 36728 MW; 3CC27400F02859FD CRC64;

Query Match 53.5%; Score 38; DB 11; Length 330;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWF 9
:|:|:|
Db 92 KPEPRQWF 100

RESULT 91
Q98952 PRELIMINARY; PRT; 356 AA.
AC Q98952;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ALPHA-(1.3)-FUCOSYLTRANSFERASE (EC 2.4.1.-)
DE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCT-IV)

DE (CTF1).
GN CFT1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
RN SEQUENCE FROM N.A.
RA MEDLINE=97115837; PubMed=8955139;
RA Lee K.P., Carlson L.M., Woodcock J.B., Ramachandra N., Schultz T.L.,
RA Davis T.A., Lowe J.B., Thompson C.B., Larsen R.D.;
RL J. Biol. Chem. 271:32960-32967(1996).
CC -!- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
THE EXPRESSION OF LEWIS X/SSEA-1 AND VIM-2 ANTIGENS.
CC -!- PATHWAY: GLYCOSYLATION.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERNAE OF GOLGI.
CC -!- TISSUE SPECIFICITY: IN THE FOLLOWING EMBRYONIC TISSUES: BRAIN,
EYE, GIZZARD, THYMUS, BURSA AND SPLEEN.
DR EMBL; U73678; AAC60060.1; -.
DR InterPro; IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
KW Signal-anchor; Golgi stack.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 51 SIGNAL-ANCHOR (POTENTIAL).
FT DOMAIN 52 356 (TYPE-II MEMBRANE PROTEIN).
FT CARBOHYD 80 80 LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 356 AA; 41494 MW; 13141627FE8AD089 CRC64;

Query Match 53.5%; Score 38; DB 13; Length 356;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKPQQWF 10
:|:|:|:|
Db 121 RPPRQRWVWM 130

RESULT 92
Q9EQ09 PRELIMINARY; PRT; 363 AA.
ID Q9EQ09;
AC Q9EQ09;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE OXIDIZED LDL RECEPTOR.
GN LOX-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RA Park S.-H., Ahn H.-J., Cho J.-J.;
RT "Mouse LOX-1 is expressed in mast cells after IgE cross-linking.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF303744; AAG44998.1; -.
DR InterPro; IPR001304; lectin_c.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 363 AA; 41613 MW; E44703D6408F15F8 CRC64;

Query Match 53.5%; Score 38; DB 11; Length 363;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 2 PKPQQWFW 9
   |||
DB 234 PCPDWFW 241

RESULT 93
ID 070156 PRELIMINARY; PRT; 364 AA.
AC O70156;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ENDOTHelial RECEPTOR FOR OXIDIZED LOW-DENSITY LIPOPROTEIN.
GN LOX-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=SHR-SP; TISSUE=KIDNEY;
RX MEDLINE=98161826; PubMed=9494115;
RA Nagase M., Hirose S., Fujita T.;
RT "Unique repetitive sequence and unexpected regulation of expression of
RT rat endothelial receptor for oxidized low-density lipoprotein (LOX-
RT 1).";
RL Biochem. J. 330:1417-1422(1998).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RX MEDLINE=99057940; PubMed=9837956;
RA Nagase M., Abe J., Takahashi K., Ando J., Hirose S., Fujita T.;
RT "Genomic organization and regulation of expression of the lectin-like
RT oxidized low-density lipoprotein receptor (LOX-1) gene.";
RL J. Biol. Chem. 273:33702-33707(1998).
DR EMBL; AB005900; BAA25785.1; -.
DR EMBL; AB018104; BAA35123.1; -.
DR EMBL; AB018097; BAA35123.1; JOINED.
DR EMBL; AB018098; BAA35123.1; JOINED.
DR EMBL; AB018099; BAA35123.1; JOINED.
DR EMBL; AB018100; BAA35123.1; JOINED.
DR EMBL; AB018101; BAA35123.1; JOINED.
DR EMBL; AB018102; BAA35123.1; JOINED.
DR EMBL; AB018103; BAA35123.1; JOINED.
DR InterPro; IPR001304; Lectin_c.
DR Pfam; PF00059; lectin_C; 1.
DR PROSITE; PSS0041; C-TYPE-LECTIN_2; 1.
DR SMART; SM00034; CLECT; 1.
KW Lipoprotein; Receptor; Lectin.
SQ SEQUENCE 364 AA; 41890 MW; 0AD2839C07206E09 CRC64;

Query Match 53.5%; Score 38; DB 11; Length 364;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQQWFW 9
   |||
DB 234 PCPDWFW 241

RESULT 94
ID 09A8W6 PRELIMINARY; PRT; 368 AA.
AC 09A8W6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL PROTEIN CC1232.
GN CC1232.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
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OC Caulobacter.
OX NCBI_TaxID=69394;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vanathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005799; AAK23214.1; -.
DR TIGR; CC1232; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 368 AA; 41087 MW; 6985682449AD7A29 CRC64;

Query Match 53.5%; Score 38; DB 2; Length 368;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPQQWFW 10
   |||
DB 194 PVPPQFWL 202

RESULT 95
ID 09PDR6 PRELIMINARY; PRT; 373 AA.
AC 09PDR6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ROD SHAPE-DETERMINING PROTEIN.
GN XFL1313.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OX Xylella.
OX NCBI_TaxID=2371;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira C.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quagatto R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
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RL Nature 406:151-159(2000).
DR EMBL: AE003964; AAF84122.1; -.
DR InterPro: IPR001182; FTSW_RoDA_SPOVE.
DR Pfam: PF01098; FTSW_RoDA_SPOVE; 1.
KW PROSITE; PS00428; FTSW_RoDA_SPOVE; 1.
KW Complete proteome.
SQ SEQUENCE 373 AA; 41436 MW; E9480421BF70EAC5 CRC64;

Query Match 53.5%; Score 38; DB 2; Length 373;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQQWFLL 11
Db 201 PFSNFWLL 208

RESULT 96
Q9FHE8 PRELIMINARY; PRT; 392 AA.
AC Q9FHE8;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE SIMILARITY TO DISEASE RESISTANCE PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
ON NCBI_TaxID=3702;
RX Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones."
RL DNA Res. 7:31-63(2000).
DR EMBL: AB019224; BAB09491.1; -.
DR InterPro: IPR000157; TIR.
DR Pfam: PF01582; TIR; 1.
DR SMART: SM00255; TIR; 1.
SQ SEQUENCE 392 AA; 44141 MW; 8E8730F454878CA2 CRC64;

Query Match 53.5%; Score 38; DB 10; Length 392;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 KPQQWF 9
Db 251 KPQKWTW 257

RESULT 97
Q9JIK2 PRELIMINARY; PRT; 401 AA.
AC Q9JIK2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-
DE FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV).
GN FUT4.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
ON NCBI_TaxID=10029;
RX Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RL Nature 388:539-547(1997).
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).

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CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,  
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.  
DR EMBL: AE000652; AAD08579.1; -.  
DR TIGR: HP1539; -.  
DR InterPro: IPR000179; Cyt_b_b6.  
DR Pfam: PF00032; cytochrome_b_c1; 1.  
DR Pfam: PF00033; cytochrome_b_c1; 1.  
DR PROSITE: PS00193; CYTOCHROME_B_00; UNKNOWN.1.  
DR Complete proteome; Electron transport; Heme; Hypothetical protein;  
KW Respiratory chain; Transmembrane.  
KW SEQUENCE 412 AA; 47510 MW; 954646D95A1F925A CRC64;  
SQ SEQUENCE 412 AA; 47510 MW; 954646D95A1F925A CRC64;  
  
Query Match 53.5%; Score 38; DB 2; Length 412;  
Best Local Similarity 54.5%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 RPXQQQFWLM 11  
|||  
Db 349 RPAPMVWFWLV 359  
|||  
  
RESULT 99  
Q9CAP2 PRELIMINARY; PRT; 421 AA.  
AC Q9CAP2;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE HYPOTHETICAL 47.7 KDA PROTEIN.  
GN T5M16.25.  
OS Arabidopsis thaliana (Mouse-ear cross).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV, COLUMBIA;  
RX MEDLINE=21016719; PubMed=11130712;  
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,  
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marzilli A.,  
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.I.,  
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,  
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
RT thaliana.";  
RL Nature 408:816-820(2000).  
DR EMBL: AC010704; AAC51667.1; -.  
DR InterPro: IPR003409; MORN.  
DR Pfam: PF02493; MORN; 7.  
KW Hypothetical protein.  
KW SEQUENCE 421 AA; 47731 MW; 08361CB916235663 CRC64;  
  
Query Match 53.5%; Score 38; DB 10; Length 421;  
Best Local Similarity 62.5%; Pred. No. 2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 RPXQQQFW 8  
:|:|:|  
  
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,  
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.  
DR EMBL: AE000652; AAD08579.1; -.  
DR TIGR: HP1539; -.  
DR InterPro: IPR000179; Cyt_b_b6.  
DR Pfam: PF00032; cytochrome_b_c1; 1.  
DR Pfam: PF00033; cytochrome_b_c1; 1.  
DR PROSITE: PS00193; CYTOCHROME_B_00; UNKNOWN.1.  
DR Complete proteome; Electron transport; Heme; Hypothetical protein;  
KW Respiratory chain; Transmembrane.  
KW SEQUENCE 412 AA; 47510 MW; 954646D95A1F925A CRC64;  
SQ SEQUENCE 412 AA; 47510 MW; 954646D95A1F925A CRC64;  
  
Query Match 53.5%; Score 38; DB 11; Length 433;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 RPXQQQFWL 10  
|||  
Db 189 RPPQQRWVM 198  
|||  
  
RESULT 101  
O63524 PRELIMINARY; PRT; 455 AA.  
ID O63524;  
AC O63524;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE HYPOTHETICAL 51.8 KDA PROTEIN.  
GN F4D11.30 OR AT4G32770.  
OS Arabidopsis thaliana (Mouse-ear cross).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bevan M., Benes V., Rechmann S., Borkova D., Ansoorge W., Hoheisel J.,  
RA Mewes H.W., Mayer K.F.X., Schueller C.,  
RA Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Benes V., Rechmann S., Borkova D., Ansoorge W., Mewes H.W., Lemcke K.,  
RA Mayer K.F.X.;  
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL022537; CAA18584.1; -.  
DR EMBL: AL161582; CAB79994.1; -.  
KW Hypothetical protein.  
KW SEQUENCE 455 AA; 51838 MW; 4A05CF5F0BFA994D CRC64;  
  
Query Match 53.5%; Score 38; DB 10; Length 455;  
Best Local Similarity 57.1%; Pred. No. 2.2e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Qy 4 PQOWFWL 10
I:||||
Db 242 PRKWFV 248

RESULT 102

Q9WID1 PRELIMINARY; PRT; 458 AA.
AC Q9WID1; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CG11388 PROTEIN.
GN CG11388.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foglek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003462; AAF47138.1; -.
DR FlyBase; FBgn0034959; CG11388.
SQ SEQUENCE 458 AA; 53563 MW; 673A3F96F7C4BA9A CRC64;

Query Match 53.5%; Score 38; DB 5; Length 458;
Best Local Similarity 45.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RPKPQOWFWL 11
I:||||
Db 50 ROKPKSAWTL 60

RESULT 103

Q9VUK7 PRELIMINARY; PRT; 635 AA.
AC Q9VUK7; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE CG6945 PROTEIN.
GN CG6945.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foglek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003532; AAF49669.1; -.
DR FlyBase; FBgn0036476; CG6945.
SQ SEQUENCE 635 AA; 70588 MW; 7F02A40BF519E5AC CRC64;

Query Match 53.5%; Score 38; DB 5; Length 635;
Best Local Similarity 71.4%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQOW 7
I:||||
Db 400 RPKPKQW 406

RESULT 104

```
Q9UAC1          PRELIMINARY;          PRT;      684 AA.
AC Q9UAC1;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
DE PUTATIVE PTERIDINE TRANSPORTER FT2.
OS Leishmania donovani.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5661;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IS2D;
RA Moore J.B., Beverley S.M.;
RT "Identification of a protein mediating folate/methotrexate uptake by
   genetic rescue of a Leishmania transport mutant.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF084470; AAD52047.1; -.
SQ SEQUENCE 684 AA; 75387 MW; 9F773E0DC562A037 CRC64;

Query Match          53.5%; Score 38; DB 5; Length 684;
Best Local Similarity 43.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

QY 2 PKPQQ-----WFWLM 11
   |||
   |||:|
Db 193 PKPGPSMVSWIWFWM 208

RESULT 105
Q9UAB7          PRELIMINARY;          PRT;      691 AA.
AC Q9UAB7;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
DE PUTATIVE PTERIDINE TRANSPORTER FT6.
OS Leishmania donovani.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5661;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IS2D;
RA Moore J.B., Beverley S.M.;
RT "Identification of a protein mediating folate/methotrexate uptake by
   genetic rescue of a Leishmania transport mutant.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF084474; AAD52051.1; -.
SQ SEQUENCE 691 AA; 76005 MW; 63D1D7671D8B45E6 CRC64;

Query Match          53.5%; Score 38; DB 5; Length 691;
Best Local Similarity 43.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

QY 2 PKPQQ-----WFWLM 11
   |||
   |||:|
Db 193 PKPGPSMVSWIWFWM 208

RESULT 106
Q9LUQ4          PRELIMINARY;          PRT;      697 AA.
AC Q9LUQ4;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE GENOMIC DNA, CHROMOSOME 3, P1 CLONE: MUK13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
```

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OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RC MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
   features of the regions of 4,504,864 bp covered by sixty P1 and TAC
   clones.";
RL DNA Res. 7:131-135(2000).
DR EMBL; AB022218; BAB02367.1; -.
DR InterPro; IPR001211; PLP_A2.
DR PROSITE; PS00118; PA2_HIS; UNKNOWN_1.
SQ SEQUENCE 697 AA; 78550 MW; 421B2F2E6CD39AA7 CRC64;

Query Match          53.5%; Score 38; DB 10; Length 697;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 PQQWFWLM 11
   |||
   |||:|
Db 525 PDHFWFWRM 532

RESULT 107
Q9UAC0          PRELIMINARY;          PRT;      698 AA.
AC Q9UAC0;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
DE PUTATIVE PTERIDINE TRANSPORTER FT3.
OS Leishmania donovani.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5661;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IS2D;
RA Moore J.B., Beverley S.M.;
RT "Identification of a protein mediating folate/methotrexate uptake by
   genetic rescue of a Leishmania transport mutant.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF084471; AAD52048.1; -.
SQ SEQUENCE 698 AA; 75779 MW; B817D80B76A1AFDB CRC64;

Query Match          53.5%; Score 38; DB 5; Length 698;
Best Local Similarity 43.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

QY 2 PKPQQ-----WFWLM 11
   |||
   |||:|
Db 194 PKPGPSMVSWIWFWM 209

RESULT 108
Q9UAB9          PRELIMINARY;          PRT;      700 AA.
AC Q9UAB9;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
DE PUTATIVE PTERIDINE TRANSPORTER FT4.
OS Leishmania donovani.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5661;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN-IS2D;
RA Moore J.B., Beverley S.M.;
RT "Identification of a Leishmania mediating folate/methotrexate uptake by
   genetic rescue of a Leishmania transport mutant.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF084472; AAD52049.1; -.
SQ SEQUENCE 700 AA; 76420 MW; 3A3450E8D57C42AE CRC64;

Query Match          53.5%; Score 38; DB 5; Length 700;
Best Local Similarity 43.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

QY 2 PKPQQ-----WFLWM 11
   ||| ||| |||
Db 194 PKPGPSMVSNIWFWM 209

RESULT 109
Q9M7X1 PRELIMINARY; PRT; 722 AA.
AC Q9M7X1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE MJK13.4 PROTEIN.
GN MJK13.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III P1 MJK13 genomic sequence.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024081; AAF35404.1; -.
SQ SEQUENCE 722 AA; 81163 MW; 7F6861ABC2AC29E9 CRC64;

Query Match          53.5%; Score 38; DB 10; Length 722;
Best Local Similarity 62.5%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 PQQWFWM 11
   | ||| |
Db 528 PDHWFWM 535

RESULT 110
Q9DXA2 PRELIMINARY; PRT; 901 AA.
AC Q9DXA2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE ENHANCIN.
OS Chortistoneura fumiferana granulovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX NCBI_TaxID=56947;
RN [1]
RP SEQUENCE FROM N.A.
RA Bourassa A., Bergeron J., Merzouki A., Guertin C.;
RT "Enhancin of Chortistoneura fumiferana granulovirus.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF319939; AAG33872.1; -.
SQ SEQUENCE 901 AA; 104208 MW; 267F182EAE85C6D8 CRC64;
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Query Match          53.5%; Score 38; DB 12; Length 901;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQQWFWM 10
   | || | ||
Db 353 PYPQIWSML 361

RESULT 111
P74693 PRELIMINARY; PRT; 909 AA.
AC P74693;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ACRIFLAVINE RESISTANCE PROTEIN.
GN ACRB OR SLR0454.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyaajima N., Hirotsawa M., Sugitara M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
   Synecocystis sp. strain PCC6803. II. Sequence determination of the
   entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; D90917; BAAL8811.1; -.
DR InterPro; IPR001036; ACR_tran.
DR Pfam; PF00873; ACR_tran; 3.
KW Complete proteome.
SQ SEQUENCE 909 AA; 97673 MW; 96E59A0AE9FF6DFB CRC64;

Query Match          53.5%; Score 38; DB 2; Length 909;
Best Local Similarity 71.4%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPQQWF 8
   | : || |
Db 445 PRPQSWF 451

RESULT 112
O00908 PRELIMINARY; PRT; 956 AA.
AC O00908;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE POLYTHREONINE PROTEIN (FRAGMENT).
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GCHI;
RA Carraway M., Tzipori S., Widmer G.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U83169; AAB61262.1; -.
FT NON_TER 1
FT NON_TER 956
SQ SEQUENCE 956 AA; 100783 MW; 61613B6D7F1895C6 CRC64;
```

Query Match 53.5%; Score 38; DB 5; Length 956;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQOQFWL 10
ID 11:1111
Db 250 KPDEWCWL 257

RESULT 113

075339 PRELIMINARY; PRT; 1184 AA.
AC O75339;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CARTILAGE INTERMEDIATE LAYER PROTEIN.
GN CILP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ARTICULAR CARTILAGE;
RX MEDLINE=98389785; PubMed=9722584;
RA Lorenzo P., Neame P., Sommarin Y., Heinegard D.;
RT "Cloning and deduced amino acid sequence of a novel cartilage protein
(CILP) identifies a proform including a nucleotide
pyrophosphohydrolase.";
RT J. Biol. Chem. 273:23469-23475(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Nakamura I., Okawa A., Ikegawa S., Takaoka K., Nakamura Y.;
RT "Genomic organization, mapping, and polymorphisms of the gene encoding
human cartilage intermediate layer protein (CILP).";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Lorenzo P., Aman P., Sommarin Y., Heinegard D.;
RT "Pro-CILP: Gene structure and chromosomal localization.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.

EMBL; AF035408; AAC33838.1; -.
EMBL; AB022430; BAA76692.1; -.
EMBL; AF035455; AAF14889.1; -.
EMBL; AF035448; AAF14889.1; JOINED.
EMBL; AF035449; AAF14889.1; JOINED.
EMBL; AF035451; AAF14889.1; JOINED.
EMBL; AF035453; AAF14889.1; JOINED.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR InterPro; IPR001451; Hexapep_transf.
DR InterPro; IPR003598; Ig_G2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR000884; TSP1.
Pfam; PF00047; Ig_1.
Pfam; PF00090; tsp_1; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00209; TSP1; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
PROSITE; PS50092; TSP1; 1.
SEQUENCE 1184 AA; 132538 MW; 4449F05537CC99C3 CRC64;

Query Match 53.5%; Score 38; DB 4; Length 1184;
Best Local Similarity 44.4%; Pred. No. 5.6e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKEQOQFW 9
ID 11:1111
Db 335 KRPDKYFW 343

RESULT 114

09QYV8 PRELIMINARY; PRT; 1216 AA.
AC 09QYV8;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE DNA POLYMERASE GAMMA (EC 2.7.7.7).
GN MIP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RA Sun Q., Popanda O., Thielmann H.W.;
RT "Mitochondrial DNA polymerase gamma from Novikoff hepatoma cells
differs from that of normal rat liver in cDNA sequence and kinetic
properties.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ245646; CAB56206.1; -.
DR InterPro; IPR001098; DNA_pol_A.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR002297; DNA_polG.
DR Pfam; PF00254; FKBP; 1.
DR Pfam; PF00476; DNA_pol_A; 1.
DR PRINTS; PR00867; DNAPOLG.
DR PROSITE; PS00447; DNA_POLYMERASE_A; 1.
DR SMART; SM00482; POLAC; 1.
KW Transferase; Nucleotidyltransferase.
SQ SEQUENCE 1216 AA; 136955 MW; A74CD68B68DB690C CRC64;

Query Match 53.5%; Score 38; DB 11; Length 1216;
Best Local Similarity 50.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KPQOQFW 9
ID 11:1111
Db 147 PQPRKVVW 154

RESULT 115

09QYV7 PRELIMINARY; PRT; 1216 AA.
AC 09QYV7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE DNA POLYMERASE GAMMA (EC 2.7.7.7).
GN MIP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RA Sun Q., Popanda O., Thielmann H.W.;
RT "Mitochondrial DNA polymerase gamma from Novikoff hepatoma cells
differs from that of normal rat liver in cDNA sequence and kinetic
properties.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ245647; CAB56207.1; -.
DR InterPro; IPR001098; DNA_pol_A.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR002297; DNA_polG.
DR Pfam; PF00254; FKBP; 1.
DR Pfam; PF00476; DNA_pol_A; 1.
DR PRINTS; PR00867; DNAPOLG.

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DR PROSITE; PS00447; DNA_POLYMERASE_A; 1.
DR SMART; SM00482; POLAC; 1.
KW Transferase; Nucleotidyltransferase.
SQ SEQUENCE 1216 AA; 136836 MW; 3E55311408373ABE CRC64;

Query Match
Best Local Similarity 53.5%; Score 38; DB 11; Length 1216;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKQOWFW 9
|:|:|:|
Db 147 PQRKQWV 154

RESULT 116
P81137
AC P81137 PRELIMINARY; PRT; 1528 AA.
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INSECTICIDAL TOXIN RECEPTOR BT-R1 PRECURSOR.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Sphingioidea; Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=MIDGUT;
RX MEDLINE=95197553; PubMed=7890666;
RA Vadlamudi R.K., Weber E., Ji I., Ji T.H., Bulla L.A. Jr.;
RT "Cloning and expression of a receptor for an insecticidal toxin of
Bacillus thuringiensis."
RL J. Biol. Chem. 270:5490-5494(1995).
CC -!- FUNCTION: BINDS TO THE CRYIA(B) TOXIN OF BACILLUS THURINGIENSIS
CC -!- SUBSP. BERLINER, LEADING TO THE DEATH OF M.SEXTA.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
CC -!- SIMILARITY: RELATED TO THE CADHERIN FAMILY OF CELL ADHESION
CC MOLECULES. CONTAINS 11 CADHERIN-TYPE REPEATS.
DR InterPro; IPR001525; C5_DNA_meth.
DR Pfam; PF00028; cadherin. 5.
DR SMART; SM00112; CA; 10.
DR PROSITE; PS00095; C5_MTASE_2; UNKNOWN_1.
DR PROSITE; PS00232; CADHERIN_1; 1.
DR PROSITE; PS0268; CADHERIN_2; 10.
KW Receptor; Glycoprotein; Transmembrane; Signal; Repeat; Cell adhesion.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 1528 INSECTICIDAL TOXIN RECEPTOR BT-R1.
FT DOMAIN 22 1405 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 72 1353 11 X APPROXIMATE TANDEM REPEATS.
FT TRANSMEM 1406 1428 POTENTIAL.
FT DOMAIN 1429 1528 CYTOPLASMIC (POTENTIAL).
FT REPEAT 72 176 CADHERIN 1.
FT REPEAT 177 289 CADHERIN 2.
FT REPEAT 290 397 CADHERIN 3.
FT REPEAT 398 500 CADHERIN 4.
FT REPEAT 501 623 CADHERIN 5.
FT REPEAT 624 757 CADHERIN 6.
FT REPEAT 758 882 CADHERIN 7.
FT REPEAT 883 1004 CADHERIN 8.
FT REPEAT 1005 1121 CADHERIN 9.
FT REPEAT 1122 1242 CADHERIN 10.
FT REPEAT 1243 1353 CADHERIN 11.
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 468 468 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 492 492 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 575 575 N-LINKED (GLCNAC. . .) (POTENTIAL).

DR PROSITE; PS00447; DNA_POLYMERASE_A; 1.
DR SMART; SM00482; POLAC; 1.
KW Transferase; Nucleotidyltransferase.
SQ SEQUENCE 1216 AA; 136836 MW; 3E55311408373ABE CRC64;

Query Match
Best Local Similarity 53.5%; Score 38; DB 5; Length 1528;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOWFWL 10
|:|:|:|
Db 233 PQOWFWL 239

RESULT 117
O9GPJ9
ID O9GPJ9 PRELIMINARY; PRT; 1717 AA.
AC O9GPJ9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CADHERIN-RELATED PROTEIN RECEPTOR BT-R1.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Sphingioidea; Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RA Dorsch J.A., Maaty W.S.A., Griko N.B., Candias M., Bulla L.A. Jr.;
RT "A Cadherin-related protein Receptor, BT-R1, in the Midgut Epithelium
of Manduca sexta Mediates Toxicity for Bacillus thuringiensis CryIa
Toxins."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO THE CADHERIN FAMILY.
DR EMBL; AF319973; AAG37912.1; -.
DR InterPro; IPR001525; C5_DNA_meth.
DR InterPro; IPR002126; Cadherin.
DR Pfam; PF00028; cadherin; 6.
DR SMART; SM00112; CA; 10.
DR PROSITE; PS00095; C5_MTASE_2; UNKNOWN_1.
DR PROSITE; PS00232; CADHERIN_1; 1.
DR PROSITE; PS0268; CADHERIN_2; 10.
KW Calcium-binding; Cell adhesion; Glycoprotein; Receptor.
SQ SEQUENCE 1717 AA; 192305 MW; FEC4A48B098B17E CRC64;

Query Match
Best Local Similarity 53.5%; Score 38; DB 5; Length 1717;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOWFWL 10
|:|:|:|
Db 234 PQOWFWL 240

RESULT 118
O96503
ID O96503 PRELIMINARY; PRT; 1832 AA.
AC O96503;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE GP900.
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
```

RA SEQUENCE FROM N.A.
RX MEDLINE-99066935; PubMed=9851610;
RA Barnes D.A., Bonnin A., Huang J.X., Gousset L., Wu J., Gut J.,
RA Doyle P., Dubremetz J.F., Ward H., Petersen C.;
RT "A novel multi-domain mucin-like glycoprotein of Cryptosporidium
RT parvum mediates invasion.";
RL Mol. Biochem. Parasitol. 96:93-110(1998).
DR EMBL: AF068065; AAC98153.1; -;
SQ SEQUENCE 1832 AA; 192653 MW; 590E6ACB16BBE0D2 CRC64;

Query Match 53.5%; Score 38; DB 5; Length 1832;
Best Local Similarity 62.5%; Pred. No. 8.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPQWFNL 10
DB 527 KPDEWCWL 534
|||:| |

RESULT 119
Q9VI22 PRELIMINARY; PRT; 2237 AA.
ID Q9VI22
AC Q9VI22
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CG10272 PROTEIN.
GN CG10272.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE-20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flossler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gortel J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam K.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny L., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J.R., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003675; AAF54122.1; -;
DR FlyBase: FBgn0037444; AA_trna_ligase_II, CGI0272.
DR InterPro: IPR002106; AA_trna_ligase_II-2; UNKNOWN_1.
DR PROSITE: PS00339; AA_trna_ligase_II-2; UNKNOWN_1.
SQ SEQUENCE 2237 AA; 242406 MW; 2E4A397306BF6E57 CRC64;

Query Match 53.5%; Score 38; DB 5; Length 2237;
Best Local Similarity 54.5%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPKPOWFWM 11
DB 2199 RPKGKDWDSM 2209
|||:| |

RESULT 120
Q99IT0 PRELIMINARY; PRT; 100 AA.
ID Q99IT0
AC Q99IT0
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 11.5 KDA PROTEIN.
OS uncultured organism.
OC unclassified; environmental samples.
OX NCBI_TaxID=155900;
RN [1]
RP SEQUENCE FROM N.A.
RA Stokes H.W., Nield B.S., Mabbutt B.C., Nevalainen H., Holmes A.J.,
RA Gillings M.R.;
RT "Novel and diverse integron-like gene cassettes are prevalent in
RT natural environments.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF349104; AAK28610.1; -;
KW Hypothetical protein.
SQ SEQUENCE 100 AA; 11451 MW; A39185CC7D9D674A CRC64;

Query Match 52.8%; Score 37.5; DB 14; Length 100;
Best Local Similarity 58.3%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 2 PKPQWF---WL 10
DB 48 PKPQWWSYRWL 59
|||:| |

RESULT 121
Q99ZD5 PRELIMINARY; PRT; 213 AA.
ID Q99ZD5
AC Q99ZD5
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PUTATIVE AMINO ACID ABC TRANSPORTER (PERMEASE PROTEIN).
GN SPY1276.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SF370;
RX MEDLINE-21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

RT *Complete genome sequence of an M1 strain of Streptococcus pyogenes.*;
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 DR EMBL; AE006566; AAK34126.1;
 KW Complete proteome.
 SQ SEQUENCE 213 AA; 23990 MW; FCAB7D5BA2E32097 CRC64;

Query Match 52.8%; Score 37.5; DB 2; Length 213;
 Best Local Similarity 50.08; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 5; Gaps 1;

Qy 3 RPQWFM-----WLM 11
 || ||| |||
 Db 45 KPLQWFLTLVYWM 58

RESULT 122

O9CY68 PRELIMINARY; PRT; 300 AA.
 ID AC O9CY68
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE 7 DAYS EMBRYO CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
 DE CLONE:C430041K09, FULL INSERT SEQUENCE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.,
 RT *Functional annotation of a full-length mouse cDNA collection.*;
 RL Nature 409:685-690(2001).
 DR EMBL; AK021249; BAB32347.1;
 SQ SEQUENCE 300 AA; 34815 MW; 94D65F47AD4A208D CRC64;

Query Match 52.8%; Score 37.5; DB 11; Length 300;
 Best Local Similarity 63.6%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 RPQPOQ-FWL 10
 || | |||
 Db 97 RPHPAYWFWL 107

RESULT 123

O921X2 PRELIMINARY; PRT; 473 AA.
 ID AC O921X2
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE PHOSPHATIDYLSERINE SYNTHASE-2.
 GN PTDSS2
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=LIVER;
 RA Stone S.J., Vance J.E.;
 RT *Phosphatidylserine synthase-2 from mouse liver.*;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF09053; AAC98383.1;
 DR MGD; MGI:1351664; Ptdss2.
 SQ SEQUENCE 473 AA; 55004 MW; 66402CE1EB7D0B07 CRC64;

Query Match 52.8%; Score 37.5; DB 11; Length 473;
 Best Local Similarity 63.6%; Pred. No. 2.7e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 RPQPOQ-FWL 10
 || | |||
 Db 97 RPHPAYWFWL 107

RESULT 124

O08888 PRELIMINARY; PRT; 474 AA.
 ID AC O08888
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
 DE PHOSPHATIDYLSERINE SYNTHASE II.
 GN PSSB.
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kuge O., Saito K., Masahiro N.;
 RL J. Biol. Chem. 0:0-0(0).
 DR EMBL; AB004109; BAA20355.1;
 SQ SEQUENCE 474 AA; 55004 MW; 81942EA310F538C2 CRC64;

Query Match 52.8%; Score 37.5; DB 11; Length 474;
 Best Local Similarity 63.6%; Pred. No. 2.7e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 RPQPOQ-FWL 10
 || | |||
 Db 97 RPHPAYWFWL 107

RESULT 125

O9BVG9 PRELIMINARY; PRT; 487 AA.
 ID AC O9BVG9
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE SIMILAR TO PHOSPHATIDYLSERINE SYNTHASE 2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-NEUROBLASTOMA;
 RA Strausberg R.;

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001210; AA01210.1; -
SQ SEQUENCE 487 AA; 56253 MW; E02508F894841A4F CRC64;

Query Match 52.8%; Score 37.5; DB 4; Length 487;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 RPKPOQW-FWL 10
|| | |||
Db 119 RPHPAYWRFWL 129

RESULT 126

ID O92611 PRELIMINARY; PRT; 1177 AA.
AC O92611;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE DNA-BINDING PROTEIN.
GN DBP.
OS Pseudorabies virus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10345;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TNL;
RX MEDLINE=98455382; PubMed=9784061;
RA Wu S.-L., Hsiang C.-Y., Ho T.-Y., Chang T.-J.;
RT "Identification, expression, and characterization of the pseudorabies
RT virus DNA-binding protein gene and gene product.";
RL Virus Res. 56:1-9(1998).
DR EMBL; U80909; AAC63429.1; -
DR InterPro; IPR000635; Viral_DNA_bind.
DR Pfam; PF00747; viral_DNA_bp; 1.
KW DNA-binding.
SQ SEQUENCE 1177 AA; 125408 MW; BA87AF9CFC961707 CRC64;

Query Match 52.8%; Score 37.5; DB 12; Length 1177;
Best Local Similarity 60.0%; Pred. No. 6.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 2 PKPOQWFWM 11
|| | |||
Db 820 PNP-QWFWM 828

RESULT 127

ID O9E1Y7 PRELIMINARY; PRT; 1194 AA.
AC O9E1Y7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SSDNA BINDING PROTEIN.
OS Carcophilacine herpesvirus 7.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=35245;
RN [1]
RP SEQUENCE FROM N.A.
RA Gray W.L., Starnes H.B., White M.W., Ashburn C.V., Mahalingam R.;
RT "Complete Sequence of the Simian Varicella Virus Genome.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF275348; AAG27202.1; -
DR InterPro; IPR000635; Viral_DNA_bind.
DR Pfam; PF00747; viral_DNA_bp; 1.
SQ SEQUENCE 1194 AA; 131968 MW; EBA7F3C841965897 CRC64;

Query Match 52.8%; Score 37.5; DB 12; Length 1194;
Best Local Similarity 60.0%; Pred. No. 6.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 2 PKPOQWFWM 11
|| | |||
Db 830 PNP-QWFWM 838

RESULT 128

ID Q69101 PRELIMINARY; PRT; 1197 AA.
AC Q69101;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE DNA BINDING PROTEIN ICP8.
OS Herpes simplex virus (type 2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10310;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KN;
RX MEDLINE=93228441; PubMed=8385914;
RA Toh Y., Tanaka S., Liu Y., Mori R.;
RT "Nucleotide sequence of the major DNA-binding protein gene of herpes
RT simplex virus type 2 and a comparison with the type 1.";
RL Arch. Virol. 129:183-196(1993).
DR EMBL; D10658; BAA01507.1; -
DR InterPro; IPR000635; Viral_DNA_bind.
DR Pfam; PF00747; viral_DNA_bp; 1.
SQ SEQUENCE 1197 AA; 128470 MW; AA3ADA75B8865BFE CRC64;

Query Match 52.8%; Score 37.5; DB 12; Length 1197;
Best Local Similarity 66.7%; Pred. No. 6.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 RPKPOQFW 9
|| | |||
Db 837 QPNP-QFW 844

RESULT 129

ID Q89549 PRELIMINARY; PRT; 1203 AA.
AC Q89549;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE UL29.
GN UL29.
OS Bovine herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COOPER;
RA Schwyzer M., Vilek C., Lowery D.E., Bello L.J., Meyer G., Misra V.,
RA Thiry E., Paces V.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COOPER;
RA Meyer G., Vilek C., Paces V., Pastoret P., Thiry E., Schwyzer M.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=JURA.
RA Schwyzer M., Vilek C., Lowery D.E., Bello L.J., Meyer G., Misra V.;

RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-JURA;
RA Schwyzer M.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z78205; CAB01596.1; -.
DR EMBL; X94677; CAA64336.1; -.
DR EMBL; AJ004801; CAA06104.1; -.
DR InterPro: IPR000635; Viral_DNA_bind.
DR Pfam; PF00747; Viral_DNA_dp; 1.
SQ SEQUENCE 1203 AA; 127409 MW; 8299D64966A9654F CRC64;

Query Match 52.8%; Score 37.5; DB 12; Length 1203;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 2 PKPQOWFWLM 11
| | | | |
Db 840 PNP-QWFWTL 848

RESULT 130

O39273
ID O39273 PRELIMINARY; PRT; 1208 AA.
AC O39273;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JUN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE COUNTERPART OF HSV-1 GENE UL29 AND VZV GENE 29.
GN 31.
OS Equine herpesvirus 4.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10331;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NS80567;
RX MEDLINE=98264497; PubMed=9603335;
RA Telford E.A., Watson M.S., Perry J., Cullinane A.A., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-4.";
RL J. Gen. Virol. 79:1197-1203(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NS80567;
RA Telford E.A., Watson M.S., Perry J., Cullinane A.A., Davison A.J.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030027; AAC59547.1; -.
DR InterPro: IPR000635; Viral_DNA_bind.
DR Pfam; PF00747; Viral_DNA_dp; 1.
SQ SEQUENCE 1208 AA; 130607 MW; 17699FBD9238C4CB CRC64;

Query Match 52.8%; Score 37.5; DB 12; Length 1208;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 2 PKPQOWFWLM 11
| | | | |
Db 844 PNP-QWFWTL 852

RESULT 131

O9TBB3
ID O9TBB3 PRELIMINARY; PRT; 53 AA.
AC O9TBB3;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE ATPASE 8 (FRAGMENT).
OS Tadorna variegata.
OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Tadorna.
OX NCBI_TaxID=107024;
RN [1]
RP SEQUENCE FROM N.A.
RA Sorenson M.D., Cooper A., Paxinos E.E., Quinn T.W., James H.F.,
RA Olson S.L., Fleischner R.C.;
RT "Relationships of the extinct moa-nalos, flightless Hawaiian waterfowl,
RT based on ancient DNA.";
RL Proc. R. Soc. Lond. B, Biol. Sci. 0:0-0(1999).
DR EMBL; AF173743; AAF07025.1; -.
DR InterPro: IPR001421; ATP-synt_8.
DR Pfam; PF00895; ATP-synt_8; 1.
DR ProDom; PD161863; Avian_mito_ATPase_8; 1.
KW Mitochondrion.
FT NON_TER 53
SQ SEQUENCE 53 AA; 6044 MW; B6AC0B525B992891 CRC64;

Query Match 52.1%; Score 37; DB 8; Length 53;
Best Local Similarity 62.5%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PKPQOWFW 9
| | | | |
Db 45 PKPTPAW 52

RESULT 132

O9TBB2
ID O9TBB2 PRELIMINARY; PRT; 53 AA.
AC O9TBB2;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE ATPASE 8 (FRAGMENT).
OS Tadorna tadorna.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Tadorna.
OX NCBI_TaxID=75865;
RN [1]
RP SEQUENCE FROM N.A.
RA Sorenson M.D., Cooper A., Paxinos E.E., Quinn T.W., James H.F.,
RA Olson S.L., Fleischner R.C.;
RT "Relationships of the extinct moa-nalos, flightless Hawaiian waterfowl,
RT based on ancient DNA.";
RL Proc. R. Soc. Lond. B, Biol. Sci. 0:0-0(1999).
DR EMBL; AF173744; AAF07026.1; -.
DR InterPro: IPR001421; ATP-synt_8.
DR InterPro: IPR003237; Avian_mito_ATPase_8.
DR Pfam; PF00895; ATP-synt_8; 1.
DR ProDom; PD161863; Avian_mito_ATPase_8; 1.
KW Mitochondrion.
FT NON_TER 53
SQ SEQUENCE 53 AA; 5970 MW; 4E1E99525B855882 CRC64;

Query Match 52.1%; Score 37; DB 8; Length 53;
Best Local Similarity 62.5%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PKPQOWFW 9
| | | | |
Db 45 PKPAPPAW 52

RESULT 133

O9RM36
ID O9RM36 PRELIMINARY; PRT; 116 AA.
AC O9RM36;
DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE HYPOTHETICAL PROTEIN (FRAGMENT).
 OS Escherichia coli.
 OG Plasmid por117.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PLASMID-POR117;
 RX MEDLINE=84067491; PubMed=6358799;
 RA Tait R.C., Kado C.I., Rodriguez R.L.;
 RT "A comparison of the origin of replication of pSA with R6K.";
 RL Mol. Gen. Genet. 192:32-38(1983).
 DR EMBL: X00060; CAB56196.1; -;
 KW Plasmid.
 FT NON_TER 1 1
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; E41EBB9C4F154A52 CRC64;

Query Match 52.1%; Score 37; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WFWLM 11
 |||||
 DB 103 WFWLM 107

RESULT 134

ID Q9ADB8 PRELIMINARY; PRT; 181 AA.
 AC Q9ADB8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE HYPOTHETICAL 20.5 KDA PROTEIN.
 GN SCBAC5H2.19.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Saunders D.C., Harris D.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL: AL589707; CAC33914.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 181 AA; 20454 MW; F7C3F5048309A3C5 CRC64;

Query Match 52.1%; Score 37; DB 2; Length 181;
 Best Local Similarity 60.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPKPQWFWL 10

DB 142 RPLPDLWPWL 151
 || | | | |

RESULT 135

ID O14264 PRELIMINARY; PRT; 220 AA.
 AC O14264;
 DT 01-MAY-1998 (TrEMBLrel. 05, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE HYPOTHETICAL 25.8 KDA PROTEIN C7D4.09C IN CHROMOSOME I.
 GN SPAC7D4.09C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Gentles S., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z99532; CAB16726.2; -;
 DR InterPro: IPR001104; S5A_redtse_C.
 KW Hypothetical protein.
 SQ SEQUENCE 220 AA; 25760 MW; 8314536BD00595C8 CRC64;

Query Match 52.1%; Score 37; DB 3; Length 220;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 POOWFW 9
 |::|||
 DB 61 PKRWF 66

RESULT 136

ID Q9V424 PRELIMINARY; PRT; 226 AA.
 AC Q9V424;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE METHYL-CPG-BINDING-DOMAIN-LIKE-PROTEIN.
 GN METHYL-CPG-BINDING-DOMAIN-LIKE-PROTEIN OR CG8208.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Niklos G.L.G.,
 RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadenot L.B., Davies P.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies I.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,


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RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong E., Wang A.H., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003683; AAP54400.1;
DR Flybase; FBgn0027930; MBD.
DR InterPro; IPR001739; MBD.
DR SMART; SM00391; MBD; 1.
SQ SEQUENCE 314 AA; 33803 MW; 7B6BDFE63873D230 CRC64;

Query Match 52.1%; Score 37; DB 5; Length 314;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPQOWFW.9
Db 198 REKPKQLEW 206

RESULT 140
Q00893 PRELIMINARY; PRT; 331 AA.
AC Q00893;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PECTATE LYASE (FRAGMENT).
GN PEL.
OS Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella
OS eugulata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC Glomerella.
OX NCBI_TaxID=5457;
RN [1]
```

01-NOV-1998 (TRENBLrel. 08, Created)
01-NOV-1998 (TRENBLrel. 08, Last sequence update)
01-JUN-2001 (TRENBLrel. 17, Last annotation update)
ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-
FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 9) (FUCT-IX) (MFUC-TIX).
FUT9.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
STRAIN=BALB/C; TISSUE=BRAIN;
MEDLINE=98434588; PubMed=9756916;
Kudo T., Ikehara Y., Togayachi A., Kaneko M., Hiraga T., Sasaki K.,
Narimatsu H.;
"Expression cloning and characterization of a novel murine alpha1, 3-
fucosyltransferase, mfuc-tix, that synthesizes the Lewis x (CD15)
epitope in brain and kidney.";
J. Biol. Chem. 273:26729-26738(1998).
-!- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
THE EXPRESSION OF LEWIS X AND LEWIS Y.
-!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,4-BETA-D-GALACTOSYL-N-
ACETYL-D-GLUCOSAMINYL-R = GDP + 1,4-BETA-D-GALACTOSYL-(ALPHA-
1,3-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
-!- PATHWAY: GLYCOSYLATION
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERNAE OF GOLGI.
-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN AND KIDNEY. IT
ALSO EXPRESSED IN THE STOMACH, COLON, UTERUS AND EPIDIDYMIS. NOT
FOUND IN THYMUS, LIVER, SPLEEN, Ovary, LUNG, HEART, TESTIS AND
SMALL INTESTINE.
EMBL; AB015426; BAA33522.1; -.
MGD; MGI:1330859; Fut9.
InterPro; IPR001503; Glyco_transf_10.
Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
Signal-anchor; Golgi stack.
FT DOMAIN 1 11 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 12 30 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 31 359 LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 359 AA; 42041 MW; 96A2394547F2A44E CRC64;
Query Match 52.1%; Score 37; DB 11; Length 359;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RPKPQWFNL 10
Db 125 RPFQKWIWM 134
RESULT 143
Q9JIG1 PRELIMINARY; PRT; 359 AA.
ID Q9JIG1
AC Q9JIG1
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-
FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 9) (FUCT-IX).
GN FUT9.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]

SEQUENCE FROM N.A.
TISSUE=OVARY;
MEDLINE=20166953; PubMed=10700388;
Patnaik S.K., Zhang A., Shi S., Stanley P.;
"Alpha(1,3)fucosyltransferases expressed by the gain-of-function
Chinese hamster ovary glycosylation mutants LEC12, LEC29, and LEC30.";
Arch. Biochem. Biophys. 375:322-332(2000).
-!- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
THE EXPRESSION OF LEWIS X AND LEWIS Y.
-!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,4-BETA-D-GALACTOSYL-N-
ACETYL-D-GLUCOSAMINYL-R = GDP + 1,4-BETA-D-GALACTOSYL-(ALPHA-
1,3-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
-!- PATHWAY: GLYCOSYLATION
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERNAE OF GOLGI.
EMBL; AF230460; AAF82412.1; -.
InterPro; IPR001503; Glyco_transf_10.
Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
Signal-anchor; Golgi stack.
FT DOMAIN 1 11 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 12 30 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 31 359 LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 359 AA; 42071 MW; 9D5CD8BFF07EA902 CRC64;
Query Match 52.1%; Score 37; DB 11; Length 359;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RPKPQWFNL 10
Db 125 RPFQKWIWM 134
RESULT 144
Q99JB3 PRELIMINARY; PRT; 359 AA.
ID Q99JB3
AC Q99JB3
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE ALPHA1,3-FUCOSYLTRANSFERASE IX.
GN FUT9.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Shimoda Y., Tajima Y., Osanai T., Katsume A., Kohara M., Kudo T.,
Narimatsu H., Osumi N., Sanai Y.;
"Expression of Lewis x epitope in embryonic forebrain by regulating
alpha1,3-fucosyltransferase IX expression.";
Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=20472964; PubMed=11020213;
RA Baboval T., Henion T., Kinnally E., Smith F.I.;
"Molecular cloning of rat alpha1,3-fucosyltransferase IX (Fuc-TIX) and
comparison of the expression of fuc-TIV and fuc-TIX genes during rat
postnatal cerebellum development.";
J. Neurosci. Res. 62:206-215(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Smith F.I., Baboval T.;
Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [1]

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DR EMBL; AB049819; BAB40953.1; -.
DR EMBL; AF345993; AAK16591.1; -.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 359 AA; 42037 MW; 369BA47BD0C6CC80 CRC64;

Query Match 52.1%; Score 37; DB 11; Length 359;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWF 10
||| | | |
Db 125 RPPQKWIW 134

RESULT 145
Q9TQO3 PRELIMINARY; PRT; 365 AA.
AC Q9TQO3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.-).
GN FUTB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN; COLON, HEART, LIVER, LUNG, TESTIS, SPLEEN, AND KIDNEY;
RX MEDLINE=20022985; PubMed=10555285;
RA Wierinckx A., Mercier D., Oulmouden A., Petit J.M., Julien R.;
RT "Complete genomic organization of futb encoding a bovine alpha3-
RT fucosyltransferase: exons in human orthologous genes emerged from
RT ancestral intronic sequences."
RL Mol. Biol. Evol. 16:1535-1547(1999).
RC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
CC THE EXPRESSION OF LEWIS X/SSEA-1 AND VIM-2 ANTIGENS.
CC -1- PATHWAY: GLYCOSYLATION.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC FORM IN TRANS CISTERNAE OF GOLGI.
DR EMBL; AJ132776; CAA10775.1; -.
DR EMBL; AJ132773; CAA10772.1; -.
DR EMBL; AJ132774; CAA10773.1; -.
DR EMBL; AJ132775; CAA10774.1; -.
DR EMBL; AJ132772; CAA10771.1; -.
DR InterPro; IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
KW Signal-anchor; Golgi stack.
FT DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 16 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 35 365 LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 111 111 F -> L (IN CAA10771).
FT CONFLICT 122 122 K -> Q (IN CAA10771).
FT CONFLICT 132 133 AD -> PG (IN CAA10771).
SQ SEQUENCE 365 AA; 42720 MW; 0E5F5F8002AF5A8D CRC64;

Query Match 52.1%; Score 37; DB 6; Length 365;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
||| | | |
Db 130 RPAQQRWV 138
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RESULT 146
Q9KQW4 PRELIMINARY; PRT; 406 AA.
AC Q9KQW4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL PROTEIN VC1884.
GN VC1884.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
DR EMBL; AE004263; AAF95032.1; -.
DR TIGR; VC1884; -.
DR InterPro; IPR003838; DUF214.
DR Pfam; PF02687; DUF214; 1.
KW Complete proteome.
SQ SEQUENCE 406 AA; 43747 MW; 4879D14D30442588 CRC64;

Query Match 52.1%; Score 37; DB 2; Length 406;
Best Local Similarity 55.8%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
||| | | |
Db 243 QPLPQDQW 251

RESULT 147
Q9EX44 PRELIMINARY; PRT; 421 AA.
AC Q9EX44;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PUTATIVE INTEGRAL MEMBRANE PROTEIN.
GN 2SCG2.07.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Brown S.P., Harris D.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denepaite D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
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RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL: AL445983; CAC14362.1; -.
 DR InterPro: IPR001958; TCR_beta.
 DR PRINTS: PR01035; TCRETA.
 SQ SEQUENCE 421 AA; 43821 MW; A0B747AFF09EA6FF CRC64;

Query Match 52.1%; Score 37; DB 2; Length 421;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WFWLM 11
 |||||
 DB 372 WFWLM 376

RESULT 148
 Q9CK08 PRELIMINARY; PRT; 467 AA.
 AC Q9CK08;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE HYPOTHETICAL PROTEIN PM1829.
 GN PM1829.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PM70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.-J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida Pm70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 DR EMBL: AE006220; AAK03913.1; -.
 DR InterPro: IPR002035; VWFA.
 DR SMART: SM00327; VWA; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 467 AA; 52878 MW; 6AF5BDABCC75A776 CRC64;

Query Match 52.1%; Score 37; DB 2; Length 467;
 Best Local Similarity 57.1%; Pred. No. 3.2e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQWF 9
 ||:|:|
 DB 156 KPTRYW 162

RESULT 149
 Q9FDI3 PRELIMINARY; PRT; 529 AA.
 AC Q9FDI3;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE CYCLOHEXANONE MONOOXYGENASE 2.
 GN CHNB2.
 OS Brevibacterium sp. HCU.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Micrococineae; Brevibacteriaceae; Brevibacterium.
 OX NCBI_TaxID=133406;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HCU;
 RX MEDLINE=20353458; PubMed=10894733;
 RA Brzostowicz P.C., Gibson K.L., Thomas S.M., Blasko M.S.,
 RA Rouviere P.E.;
 RT "Simultaneous Identification of Two Cyclohexanone Oxidation Genes from

RT an Environmental Brevibacterium Isolate Using mRNA Differential
 RT Display.";
 RL J. Bacteriol. 182:4241-4248(2000).
 CC -I- COFACTOR: FAD (BY SIMILARITY).
 DR EMBL: AF257215; AAG01290.1; -.
 DR InterPro: IPR001327; FAD_pyr_redox.
 DR PRINTS: PR001100; pyr_redox.
 DR PRINTS: PR00368; FADPNR.
 DR PRINTS: PR00411; PNDRDTASEI.
 DR FAD: Flavoprotein; Monooxygenase; Oxidoreductase.
 SQ SEQUENCE 529 AA; 59143 MW; 71DE09C8A4E441BF CRC64;

Query Match 52.1%; Score 37; DB 2; Length 529;
 Best Local Similarity 50.0%; Pred. No. 3.6e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOQWF 9
 ||:|:|
 DB 501 PKAKSNW 508

RESULT 150
 Q9KLT3 PRELIMINARY; PRT; 536 AA.
 AC Q9KLT3;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE METHYL-ACCEPTING CHEMOTAXIS PROTEIN.
 GN VCA0658.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=686;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae.";
 RL Nature 406:477-483(2000).
 DR EMBL: AE004395; AAF96559.1; -.
 DR TIGR: VCA0658; -.
 DR InterPro: IPR000122; Chemotaxis_transducer.
 DR InterPro: IPR001610; PAC.
 DR Pfam: PF00015; MCPsignal; 1.
 DR Pfam: PF00785; PAC; 1.
 DR Pfam: PF00989; PAC; 1.
 DR SMART: SM00283; NA; 1.
 DR SMART: SM00086; PAC; 1.
 DR SMART: SM00091; PAC; 1.
 KW Complete proteome.
 SQ SEQUENCE 536 AA; 59005 MW; C56D363FDD020CA45 CRC64;

Query Match 52.1%; Score 37; DB 2; Length 536;
 Best Local Similarity 71.4%; Pred. No. 3.7e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQOWFWL 10
 |:|:| |
 DB 188 PQOWWL 194

RESULT 151

Q9RPG1 Q9RPG1 PRELIMINARY; PRT; 565 AA.
AC Q9RPG1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PRNC.
GN PRNC.
OS Myxococcus fulvus.
OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
OC Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=33;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=MX F147;
RX MEDLINE=20016567; PubMed=10547442;
RA Hammer P.E., Burd W., Hill D.S., Ligon J.M., van Pee K.-H.;
RT "Conservation of the pyrrolnitrin biosynthetic gene cluster among six
RT pyrrolnitrin-producing strains."
RL FEMS Microbiol. Lett. 180:39-44(1999).
DR EMBL: AF1611185; AAD46367.1; -.
DR InterPro: IPR003042; Rng_mnxygenase.
DR PRINTS; PR00420; RNMNOXGNASE.
SQ SEQUENCE 565 AA; 64513 MW; C308826D69CA4921 CRC64;

Query Match 52.1%; Score 37; DB 2; Length 565;
Best Local Similarity 55.6%; Pred. No. 3.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
:|:|:|:
DB 227 KPGQRWRW 235

RESULT 152
Q9RJ38 Q9RJ38 PRELIMINARY; PRT; 595 AA.
AC Q9RJ38;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE HYPOTHETICAL 66.3 KDA PROTEIN.
GN SC18.15.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Oliver K., Harris D.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapait D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL: AL132644; CAB59446.1; -.
KW Hypothetical protein.
SQ SEQUENCE 595 AA; 66269 MW; BDB2911451B27282 CRC64;

Query Match 52.1%; Score 37; DB 2; Length 595;

Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQW 7
:|:|:|:
DB 362 RPRPQW 368

RESULT 153
Q9XMR9 Q9XMR9 PRELIMINARY; PRT; 604 AA.
AC Q9XMR9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT 2 (EC 1.9.3.1).
GN COX2.
OS Tetrahymena pyriformis.
OG Mitochondrion.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymena.
OX NCBI_TaxID=5908;
RN [1]
RN SEQUENCE FROM N.A.
RA Edqvist J., Burger G., Gray M.W.;
RT "Expression of mitochondrial protein-coding genes in Tetrahymena
RT pyriformis."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RA Burger G., Zhu Y., Littlejohn T.G., Greenwood S.J., Schnare M.N.,
RA Lang B.F., Gray M.W.;
RT "Complete sequence, gene content and organization of the mitochondrial
RT genome of Tetrahymena pyriformis. Comparison with Paramecium aurelia
RT mitochondrial DNA."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF160864; AAD41945.1; -.
DR InterPro: IPR001505; COX2.
DR Pfam: PF00116; COX2; 1.
DR ProDom: PD000131; COX2; 1.
KW Oxidoreductase; Mitochondrion.
SQ SEQUENCE 604 AA; 72130 MW; 87F1E59532E0D064 CRC64;

Query Match 52.1%; Score 37; DB 8; Length 604;
Best Local Similarity 40.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWF 10
:|:|:|:
DB 116 RVRARQWYI 125

RESULT 154
Q62094 Q62094 PRELIMINARY; PRT; 645 AA.
AC Q62094;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PROTEIN CONVERTASE 4.
GN PC4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=LIVER;
RX MEDLINE=92210552; PubMed=1372895;
RA Nakayama K., Kim W.S., Torii S., Hosaka M., Nakagawa T., Ikemizu J.,
RA Baba T., Murakami K.;

RT "Identification of the fourth member of the mammalian endoprotease
RT family homologous to the yeast Kex2 protease. Its testis-specific
RT expression.";
RL J. Biol. Chem. 267:5897-5900(1992).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=LIVER;
RX MEDLINE=93078790; PubMed=1448111;
RA Seidah N.G., Day R., Hamelin J., Gaspar A., Collard M.W., Chretien M.;
RT "Testicular expression of PC4 in the rat: molecular diversity of a
RT novel germ cell-specific Kex2/subtilisin-like proprotein convertase.";
RT Mol. Endocrinol. 6:1559-1570(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=LIVER;
RX MEDLINE=94292203; PubMed=8020970;
RA Minkay M., Raffin-Sanson M.L., Tadros H., Sirolis F., Seidah N.G.,
RA Chretien M.;
RT "Structure of the gene for the testis-specific proprotein convertase 4
RT and of its alternate messenger RNA isoforms.";
RL Genomics 20:231-237(1994).
DR EMBL; L21221; AAA39973.1; JOINED.
DR EMBL; L21210; AAA39973.1; JOINED.
DR EMBL; L21211; AAA39973.1; JOINED.
DR EMBL; L21212; AAA39973.1; JOINED.
DR EMBL; L21213; AAA39973.1; JOINED.
DR EMBL; L21214; AAA39973.1; JOINED.
DR EMBL; L21215; AAA39973.1; JOINED.
DR EMBL; L21216; AAA39973.1; JOINED.
DR EMBL; L21217; AAA39973.1; JOINED.
DR EMBL; L21218; AAA39973.1; JOINED.
DR EMBL; L21219; AAA39973.1; JOINED.
DR EMBL; L21220; AAA39973.1; JOINED.
DR EMBL; L21223; AAA39973.1; JOINED.
DR HSPF; Q99405; IMPT.
DR InterPro; IPR000209; Peptidase_S8.
DR InterPro; IPR002884; P_domain.
DR Pfam; PF01483; P. 1.
DR Pfam; PF00082; Peptidase_S8. 1.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000717; P_domain; 1.
DR PROSITE; PS00136; SUBTILASE_ASP. 1.
DR PROSITE; PS00137; SUBTILASE_HIS. 1.
DR PROSITE; PS00138; SUBTILASE_SER. 1.
KW Serine protease
SQ SEQUENCE 645 AA; 71980 MW; 54B07AA4A97D8AA0 CRC64;

Query Match 52.1%; Score 37; DB 11; Length 645;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 QQFWL 10
Db 615 QQWWL 620
|||:|

RESULT 155
Q9QU36 PRELIMINARY; PRT; 656 AA.
AC Q9QU36;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE DNA, COMPLETE GENOME, ISOLATE:TLMV-CBD203.
OS TTV-like mini virus.
OC Viruses; ssDNA viruses; Circoviridae.
OX NCBI_TaxID=93678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TLMV-CBD203;
RA Mishiro S.;
RA Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TLMV-CBD203;
RA Takahashi K., Iwasa Y., Hijikata M., Mishiro S.;
RT "Identification of a new human DNA virus (TTV-like mini virus: TLMV)
RT immediately related to TT virus and chicken anemia virus.";
RL Arch. Virol. 0:0-0(1999).
DR EMBL; AB026929; BAA86945.1; -.
SQ SEQUENCE 656 AA; 76983 MW; DA2CA1D3C2D83A37 CRC64;

Query Match 52.1%; Score 37; DB 12; Length 656;
Best Local Similarity 44.4%; Pred. No. 4.5e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKQOWFW 9
Db 268 KPQNNMFW 276
|||:

RESULT 156
Q9PVX6 PRELIMINARY; PRT; 669 AA.
AC Q9PVX6;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CPEOMESODERMIN PROTEIN.
GN CPEOMESODERMIN.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroides; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RX MEDLINE=99325981; PubMed=10400394;
RA Sone K., Takahashi T.C., Takabatake Y., Takeshima K., Takabatake T.;
RT "Expression of five novel T-box genes and brachyury during
RT embryogenesis, and in developing and regenerating limbs and tails of
RT newts.";
RL Dev. Growth Differ. 41:321-333(1999).
DR EMBL; AB019785; BAA84718.1; -.
DR HSPF; P24781; 1XBR.
DR InterPro; IPR001699; T-box.
DR Pfam; PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR SMART; SM00425; TBOX. 1.
DR PROSITE; PS01283; TBOX_1; 1.
DR PROSITE; PS01264; TBOX_2; 1.
DR PROSITE; PS02552; TBOX_3; 1.
SQ SEQUENCE 669 AA; 72294 MW; 58D870CCF057C0FA CRC64;

Query Match 52.1%; Score 37; DB 13; Length 669;
Best Local Similarity 71.4%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RPKQOWFW 8
Db 489 PSPQWF 495
|||:

RESULT 157
Q9SRV5 PRELIMINARY; PRT; 765 AA.
AC Q9SRV5;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE PUTATIVE METHIONINE SYNTHASE.
GN F20H23.19.
OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.I., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC F20H23 genomic sequence."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC009540; AAF00639.1; -
DR InterPro; IPR002629; Methionine_synth.
DR Pfam; PF01717; Methionine_synth; 1
SQ SEQUENCE 765 AA; 84583 MW; EB478D815910E701 CRC64;

Query Match 52.1%; Score 37; DB 10; Length 765;
Best Local Similarity 66.7%; Pred. No. 5.2e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWFW 9
|||||
DB 534 RPKPMTVFW 542

RESULT 158

ID Q9LM03 PRELIMINARY; PRT; 765 AA.
AC Q9LM03;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE METHIONINE SYNTHASE (EC 2.1.1.14).
GN MS.
OS Solanum tuberosum (potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeh M., Leggewie G., Hoefgen R., Hesse H.;
RT "Isolation and characterization of a cDNA encoding methionine synthase
from Solanum tuberosum."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF082893; AAF74393.1; -
DR InterPro; IPR002629; Methionine_synth.
DR Pfam; PF01717; Methionine_synth; 1.
KW Transferase; Methyltransferase.
SQ SEQUENCE 765 AA; 84665 MW; 6112AF7047DAD485 CRC64;

Query Match 52.1%; Score 37; DB 10; Length 765;
Best Local Similarity 66.7%; Pred. No. 5.2e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWFW 9
|||||
DB 534 RPKPMTVFW 542

RESULT 159

ID Q9FFZ5 PRELIMINARY; PRT; 806 AA.
AC Q9FFZ5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GB|AA|00669.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002544; BAB09687.1; -
SQ SEQUENCE 806 AA; 89645 MW; 71645A5EE9E7746C CRC64;

Query Match 52.1%; Score 37; DB 10; Length 806;
Best Local Similarity 50.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPQQWFW 9
|||
DB 197 PEANEWFW 204

RESULT 160

Q9HEW7
ID Q9HEW7 PRELIMINARY; PRT; 918 AA.
AC Q9HEW7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE NITROGEN RESPONSE FACTOR NR1.
OS Cladosporium fulvum (Fulvia fulva).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC Dothideomycetes et Chaetothyriomycetes incertae sedis;
OC Mycosphaerellaceae; mitosporic Mycosphaerellaceae; Cladosporium.
OX NCBI_TaxID=5499;
RN [1]
RP SEQUENCE FROM N.A.
RA Perez-Garcia A., Snoeijers S.S., Joosten M.H.A.J., Goosen T.,
RA De Wit P.J.G.M.;
RT "Expression of the avirulence gene Avr9 of the fungal tomato pathogen
Cladosporium fulvum is regulated by the global nitrogen response
factor NR1."
RL Mol. Plant Microbe Interact. 0:0-0(2001).
DR EMBL; AF312694; AAG48616.1; -
DR InterPro; IPR002965; P-rich_extensn.
DR InterPro; IPR000679; ZnF_GATA.
DR Pfam; PF00320; GATA; 1.
DR PRINTS; PR00619; GATAZNFINGER.
DR PRINTS; PR01217; PRICHEXTENS.
DR SMART; SM00401; ZnF_GATA; 1.
DR PROSITE; PS00344; GATA_ZN_FINGER_1; 1.
DR PROSITE; PS01114; GATA_ZN_FINGER_2; 1.
SQ SEQUENCE 918 AA; 99077 MW; E98198D999BCA899 CRC64;

Query Match 52.1%; Score 37; DB 3; Length 918;
Best Local Similarity 71.4%; Pred. No. 6.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQWFWL 10
|||
DB 908 PQEWFWL 914

RESULT 161

O60043
ID O60043 PRELIMINARY; PRT; 944 AA.
AC O60043;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE NITROGEN RESPONSE REGULATOR.

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GN NRRI.
OS Metarhizium anisopliae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae; Metarhizium.
OX NCBI_TaxID=5530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MEL;
RA Screen S., Bailey A., Charnley K., Cooper R., Clarkson J.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006468; CAA07052.1; -.
DR HSSP; P17429; 4GAT.
DR InterPro; IPR000679; ZNF_GATA.
DR Pfam; PF00320; GATA; 1.
DR PRINTS; PR00619; GATAZNFINGER.
DR SMART; SM00401; ZNF_GATA; 1.
DR PROSITE; PS00344; GATA_ZN_FINGER_1; 1.
DR PROSITE; PS00114; GATA_ZN_FINGER_2; 1.
SQ SEQUENCE 944 AA; 99686 MW; A1A723E658C23EA0 CRC64;

Query Match 52.1%; Score 37; DB 3; Length 944;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PQQFWL 10
   ||:| ||
Db 934 PQQFWL 940

RESULT 162
Q9W570 PRELIMINARY; PRT; 1002 AA.
ID Q9W570
AC Q9W570
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-JUN-2001 (Tremblrel. 13, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE DOR OR EG:171E4.1 OR CG3093.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

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RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kimos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003421; AAF45652.1; -.
DR FlyBase; FBgn0000482; dor.
DR InterPro; IPR000547; Clathrin_repeat.
DR InterPro; IPR001841; Znf_ring.
DR SMART; SM00299; CLH; 1.
DR SMART; SM00184; RING; 1.
SQ SEQUENCE 1002 AA; 115319 MW; 5B56BFE9040256BB CRC64;

Query Match 52.1%; Score 37; DB 5; Length 1002;
Best Local Similarity 71.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PQQFWL 10
   ||:| ||
Db 301 PQQFWL 307

RESULT 163
Q9H8F3 PRELIMINARY; PRT; 1081 AA.
ID Q9H8F3
AC Q9H8F3
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CDNA FLJ13680 FIS, CLONE PLACE2000007, HIGHLY SIMILAR TO HOMO SAPIENS
DE KIA0913 PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Naganari K., Masuho Y., Oshima A.;
RT "NEDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK023742; BAB14664.1; -.
SQ SEQUENCE 1081 AA; 115370 MW; 01975A049C70A001 CRC64;

Query Match 52.1%; Score 37; DB 4; Length 1081;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QNFWL 10
   |||||
Db 663 QNFWL 667

RESULT 164
Q94987 PRELIMINARY; PRT; 1301 AA.
ID Q94987
AC Q94987
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)

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DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE KIAA0913 PROTEIN (FRAGMENT).
GN KIAA0913.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosewa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT *Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.*;
RL DNA Res. 5:355-364(1998).
DR EMBL; AB020720; BAA74936.1; -.
FT NON_TER 1
SQ SEQUENCE 1301 AA; 138677 MW; E0F0C4CE12615646 CRC64;

Query Match 52.1%; Score 37; DB 4; Length 1301;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QWFWL 10
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|
Db 1134 QWFWL 1138

RESULT 165
O93457 PRELIMINARY; PRT; 1418 AA.
AC O93457;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INSULIN-LIKE GROWTH FACTOR 1 RECEPTOR PRECURSOR.
OS Scophthalmus maximus (turbot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronotoidei; Scophthalmidae; Scophthalmus.
OX NCBI_TaxID=52904;
RN [1]
RP SEQUENCE FROM N.A.
RA Elies G., Duval H., Bonnet G., Wolff J., Boeuf G., Boujard D.;
RT *Turbot insulin and insulin-like growth factor-1 receptors: cDNAs
RT cloning and messenger RNAs expression during development.*;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; AJ224993; CAA12278.1; -.
DR HSP; P06213; IIRK.
DR InterPro; IPR000494; EGFR_L.
DR InterPro; IPR000719; Euk.pkinase.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR002011; Receptor_tyr_kin_II.
DR InterPro; IPR001245; Tyr_kin.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 1.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00261; FU; 1.
DR SMART; SM00219; TYRKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Signal;
KW Transferase; Transmembrane; Tyrosine-protein kinase.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 1418 INSULIN-LIKE GROWTH FACTOR 1 RECEPTOR.
SQ SEQUENCE 1418 AA; 159826 MW; 5D9921332113C4AE CRC64;

Query Match 52.1%; Score 37; DB 13; Length 1418;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQW 7
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|
Db 1099 RPKPQQW 1105

RESULT 166
Q91588 PRELIMINARY; PRT; 1589 AA.
ID Q91588
AC Q91588;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE COMPLEMENT COMPONENT C3 (FRAGMENT).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=95180322; PubMed=7875221;
RA Lambiris J.D., Fappas J., Mavroidis M., Wang Y., Manzone H., Swager J.,
RA Du Pasquier L., Silibovsky R.;
RT *The third component of Xenopus complement: cDNA cloning, structural
RT and functional analysis, and evidence for an alternate C3
RT transcript.*;
RL Eur. J. Immunol. 25:572-578(1995).
DR EMBL; U15253; AAB60608.1; -.
DR HSP; P01024; IC3D.
DR InterPro; IPR002890; A2M_N.
DR InterPro; IPR001599; Alpha_2_macrogllobln.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR001840; Anaphylatoxn.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF00207; A2M; 1.
DR Pfam; PF01835; A2M_N; 1.
DR Pfam; PF01821; ANATO; 1.
DR Pfam; PF01759; NTR; 1.
DR PRINTS; PR00004; ANAPHYLATOXN.
DR SMART; SM00104; ANATO; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
FT NON_TER 1 588 COMPLEMENT COMPONENT C3 BETA CHAIN.
FT CHAIN 592 1489 COMPLEMENT COMPONENT C3 ALPHA CHAIN.
FT CHAIN 1589 AA; 177904 MW; DCB777FB4B11456A CRC64;
SQ SEQUENCE 1589 AA; 177904 MW; DCB777FB4B11456A CRC64;

Query Match 52.1%; Score 37; DB 13; Length 1589;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PQQWFW 9
|
|
|
Db 691 PESWFW 696

RESULT 167
O17368

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ID O17368 PRELIMINARY; PRT; 1635 AA.
AC O17368;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE F48A11.1 PROTEIN.
GN F48A11.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden K., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;
RC Bradshaw H.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;
RC Waterston R.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF026210; AAB71283.1; -.
SQ SEQUENCE 1635 AA; 186341 MW; F07C3281935A2E98 CRC64;

Query Match 52.1%; Score 37; DB 5; Length 1635;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQQFWL 10
Db 580 PQTWL 586

RESULT 168
ID O51827 PRELIMINARY; PRT; 2458 AA.
AC O51827;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE POLYKETIDE SYNTHASE TYPE I.
GN PLTB.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=294;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=PF-5;
RX MEDLINE=98094250; PubMed=9434161;
RA Nowak-Thompson B., Gould S.J., Loper J.E.;
RT "Identification and sequence analysis of the genes encoding a
RT polyketide synthase required for pyoluteorin biosynthesis in
RT Pseudomonas fluorescens Pf-5.";
RL Gene 204:17-24(1997).
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RN SEQUENCE FROM N.A.
RP STRAIN=PF-5;
RA Nowak-Thompson B., Gould S.J., Loper J.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF081920; AAC38075.1; -.
DR InterPro; IPR001227; Acyltransf_domain.
DR InterPro; IPR000794; Ketoacyl-synt.
DR InterPro; IPR003880; Phosphopant_attach.
DR InterPro; IPR002155; Thiolase.
DR Pfam; PF00698; Acyl_transf; 1.
DR Pfam; PF00109; ketoacyl-synt; 2.
DR Pfam; PF00550; pp-binding; 2.
DR PROSITE; PS00075; ACP_DOMAIN; 2.
DR PROSITE; PS00606; B-KETOACYL SYNTHASE; 2.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
DR PROSITE; PS00098; THIOLEASE_1; UNKNOWN_1.
KW Phosphopantetheine; Transferase.
SQ SEQUENCE 2458 AA; 262676 MW; AE756080AE1A5FB1 CRC64;

Query Match 52.1%; Score 37; DB 2; Length 2458;
Best Local Similarity 55.6%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKQOWFW 9
Db 1613 RPAQLWV 1621

RESULT 169
Q99N19
ID Q99N19 PRELIMINARY; PRT; 523 AA.
AC Q99N19;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYTOCHROME P450 CYP4F13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=129/SV+TP TYR C-CH TER/+; TISSUE=KIDNEY;
RA Antonovic L., Kawashima H., Strobel H.;
RT "Protein expression and catalytic activity assessment of mouse 4F
RT clones.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF233643; AAK15009.1; -.
SQ SEQUENCE 523 AA; 59823 MW; 47E0E7840940CE21 CRC64;

Query Match 51.4%; Score 36.5; DB 11; Length 523;
Best Local Similarity 75.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 2 PKPQOWFW 9
Db 55 PKP-SNFW 61

RESULT 170
Q99KY6
ID Q99KY6 PRELIMINARY; PRT; 523 AA.
AC Q99KY6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE SIMILAR TO RIKEN CDNA I810054N16 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=MAMMARY TUMOR;

RA Strausberg R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL: BC003954; AAB03954.1; -

SQ SEQUENCE 523 AA; 59894 MW; 3927661E5FBD20CD CRC64;

Query Match

51.4%; Score 36.5; DB 11; Length 523;

Best Local Similarity 75.0%; Pred. No. 4.3e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 PKPQOWFW 9

||| |||

Db 55 PKP-SWFW 61

RESULT 171

Q9SDN8

ID Q9SDN8 PRELIMINARY; PRT; 93 AA.

AC Q9SDN8;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE ELICITIN-LIKE PROTEIN (FRAGMENT).

OS Phytophthora capsici.

OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;

OC Phytophthora.

OX NCBI_TaxID=4784;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PI314-T1;

RA Bailey A.M.;

RL "Detection and Identification of additional gene products induced by

RT the interaction between Phytophthora capsici and its host, Capsicum

RT annum."

RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

DR EMBL: AF212434; AAF18483.1; -

FT NON_TER 1

FT NON_TER 93

SQ SEQUENCE 93 AA; 11050 MW; E57D17B614107060 CRC64;

Query Match

50.7%; Score 36; DB 10; Length 93;

Best Local Similarity 85.7%; Pred. No. 96;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOOW 7

||| |||

Db 52 RPKVQOW 58

RESULT 172

P73564

ID P73564 PRELIMINARY; PRT; 103 AA.

AC P73564;

DT 01-FEB-1997 (TREMBLrel. 02, Created)

DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)

DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE HYPOTHETICAL 12.2 KDA PROTEIN.

GN SLR0881

OS Synechocystis sp. (strain PCC 6803).

OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.

OX NCBI_TaxID=1148;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97061201; PubMed=8905231;

RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

RA Miyajima N., Hirose M., Sugiyama M., Sugiyama S., Kimura T.,

RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,

RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,

RA Tabata S.;

RT "Sequence analysis of the genome of the unicellular cyanobacterium

RT Synechocystis sp. strain PCC6803. II. Sequence determination of the

RT entire genome and assignment of potential protein-coding regions.";

RL DNA Res 3:109-136(1996).

DR EMBL: D90907; BAA17604.1; -

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 103 AA; 12174 MW; 24EE96F034055C71 CRC64;

Query Match

50.7%; Score 36; DB 2; Length 103;

Best Local Similarity 42.9%; Pred. No. 1.1e+02;

Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQWFW 9

||: ||:

Db 84 RPEHWYW 90

RESULT 173

O76548

ID O76548 PRELIMINARY; PRT; 104 AA.

AC O76548;

DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)

DE GGTA (FRAGMENT).

GN GGTA.

OS Dictyostelium discoideum (Slime mold).

OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

OX NCBI_TaxID=44689;

RN [1]

RP SEQUENCE FROM N.A.

RA Iraufar N., Loomis W.F.;

RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

DR EMBL: AF076603; AAC31542.1; -

FT NON_TER 1

FT NON_TER 1

SQ SEQUENCE 104 AA; 12263 MW; 6150084AE4714CFB CRC64;

Query Match

50.7%; Score 36; DB 5; Length 104;

Best Local Similarity 66.7%; Pred. No. 1.1e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQWFW 9

||: ||:

Db 5 PQEWLW 10

RESULT 174

O9AFZ7

ID O9AFZ7 PRELIMINARY; PRT; 105 AA.

AC O9AFZ7;

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE ORF, HYPOTHETICAL.

GN S0011.

OS Shigella flexneri.

OG Plasmid virulence pWR501.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Shigella.

OX NCBI_TaxID=623;

RN [1]

RP SEQUENCE FROM N.A.

RA Venkatesan M.M., Goldberg M.B., Rose D.J., Grotbeck E.J., Burland V.,

RA Blattner F.R.;

RT "Complete DNA Sequence and Analysis of the Large Virulence Plasmid of

RT Shigella flexneri";

RL Infect. Immun. 0:0-0(2001).

DR EMBL: AF348706; AAK18322.1; -

KW Plasmid.

SQ SEQUENCE 105 AA; 11765 MW; 4D17F10F5FFBCBCC CRC64;

Query Match 50.7%; Score 36; DB 2; Length 105;
 Best Local Similarity 60.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKPQWFNL 10
 |||||
 Db 26 RPYDQWAF 35

RESULT 175

O9DCS0 PRELIMINARY; PRT; 125 AA.
 AC Q9DCS0
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE DETODINASE, IODOTHYRONINE, TYPE I.
 GN DIOL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Sakimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK002549; BAB22180.1; -.
 DR MGD; MGI:94896; Diol.
 SQ SEQUENCE 125 AA; 14309 MW; 2C06DEC77C5F9E21 CRC64;

Query Match 50.7%; Score 36; DB 11; Length 125;
 Best Local Similarity 71.4%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQQWFWL 10
 |||||
 Db 4 PQLWLWL 10

RESULT 176

Q36742 PRELIMINARY; PRT; 135 AA.
 AC Q36742
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ATPASE 8 PROTEIN (FRAGMENT).
 GN ATPASE 8.
 OS Cottus kessleri.
 OC Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
 OC Cottoidel; Cottidae; Cottus.
 OX NCBI_TaxID=8099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95287403; PubMed=7769616;
 RA Slobodyanyuk S.Ja., Kirilchik S.V., Pavlova M.E., Belikov S.I.,
 RA Novitsky A.L.;
 RT "The evolutionary relationships of two families of cottoid fishes of
 RT Lake Baikal (east Siberia) as suggested by analysis of mitochondrial
 RT DNA";
 RL J. Mol. Evol. 40:392-399(1995).
 DR EMBL; S78299; AAD14277.1; -.
 DR InterPro; IPR001421; ATP-synt_8.
 DR Pfam; PF00895; ATP-synt_8; 1.
 KW Mitochondrion.
 FT NON_TER 135 135
 SQ SEQUENCE 135 AA; 15430 MW; B417E429E935357F CRC64;

Query Match 50.7%; Score 36; DB 8; Length 135;
 Best Local Similarity 45.5%; Pred. No. 1.4e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RPKPQWFWM 11
 :||:|
 Db 44 RPKTEPTWPM 54

RESULT 177

Q9RVC1 PRELIMINARY; PRT; 154 AA.
 ID Q9RVC1
 AC Q9RVC1
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE HYPOTHETICAL 16.7 KDA PROTEIN.
 GN DR1108.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RL.
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vanathavan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans RL";
 RL Science 286:1571-1577(1999).
 DR EMBL; AE001961; AAF10689.1; -.
 DR TIGR; DR1108; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 154 AA; 16714 MW; D888E4ACFFE70234 CRC64;

Query Match 50.7%; Score 36; DB 2; Length 154;
 Best Local Similarity 54.5%; Pred. No. 1.6e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKPQWFWM 11
 |:|||||
 Db 46 RQOPQAFWLL 56

RESULT 178

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Q9HWX8          PRELIMINARY;      PRT;    171 AA.
AC Q9HWX8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PHOSPHATIDYLGLYCEROPHOSPHATASE A.
GN PG OR PA4050.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Hickey C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964 (2000).
DR EMBL; AE004821; AAG07437.1; -.
KW Complete proteome.
SQ SEQUENCE 171 AA; 19606 MW; 4C8D5C86276F892D CRC64;

Query Match          50.7%; Score 36; DB 2; Length 171;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQWFWM 11
DB 107 PEGWWLL 114

RESULT 179
Q9FRE0
ID Q9FRE0          PRELIMINARY;      PRT;    241 AA.
AC Q9FRE0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE HYPOTHETICAL 25.1 KDA PROTEIN.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
RA Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSJNBa0013M12 genomic sequence."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC082644; AA46138.1; -.
KW Hypothetical protein.
SQ SEQUENCE 241 AA; 25126 MW; F07B4F4BF05DB6AC CRC64;

Query Match          50.7%; Score 36; DB 10; Length 241;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 QQWFWM 10
DB 149 QQWFWL 154
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RESULT 180
Q9TAK3          PRELIMINARY;      PRT;    250 AA.
AC Q9TAK3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE NADH DEHYDROGENASE SUBUNIT 6 (EC 1.6.5.3).
GN NAD6.
OS Cafeteria roenbergensis.
OC Eukaryota; stramenopiles; Bicosoecida; Cafeteria.
OX NCBI_TaxID=33653;
RN [1]
RP SEQUENCE FROM N.A.
RA Burger G.;
RT "The mitochondrial genome of Cafeteria roenbergensis."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193903; AAF05783.1; -.
DR InterPro; IPR001457; Oxidored_q3.
DR Pfam; PF004499; Oxidored_q3; 1.
KW Oxidoreductase; Mitochondrion.
SQ SEQUENCE 250 AA; 29049 MW; E992796F89D8255B CRC64;

Query Match          50.7%; Score 36; DB 8; Length 250;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPQQWF 9
DB 235 PKPKGFFW 242

RESULT 181
O19110          PRELIMINARY;      PRT;    254 AA.
AC O19110;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE TESTIS-SPECIFIC PROTEIN (FRAGMENT).
GN TSPY.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTES;
RX MEDLINE=97341111; PubMed=9195993;
RA Vogel T., Dechend F., Manz E., Jung C., Jakubiczka S., Fehr S.,
RA Schmidtke J., Schmieders F.;
RT "Organization and expression of bovine TSPY."
RL Mamm. Genome 8:491-496 (1997).
DR EMBL; U75896; AAB72143.1; -.
DR InterPro; IPR002164; NAP_family.
DR Pfam; PF00956; NAP_family; 1.
FT NON_TER 1
SQ SEQUENCE 254 AA; 29745 MW; B36A293999A9132DC CRC64;

Query Match          50.7%; Score 36; DB 6; Length 254;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
DB 186 RSTPVHFW 194
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RESULT 182
Q21187          PRELIMINARY;      PRT;    268 AA.
AC Q21187;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE SIMILARITY TO THE FORK-HEAD DNA BINDING DOMAIN.
GN K03C7.2
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150716; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinon-Sproat J., Wohlman P.; et al.
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Leimbach D.;
RP SEQUENCE (NOV-1995) to the EMBL/GenBank/DBJ databases.
[3]
RA waterston R.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U40059; AAA81139.1; -.
DR HSPF; Q63245; 2HPH.
DR InterPro; IPR001766; Fork_head.
DR Pfam; PF00250; Fork_head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS00339; FORK_HEAD_3; 1.
SQ SEQUENCE 268 AA; 30361 MW; 3AE5FCC8E84F6783 CRC64;

Query Match      50.7%; Score 36; DB 5; Length 268;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQWFW 9
DB 116 RHRPDQGW 124

RESULT 183
Q9KRT5          PRELIMINARY;      PRT;    280 AA.
AC Q9KRT5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE GLYCEROL-3-PHOSPHATE ABC TRANSPORTER, PERMEASE PROTEIN.
GN VC1551
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;

Query Match      50.7%; Score 36; DB 5; Length 268;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQWFW 9
DB 116 RHRPDQGW 124

RESULT 184
Q9RX15          PRELIMINARY;      PRT;    287 AA.
AC Q9RX15;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CONSERVED HYPOTHETICAL PROTEIN.
GN DR0500.
OS Deinococcus radiodurans
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1."
RL Science 286:1571-1577(1999).
DR EMBL; AF001909; AAF10080.1; -.
DR TIGR; DR0500; -.
DR InterPro; IPR003797; DUF194.
DR Pfam; PF02645; DUF194; 1.
KW Complete proteome.
SQ SEQUENCE 287 AA; 30591 MW; 4E247F9B2D278771 CRC64;

Query Match      50.7%; Score 36; DB 2; Length 287;
Best Local Similarity 71.4%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQW 7
DB 64 QPSPOOW 70

RESULT 185
Q53945
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ID Q53945 PRELIMINARY; PRT; 302 AA.
AC Q53945;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE BACTERIOPHAGE (PHIC31) RESISTANCE (PGLY AND PGL2) GENES, COMPLETE
DE CDS S. (FRAGMENT)
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=95370146; PubMed=7642495;
RA Bedford D.J., Laity C., Buttner M.J.;
RT "Two genes involved in the phase-variable phi C31 resistance mechanism
of Streptomyces coelicolor A3(2).";
RL J. Bacteriol. 177:4681-4689(1995).
EMBL; L37531; AAB00368.1; -.
DR InterPro: IPR001969; Asp.protease.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 302 AA; 34027 MW; 7E9DFC5A218402D7 CRC64;

Query Match 50.7%; Score 36; DB 2; Length 302;
Best Local Similarity 57.1%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQWF 9
I :|||
DB 93 KTEQWY 99

RESULT 186
Q9CYX6 PRELIMINARY; PRT; 320 AA.
ID Q9CYX6
AC Q9CYX6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE WINGLESS-RELATED MTW INTEGRATION SITE 5B.
GN WNT5B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALLING
```

```
CC MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC -!- EXTRACELLULAR MATRIX (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.
DR EMBL; AK013218; BAB28720.1; -.
DR MGD; MGI:98959; Wnt5b.
DR InterPro: IPR000970; Wnt1.
DR Pfam: PF00110; wnt; 1.
DR PRINTS; PRQ1349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Glycoprotein.
SQ SEQUENCE 320 AA; 35600 MW; DF75DEDF755B139B CRC64;

Query Match 50.7%; Score 36; DB 11; Length 320;
Best Local Similarity 54.5%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 RPK--PQWFW 9
I :|||
DB 161 RPKDLPDRLW 171

RESULT 187
Q9B4H0 PRELIMINARY; PRT; 343 AA.
ID Q9B4H0
AC Q9B4H0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
OS Callisaurus draconoides.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Phrynosomatinae;
OC Callisaurus.
OX NCBI_TaxID=43586;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ROM4146;
RX MEDLINE=21175753; PubMed=11277627;
RA Trepanier T.L., Murphy R.W.;
RT "The Coachella Valley Fringe-Toed Lizard (Uma inornata): Genetic
Diversity and Phylogenetic Relationships of an Endangered Species.";
RL Mol. Phylogenet. Evol. 18:327-334(2001).
DR EMBL; AF302008; AAK32108.1; -.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 343
SQ SEQUENCE 343 AA; 38734 MW; 812A8815D6A2E331 CRC64;

Query Match 50.7%; Score 36; DB 8; Length 343;
Best Local Similarity 54.5%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPKPQWFWLM 11
I :|||
DB 282 RPKSQTWFWLL 292

RESULT 188
Q47471 PRELIMINARY; PRT; 347 AA.
ID Q47471
AC Q47471;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE PECTATE LIASE.
GN PELB.
```

```
OS Erwinia carotovora.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID=554;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SCC3193;
RA Heikinheimo R., Flego D., Pirhonen M., Karlsson M.B., Eriksson A.,
MAE A., Koiv V., Palva E.T.;
RT "Characterization of a novel pectate lyase from Erwinia carotovora
subsp. carotovora.";
RL MOL. Plant Microbe Interact. 8:207-217(1995).
DR EMBL; X79232; CAA55814.1; -.
KW Lyase.
SQ SEQUENCE 347 AA; 37432 MW; 3E70EECB120D799. CRC64;

Query Match 50.7%; Score 36; DB 2; Length 347;
Best Local Similarity 44.4%; Pred. No. 3.5e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RPKQOQFWL 10
|| | |
Db 82 PKSDYVYVW 90

RESULT 189
ID Q9MW76 PRELIMINARY; PRT; 347 AA.
AC Q9MW76;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN CYTB.
OS Gallotia galloti.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Scincomorpha; Lacertioidea;
OC Lacertidae; Gallotia.
OX NCBI_TaxID=39310;
RN [1]
RP SEQUENCE FROM N.A.
RA Fu J.;
RT "Toward the phylogeny of the family Lacertidae - why 4708 base pairs
of mtDNA sequences cannot draw the picture.";
RL Biol. J. Linn. Soc. Lond. 71:203-217(2000).
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -!- COPFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
DR EMBL; AF206534; AAF70424.1; -.
DR InterPro; IPR001179; Cyt_b.b6.
DR Pfam; PF00033; cytochrome_b.c.1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QQ; UNKNOWN_1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
Transmembrane.
FT NON_TER 1
SQ SEQUENCE 347 AA; 39168 MW; 258F788D4485A139. CRC64;

Query Match 50.7%; Score 36; DB 8; Length 347;
Best Local Similarity 54.5%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OS Erwinia carotovora.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID=554;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SCC3193;
RA Heikinheimo R., Flego D., Pirhonen M., Karlsson M.B., Eriksson A.,
MAE A., Koiv V., Palva E.T.;
RT "Characterization of a novel pectate lyase from Erwinia carotovora
subsp. carotovora.";
RL MOL. Plant Microbe Interact. 8:207-217(1995).
DR EMBL; X79232; CAA55814.1; -.
KW Lyase.
SQ SEQUENCE 347 AA; 37432 MW; 3E70EECB120D799. CRC64;

Query Match 50.7%; Score 36; DB 4; Length 359;
Best Local Similarity 54.5%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 RPK--POQWFW 9
||| | | |
Db 148 RPKDLPRDLW 158

RESULT 191
ID Q9XT34 PRELIMINARY; PRT; 360 AA.
AC Q9XT34;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ALPHA-1,3-FUCOSYLTRANSFERASE (FRAGMENT).
GN FUT3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Meijerink E., Voegel P., Stranzinger G.;
RT "Sus scrofa alpha(1,3)fucosyltransferase gene.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF130972; AAD39143.1; -.
DR InterPro; IPR001503; Glyco.transf_10.
DR Pfam; PF00852; Glyco.transf_10; 1.
KW Transferase; Glycosyltransferase.
FT NON_TER 1
SQ SEQUENCE 360 AA; 42160 MW; 46405E5AF9E7A3A. CRC64;

Query Match 50.7%; Score 36; DB 6; Length 360;
Best Local Similarity 55.6%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKQOQFW 9
|| | | |
Db 125 RPPGQWVW 133

RESULT 192
ID O35886 PRELIMINARY; PRT; 362 AA.
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AC Q35886;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ALPHA(1.3) FUCOSYLTRANSFERASE.
GN ALPHA.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RL Zhang A., Potvin B., Kumar R., Zaiman A., Stanley P.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U78737; AAB64355.1; -.
DR InterPro: IPR001503; Glyco_transf_10.
DR Pfam: PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 362 AA; 41810 MW; A67940D57D47004C CRC64;

Query Match 50.7%; Score 36; DB 11; Length 362;
Best Local Similarity 55.6%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWFW 9
||| |||
DB 127 RPPGQRWVW 135

RESULT 193
Q9R220
ID Q9R220 PRELIMINARY; PRT; 362 AA.
AC Q9R220;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ALPHA(1.3) FUCOSYLTRANSFERASE 6A.
GN FUT6A.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RL Zhang A., Potvin B., Zaiman A., Chen W., Kumar R., Phillips L.,
RL Stanley P.;
RL "The gain-of-function Chinese hamster ovary mutant LEC1B expresses
RT one of two Chinese hamster FUT6 genes due to the loss of a negative
RT regulatory factor.";
RL J. Biol. Chem. 274:10439-10450(1999).
DR EMBL: AF090450; AAD24888.1; -.
DR InterPro: IPR001503; Glyco_transf_10.
DR Pfam: PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 362 AA; 41767 MW; 2256EA145B03DA13 CRC64;

Query Match 50.7%; Score 36; DB 11; Length 362;
Best Local Similarity 55.6%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWFW 9
||| |||
DB 127 RPPGQRWVW 135

RESULT 194
Q9R219
ID Q9R219 PRELIMINARY; PRT; 362 AA.
AC Q9R219;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ALPHA(1.3) FUCOSYLTRANSFERASE 6B.
GN FUT6B.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RL Zhang A., Potvin B., Zaiman A., Chen W., Kumar R., Phillips L.,
RL Stanley P.;
RL "The gain-of-function Chinese hamster ovary mutant LEC1B expresses
RT one of two Chinese hamster FUT6 genes due to the loss of a negative
RT regulatory factor.";
RL J. Biol. Chem. 274:10439-10450(1999).
DR EMBL: AF090449; AAD24887.1; -.
DR InterPro: IPR001503; Glyco_transf_10.
DR Pfam: PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 362 AA; 41743 MW; 480D106C40DE5F30 CRC64;

Query Match 50.7%; Score 36; DB 11; Length 362;
Best Local Similarity 55.6%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWFW 9
||| |||
DB 127 RPPGQRWVW 135

RESULT 195
P73843
ID P73843 PRELIMINARY; PRT; 369 AA.
AC P73843;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 42.2 KDA PROTEIN.
GN SLL1611.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; Pubmed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hikosawa M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL: D90910; BAA17900.1; -.
DR InterPro: IPR001225; FA_desaturase.
DR ProDom: PD001081; FA_desaturase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 369 AA; 42180 MW; 25F3FDE2250520F9 CRC64;

Query Match 50.7%; Score 36; DB 2; Length 369;
Best Local Similarity 71.4%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQQWFWL 10
||| |||
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AC Q35886;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ALPHA(1.3) FUCOSYLTRANSFERASE.
GN ALPHA.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RL Zhang A., Potvin B., Kumar R., Zaiman A., Stanley P.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U78737; AAB64355.1; -.
DR InterPro: IPR001503; Glyco_transf_10.
DR Pfam: PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 362 AA; 41810 MW; A67940D57D47004C CRC64;

Query Match 50.7%; Score 36; DB 11; Length 362;
Best Local Similarity 55.6%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWFW 9
||| |||
DB 127 RPPGQRWVW 135

RESULT 193
Q9R220
ID Q9R220 PRELIMINARY; PRT; 362 AA.
AC Q9R220;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ALPHA(1.3) FUCOSYLTRANSFERASE 6A.
GN FUT6A.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RL Zhang A., Potvin B., Zaiman A., Chen W., Kumar R., Phillips L.,
RL Stanley P.;
RL "The gain-of-function Chinese hamster ovary mutant LEC1B expresses
RT one of two Chinese hamster FUT6 genes due to the loss of a negative
RT regulatory factor.";
RL J. Biol. Chem. 274:10439-10450(1999).
DR EMBL: AF090450; AAD24888.1; -.
DR InterPro: IPR001503; Glyco_transf_10.
DR Pfam: PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 362 AA; 41767 MW; 2256EA145B03DA13 CRC64;

Query Match 50.7%; Score 36; DB 11; Length 362;
Best Local Similarity 55.6%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWFW 9
||| |||
DB 127 RPPGQRWVW 135

RESULT 194
Q9R219
ID Q9R219 PRELIMINARY; PRT; 362 AA.
AC Q9R219;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ALPHA(1.3) FUCOSYLTRANSFERASE 6B.
GN FUT6B.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RL Zhang A., Potvin B., Zaiman A., Chen W., Kumar R., Phillips L.,
RL Stanley P.;
RL "The gain-of-function Chinese hamster ovary mutant LEC1B expresses
RT one of two Chinese hamster FUT6 genes due to the loss of a negative
RT regulatory factor.";
RL J. Biol. Chem. 274:10439-10450(1999).
DR EMBL: AF090449; AAD24887.1; -.
DR InterPro: IPR001503; Glyco_transf_10.
DR Pfam: PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 362 AA; 41743 MW; 480D106C40DE5F30 CRC64;

Query Match 50.7%; Score 36; DB 11; Length 362;
Best Local Similarity 55.6%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWFW 9
||| |||
DB 127 RPPGQRWVW 135

RESULT 195
P73843
ID P73843 PRELIMINARY; PRT; 369 AA.
AC P73843;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 42.2 KDA PROTEIN.
GN SLL1611.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; Pubmed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hikosawa M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL: D90910; BAA17900.1; -.
DR InterPro: IPR001225; FA_desaturase.
DR ProDom: PD001081; FA_desaturase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 369 AA; 42180 MW; 25F3FDE2250520F9 CRC64;

Query Match 50.7%; Score 36; DB 2; Length 369;
Best Local Similarity 71.4%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQQWFWL 10
||| |||
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Db 52 PGQWLWL 58

RESULT 196

Q9XPE2 PRELIMINARY; PRT; 380 AA.

AC Q9XPE2; 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DE CYTOCHROME B.

GN CYTB.

OS Eumeces egregius.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scieroglossa; Scincomorpha; Scincoidae;

OC Scincidae; Eumeces.

OX NCBI_TaxID=52436;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99297345; PubMed=10368956;

RA Kumazawa Y., Nishida M.;

RT "Variations in mitochondrial trna gene organization of reptiles as phylogenetic markers."

RL Mol. Biol. Evol. 12:759-772(1995).

CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).

CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.

DR EMBL; AB016606; BAA79222.1; -.

DR InterPro: IPR000179; Cyt_b.b6.

DR Pfam; PF00032; cytochrome_b_c; 1.

DR Pfam; PF00033; cytochrome_b_n; 1.

DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.

DR PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN1.

KW Electron transport; Heme; Mitochondrion; Respiratory chain; Transmembrane.

SQ SEQUENCE 380 AA; 42527 MW; 81844197B9CFB471 CRC64;

Query Match 50.7%; Score 36; DB 8; Length 380;

Best Local Similarity 54.5%; Pred. No. 3.8e+02;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPKPQQWFILM 11

Db 319 RPASQTMFWLL 329

RESULT 197

Q9YGX6 PRELIMINARY; PRT; 385 AA.

AC Q9YGX6;

DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DE WNT-5A.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=EMBRYO;

RX MEDLINE=99372672; PubMed=10445500;

RA Kawakami Y., Wada N., Nishimatsu S., Ishikawa T., Noji S., Nohno T.;

RT "Involvement of Wnt-5a in chondrogenic pattern formation in the chick limb bud."

RL Dev. Growth Differ. 41:29-40(1999).

CC -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALLING MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX.

CC -!- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.

DR EMBL; AB006014; BAA75242.1; -.

DR InterPro: IPR000970; Wnt1.

DR Pfam; PF00110; wnt; 1.

DR PRINTS; PR01349; WNTPROTEIN.

DR SMART; SM00097; WNT1; 1.

DR PROSITE; PS00246; WNT1; 1.

KW Developmental protein; Glycoprotein.

SQ SEQUENCE 385 AA; 43005 MW; 409F7440368B2360 CRC64;

Query Match 50.7%; Score 36; DB 13; Length 385;

Best Local Similarity 54.5%; Pred. No. 3.8e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 RPK--PQQWF 9

Db 174 RPKDLPRDLW 184

RESULT 198

Q99JJ4 PRELIMINARY; PRT; 418 AA.

AC Q99JJ4;

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE SIMILAR TO KIAA0317 GENE PRODUCT (FRAGMENT).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC006074; AAB06074.1; -.

FT NON_TER 1

SQ SEQUENCE 418 AA; 47675 MW; B95D5FF0D0AE6863 CRC64;

Query Match 50.7%; Score 36; DB 11; Length 418;

Best Local Similarity 55.6%; Pred. No. 4.1e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9

Db 324 REKVMRWF 332

RESULT 199

Q9VNP0 PRELIMINARY; PRT; 454 AA.

AC Q9VNP0;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

DE CG1169 PROTEIN.
 GN CG1169.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 ON NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003600; AAF51889.1; -
 DR FlyBase; FBgn0037428; CG1169.
 SQ SEQUENCE 454 AA; 51320 MW; A75AAAD97E716573 CRC64;

Query Match 50.7%; Score 36; DB 5; Length 454;
 Best Local Similarity 75.0%; Pred. NO. 4.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKQOWF 8
 ||| |||
 Db 53 RPKALQWF 60

RESULT 200

Q9MGA9
 ID Q9MGA9 PRELIMINARY; PRT; 482 AA.
 AC Q9MGA9;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE NADH DEHYDROGENASE SUBUNIT 4 (EC 1.6.5.3).
 GN NAD4.
 OS Chrysodidymus synuroideus.

OG Mitochondrion.
 OC Eukaryota; Stramenopiles; Chrysophyceae; Synurales; Chrysodidymus.
 ON NCBI_TaxID=47573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chesnick J.M., Goff M., Graham J., Ocampo C., Lang B.F., Self E.,
 RA Burger G.;
 RT "The mitochondrial genome of the stramenopile alga, Chrysodidymus
 RT synuroideus. Complete sequence, gene content and genome
 RT organization."
 RL Nucleic Acids Res. 0:0-0(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Burger G.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
 CC -1- SIMILARITY: TO NADH-UBIQUINONE/PLASTOQUINONE (COMPLEX I), VARIOUS
 CC CHAINS.
 DR EMBL; AF222718; AAF36940.1; -
 DR InterPro; IPR001750; Oxidored_q1.
 DR Pfam; PF00361; oxidored_q1; 1.
 KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
 SQ SEQUENCE 482 AA; 55109 MW; 731DFC959E4A7574 CRC64;

Query Match 50.7%; Score 36; DB 8; Length 482;
 Best Local Similarity 83.3%; Pred. NO. 4.7e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QQFWL 10
 ||| ||
 Db 203 QQWLWL 208

Search completed: April 1, 2002, 16:20:10
 Job time: 156 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 1, 2002, 16:17:34 ; Search time 13.22 Seconds
(without alignments)
30.508 Million cell updates/sec

Title: US-09-988-792-1

Perfect score: 61

Sequence: 1 RPKPQQFFGLM 11

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 127

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 50%

Maximum Match 100%

Listing first 1000 summaries

Database :

SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	61	100.0	11	TKNA_HORSE	P01290 equus caball
2	61	100.0	115	TKN1_RABIT	P41540 oryctolagus
3	61	100.0	129	TKN1_HUMAN	P20366 homo sapien
4	61	100.0	130	TKN1_BOVIN	P01289 bos taurus
5	61	100.0	130	TKN1_MESAU	Q60541 mesocricetu
6	61	100.0	130	TKN1_MOUSE	P41539 mus musculus
7	61	100.0	130	TKN1_RAT	P06767 rattus norv
8	58	95.1	11	TKNA_CHICK	P19850 gallus gall
9	50	82.0	11	TKNA_ONCMY	P28499 oncorhynchu
10	49	80.3	11	TKNA_GADMO	P28498 gadus morhu
11	48	78.7	11	TKNA_SCYCA	P41333 scyllorhinu
12	44	72.1	11	TKN4_PSEGU	P42989 pseudophryn
13	44	72.1	11	TKN5_PSEGU	P42990 pseudophryn
14	44	72.1	12	TKN1_KASMA	P08613 kassina mac
15	43	70.5	11	TKNA_RANRI	P29207 rana ridibu
16	41	67.2	11	TKNA_RANCA	P22688 rana catesb
17	41	67.2	3828	TRX_DROVI	Q24742 drosophila
18	37	60.7	11	TKN1_UPERU	P08612 uperoleia r
19	37	60.7	11	TKN2_PSEGU	P42987 pseudophryn
20	36	59.0	11	TKN1_PSEGU	P42986 pseudophryn
21	36	59.0	11	TKN3_PSEGU	P42988 pseudophryn
22	36	59.0	12	TKN2_KASMA	P08614 kassina mac
23	36	59.0	12	TKN_KASSE	P08611 kassina sen
24	36	59.0	167	SERO_GALME	O76192 gallieria me
25	36	59.0	313	ISPE_HAEIN	P45271 haemophilus
26	36	59.0	728	EF2_ARCFU	O28385 archaeoglob
27	35	57.4	512	SYK_VIBCH	Q8ku60 vibrio chol
28	35	57.4	518	CP3R_ONCMY	O42563 oncorhynchu
29	35	57.4	1092	RELA_MYXXA	O52177 myxococcu
30	35	57.4	1093	DP2L_METTH	O27579 methanobact
31	34	55.7	493	Y130_MYCPN	P75506 mycoplasma
32	34	55.7	498	C6B1_PAPPO	Q04552 papilio pol
33	34	55.7	503	CP3A_MESAU	Q64148 mesocricetu

34	55.7	504	1	CP31_RAT	P04800 rattus norv
35	55.7	585	1	PPOE_LYCES	Q08296 lycopersico
36	55.7	587	1	PPOE_LYCES	Q08307 lycopersico
37	55.7	588	1	PPOB_SOLFU	Q06355 solanum tub
38	55.7	666	1	XJB0_YEAST	P47077 saccharomyc
39	55.7	1799	1	Y025_CAEEL	P34675 caenorhabdi
40	55.7	282	1	YK00_CAEEL	P42001 caenorhabdi
41	54.1	404	1	CAG5_CHICK	O92184 gallus gall
42	54.1	420	1	CRF1_CHICK	Q08012 gallus gall
43	54.1	495	1	SYK_STAAU	Q56338 staphylococ
44	54.1	498	1	C6B3_PAPPO	P57822 papilio pol
45	54.1	501	1	SYK_HAEIN	P43825 haemophilus
46	54.1	502	1	SYK_PASMU	P13030 escherichia
47	54.1	504	1	SYK1_ECOLI	P14825 escherichia
48	54.1	504	1	SYK2_ECOLI	P42685 homo sapien
49	54.1	505	1	FRK_HUMAN	P43990 acinetobact
50	54.1	509	1	SYK_ACICA	Q96321 arabidopsis
51	54.1	521	1	COX1_APILI	P25723 drosophila
52	54.1	596	1	IMAI_ARATH	P21874 bacillus st
53	54.1	1057	1	TLD_DROME	P08615 physalaemus
54	53.3	324	1	ODPB_BACST	P24591 bos taurus
55	52.5	11	1	TKN1_PHYFU	P16608 thermus aqu
56	52.5	263	1	IBP1_BOVIN	P44861 haemophilus
57	52.5	271	1	TRPA_THETH	O92734 chlamydia p
58	52.5	382	1	YDHH_HAEIN	P33561 borrelia bu
59	52.5	418	1	GCH2_CHLPN	P35527 thermotoga
60	52.5	419	1	RHO_BORBU	P34960 mus musculu
61	52.5	419	1	RHO_PSEFL	O63341 rattus norv
62	52.5	427	1	RHO_THEMA	P21692 sus scrofa
63	52.5	462	1	MM12_MOUSE	Q9rhv9 bacillus st
64	52.5	465	1	MM12_RAT	Q9gv58 mus musculu
65	52.5	469	1	MM01_PIG	O9v5p3 homo sapien
66	52.5	494	1	SYK_BACST	O9v5p3 drosophila
67	52.5	519	1	RHO_TREPA	O02768 oryctolagus
68	52.5	529	1	RAI2_MOUSE	P98078 mus musculu
69	52.5	530	1	RAI2_HUMAN	Q28060 bos taurus
70	52.5	535	1	C4C3_DROME	Q9wv12 mus musculu
71	52.5	604	1	PGH2_RABIT	P36440 heterosigma
72	52.5	766	1	DAB2_MOUSE	Q05859 mus musculu
73	52.5	896	1	DSC3_BOVIN	Q05858 gallus gall
74	52.5	923	1	STA2_MOUSE	P18948 caenorhabdi
75	52.5	1075	1	Y124_METJA	P48415 saccharomyc
76	52.5	1116	1	ROB_HETCA	P08616 uperoleia r
77	52.5	1206	1	FM14_MOUSE	O33440 meriones un
78	52.5	1213	1	FMN_CHICK	P80680 zea mays (m
79	52.5	1468	1	FMN1_MOUSE	P54134 mycobacteri
80	52.5	1651	1	VIT6_CAEEL	P40213 saccharomyc
81	52.5	2194	1	SC16_YEAST	P80054 sus scrofa
82	50.8	11	1	TKN2_UPERU	O28974 archaeoglob
83	50.8	71	1	MOT2_MERU	P03584 tomato mosa
84	50.8	97	1	FTRV_MAIZE	P29800 tomato mosa
85	50.8	126	1	YD43_MYCLE	Q9vjg9 tomato mosa
86	50.8	142	1	RS16_YEAST	P34657 caenorhabdi
87	50.8	172	1	PR39_PIG	P57931 pasteurilla
88	50.8	183	1	TBP_ARCFU	P01822 saccharomyc
89	50.8	264	1	MOVV_TOML	P33178 saccharomyc
90	50.8	264	1	MOVV_TOML2	P23710 neurospora
91	50.8	264	1	MOVV_TOML1	Q48211 haemophilus
92	50.8	266	1	YOTB_CAEEL	P73948 methanococc
93	50.8	267	1	THIM_PASMU	O21407 squirrel mo
94	50.8	269	1	CCHL_YEAST	O27272 methanobact
95	50.8	278	1	RRP1_YEAST	P57858 pasteurilla
96	50.8	283	1	NUGM_NEUCR	P18326 streptomyce
97	50.8	304	1	LST_HAEIN	O53189 mycobacteri
98	50.8	322	1	RADA_METVO	P74130 synechocyst
99	50.8	323	1	VPRT_SMRVH	P24447 human herpe
100	50.8	338	1	PUR5_METHH	P52448 human herpe
101	50.8	339	1	PYRD_PASMU	
102	50.8	405	1	CPXE_STRGO	
103	50.8	466	1	TIG_MYCTO	
104	50.8	485	1	TRE2_SYNV3	
105	50.8	488	1	EXON_HSV6U	
106	50.8	488	1	EXON_HSV6Z	

107 31 50.8 488 1 SYK_MYCHO
 108 31 50.8 509 1 CPV1_BRARE
 109 31 50.8 510 1 DHAF_VIBHA
 110 31 50.8 546 1 YTE4_CAEEL
 111 31 50.8 558 1 GPC1_RAT
 112 31 50.8 660 1 MM02_HUMAN
 113 31 50.8 662 1 MM02_MOUSE
 114 31 50.8 662 1 MM02_RABIT
 115 31 50.8 662 1 MM02_RAT
 116 31 50.8 663 1 MM02_CHICK
 117 31 50.8 685 1 SNWA_DICDI
 118 31 50.8 687 1 AKAB_RAT
 119 31 50.8 692 1 AKAB_HUMAN
 120 31 50.8 704 1 PNP_BACSU
 121 31 50.8 768 1 LIPS_RAT
 122 31 50.8 864 1 Y78A_DROME
 123 31 50.8 922 1 YB1C_SCHPO
 124 31 50.8 956 1 PMAB_ARATH
 125 31 50.8 1629 1 AT59_HUMAN
 126 31 50.8 3712 1 ACVS_CEPAC
 127 30.5 50.0 2261 1 ABC1_MOUSE

ALIGNMENTS

RESULT 1
 ID TKNA_HORSE STANDARD; PRT; 11 AA.
 AC P01250;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P.
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Equus caballus (Horse), and Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796, 10141;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Horse;
 RA Studer R.O., Trzeciak A., Lergler W.;
 RT "Isolation and amino-acid sequence of substance P from horse
 intestine.";
 RL Helv. Chim. Acta 56:860-866(1973).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=C.porcellus;
 RX MEDLINE=90044685; PubMed=2478925;
 RA Murphy R.;
 RT "Primary amino acid sequence of guinea-pig substance P.";
 RL Neuropeptides 14:105-110(1989).
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR; A01558; SPHO.
 DR PIR; A0654; A60654.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION
 SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFFLM 11
 Db 1 RPKPQOFFFLM 11
 RESULT 2
 TKNL_RABIT STANDARD; PRT; 115 AA.
 ID TKNL_RABIT
 AC P41540;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE GAMMA; C-TERMINAL
 FLANKING PEPTIDE].
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93371392; PubMed=8363593;
 RA Maegert H.J., Heitland A., Rose M., Forssmann W.G.;
 RT "Nucleotide sequence of the rabbit gamma-preprotachykinin I CDNA.";
 RL Biochem. Biophys. Res. Commun. 195:128-131(1993).
 RN [2]
 RP SEQUENCE OF 72-92.
 RA Kage R., McGregor G.P., Thim L., Conlon J.M.;
 RT "Gamma-neuropeptide K: a peptide isolated from rabbit gut that is
 derived from gamma-preprotachykinin.";
 RL Regul. Pept. 18:346-346(1987).
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
 CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X62994; CAA44728.1; -
 DR PIR; S18922; S18922.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR Prodom; PD005598; Protachykinin; 1.
 DR SMART; SM00203; TK; 2.
 DR PROSITE; PS00267; TACHYKININ; 2.
 KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 FT MOD_RES 19 POTENTIAL.
 FT SIGNAL 1 19
 FT PEPTIDE 20 56
 FT PEPTIDE 58 68
 FT PEPTIDE 72 92
 FT PEPTIDE 83 92
 FT PEPTIDE 96 111
 FT MOD_RES 68 88
 FT MOD_RES 92 92
 SQ SEQUENCE 115 AA; 13370 MW; 5EC76F7C9B10E1C6 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 0.00014;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKEQFFGLM 11
|||||

Db 58 RPKEQFFGLM 68

RESULT 3

TKNL_HUMAN STANDARD; PRT; 129 AA.
AC P20366; Q00072; O60600; O60601;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROTAACHYKININ 1 PRECURSOR (PT) [CONTAINS: SUBSTANCE P; NEUROKININ A
DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
DE GAMMA, C-TERMINAL FLANKING PEPTIDE].
GN TACI OR NKNA OR TAC2 OR NKA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RX MEDLINE=87030957; PubMed=3770210;
RA Harmar A.J., Armstrong A., Pascall J.C., Chapman K., Rosie R.,
RA Curtis A., Going J., Edwards C.R.W., Fink G.,
RT "cDNA sequence of human beta-preprotachykinin, the common precursor
RL FEBS Lett. 208:67-72(1986).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC TISSUE=Brain;
RA Tan A., Too H.P.;
RN [3]
RP SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
RX MEDLINE=91209287; PubMed=1708336;
RA Chikakata C., Brackmann B., Hunt N., Davidoff M., Schulze W.,
RA Ivell R.;
RT "Tachykinin (substance-P) gene expression in Leydig cells of the
RL human and mouse testis.";
RL Endocrinology 128:2441-2448(1991).
RN [4]
RP SEQUENCE OF 98-107.
RX MEDLINE=87275962; PubMed=3038549;
RA Theodorsson-Norheim E., Joernvall H., Andersson M., Norheim I.,
RA Oberg K., Jacobsson G.;
RT "Isolation and characterization of neurokinin A, neurokinin A(3-10)
RT and neurokinin A(4-10) from a neutral water extract of a metastatic
RT ileal carcinoma tumour.";
RL Eur. J. Biochem. 166:693-697(1987).
RN [5]
RP SEQUENCE OF 36-118 FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Blood, and Brain;
RA Lai J.P., Douglas S.D., Rappaport E., Wu J.M., Ho W.Z.;
RT "Identification of a delta isoform of preprotachykinin mRNA in human
RT mononuclear phagocytes and lymphocytes.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 111-126.
RC TISSUE=Adrenal medulla;
RX MEDLINE=91133994; PubMed=2284201;
RA McGregor G.P., Conlon J.M.;
RT "Characterization of the C-terminal flanking peptide of human
RT beta-preprotachykinin.";
RL Peptides 11:907-910(1990).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),

CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL; X54469; CAA38351.1; -
DR EMBL; U37529; AAA79195.1; -
DR EMBL; M68906; AAA60159.1; -
DR EMBL; M68907; AAA60160.1; -
DR EMBL; AF050656; AAC15702.1; -
DR EMBL; AF050658; AAC15704.1; -
DR PIR; A24805; A24805.
DR PIR; S00069; S00069.
DR MIM; 162320; -

DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; tachykinin; 1.
DR ProDom: PD005598; Protachykinin; 1.
DR SMART; SM00203; TK; 2.

DR PROSITE; PS00267; TACHYKININ; 2.
KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
KW Amidation; Alternative splicing; Signal; Neurotransmitter.

FT SIGNAL 1 19
FT PROPEP 20 56
FT PEPTIDE 58 68
FT PEPTIDE 72 107
FT PEPTIDE 72 73
FT PEPTIDE 89 107
FT PEPTIDE 98 107
FT PEPTIDE 111 126
FT MOD_RES 68 68
FT MOD_RES 107 107
FT VARSPIC 74 88
FT VARSPIC 97 114
FT VARSPIC 115 115
FT VARSPIC 87 87
FT CONFLICT 87 87
SQ SEQUENCE 129 AA; 15003 MW; 51412C1692368DE4 CRC64;
L -> P (IN REF. 4).

Query Match 100.0%; Score 61; DB 1; Length 129;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKEQFFGLM 11

|||||

Db 58 RPKEQFFGLM 68

RESULT 4

TKNL_BOVIN STANDARD; PRT; 130 AA.
AC P01289; P01291; P04091; P20773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROTAACHYKININ 1 PRECURSOR (PT) [CONTAINS: SUBSTANCE P; NEUROKININ A
DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
DE GAMMA, C-TERMINAL FLANKING PEPTIDE].
GN TACI OR NKNA OR TAC2 OR NKA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

[1]
RN SEQUENCE FROM N.A. (ISOFORM BETA).
RX MEDLINE=85086245; PubMed=6083453;
RA Nawa H., Kotani H., Nakanishi S.
RT "Tissue-specific generation of two preprotachykinin mRNAs from one
RL gene by alternative RNA splicing.";
RL Nature 312:729-734(1984).
[2]
RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RX MEDLINE=84039802; PubMed=6195531;
RA Nawa H., Hirose T., Takashima H., Inayama S., Nakanishi S.;
RT "Nucleotide sequences of cloned cDNAs for two types of bovine brain
RL substance P precursor.";
RL Nature 306:32-36(1983).
[3]
RN SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
RP TISSUE-HYPOTHALAMUS;
RX MEDLINE=91209287; PubMed=1708336;
RA Chikakata C., Brackmann B., Hunt N., Davidoff M., Schulze W.,
RA Ivell R.;
RT "Tachykinin (substance-P) gene expression in Leydig cells of the
RL human and mouse testis.";
RL Endocrinology 128:2441-2448(1991).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC -----
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CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL; X00075; CAA24939.1; -;
DR EMBL; X00075; CAA24940.1; -;
DR EMBL; X00075; CAA24941.1; -;
DR EMBL; X00076; CAA24942.1; -;
DR EMBL; X00076; CAA24943.1; ALT_SEQ.
DR EMBL; X02351; CAA26206.1; -;
DR EMBL; X01396; CAA26206.1; JOINED.
DR EMBL; X01397; CAA26206.1; JOINED.
DR EMBL; X01398; CAA26206.1; JOINED.
DR EMBL; X01399; CAA26206.1; JOINED.
DR EMBL; X01400; CAA26206.1; JOINED.
DR EMBL; M68911; AAA30724.1; -;
DR EMBL; M68912; AAA30725.1; -;
DR PIR; A01557; SPBOA.
DR PIR; A01559; SPBOB.
DR PIR; A05093; A05093.
DR PIR; B25067; B25067.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR ProDom; PD005598; Protachykinin; 1.
DR SMART; SM00203; TK; 2.
DR PROSITE; PS00267; TACHYKININ; 2.
KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
KW Amidation; Alternative splicing; Signal; Neurotransmitter.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 56 POTENTIAL.
FT PEPTIDE 58 68 SUBSTANCE P.
FT PEPTIDE 72 107 NEUROPEPTIDE K.
FT PEPTIDE 72 73 NEUROPEPTIDE GAMMA 1ST PART.
FT PEPTIDE 89 107 NEUROPEPTIDE GAMMA 2ND PART.
FT PEPTIDE 98 107 NEUROKININ A.
FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
FT MOD_RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
FT

FT MOD_RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
FT VARSPLIC 74 88 MISSING (IN ISOFORM GAMMA AND ISOFORM
FT DELTA).
FT VARSPLIC 97 114 MISSING (IN ISOFORM ALPHA AND ISOFORM
FT DELTA).
FT VARSPLIC 115 115 V -> M (IN ISOFORM ALPHA AND ISOFORM
FT DELTA).
FT CONFLICT 121 121 V -> A (IN REF. 3).
SQ SEQUENCE 130 AA; 15076 MW; CE2A28572305DEB7 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
Db 58 RPKPQQFFGLM 68
|||||

RESULT 5
TKNL_MESAU STANDARD; PRT; 130 AA.
ID TXNL_MESAU
AC Q60541; P49110;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
GN TAC1 OR NKNA OR TAC2 OR NKA.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS BETA AND GAMMA).
RC STRAIN=AURA; TISSUE=Brain;
RA Heitland A., Kruhoffer M., Juerger Maegert H.J., Forssmann W.G.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC -----
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CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL; X80662; CAA56691.1; -;
DR EMBL; X80663; CAA56692.1; -;
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR ProDom; PD005598; Protachykinin; 1.
DR SMART; SM00203; TK; 2.
DR PROSITE; PS00267; TACHYKININ; 2.
KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
KW Amidation; Alternative splicing; Signal; Neurotransmitter.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 56 POTENTIAL.
FT PEPTIDE 58 68 SUBSTANCE P.
FT PEPTIDE 72 107 NEUROPEPTIDE K.
FT PEPTIDE 72 73 NEUROPEPTIDE GAMMA 1ST PART.
FT PEPTIDE 89 107 NEUROPEPTIDE GAMMA 2ND PART.
FT

FT PEPTIDE 98 107 NEUROKININ A.
FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
FT MOD_RES 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
FT MOD_RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
FT VARSPLIC 74 88 MISSING (IN ISOFORM GAMMA).
SQ SEQUENCE 130 AA; 14907 MW; CC92E9371A646F2E CRC64;

Query Match 100.0%; Score 61; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQQFFGLM 11
| | | | | | | | | |
DB 58 RPKPQQFFGLM 68

RESULT 6
TKNL_MOUSE STANDARD; PRT; 130 AA.
AC P41539; Q00073;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
DE GAMMA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
GN TAC1 OR NKNA OR TAC2 OR NKA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=ICR; TISSUE=Brain;
RA Kako K., Muneoka E., Hosaka M., Murakami K., Nakayama K.;
RT "Cloning and sequence analysis of mouse cDNAs encoding
preprotachykinin A and B."
RL Biomed. Res. 14:253-259(1993).
RN [2]
RP SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
RC TISSUE=Brain;
RX MEDLINE=91209287; PubMed=1708336;
RA Chiwakata C., Brackmann B., Hunt N., Davidoff M., Schulze W.,
RA Ivell R.;
RT "Tachykinin (substance-P) gene expression in Leydig cells of the
human and mouse testis."
RL Endocrinology 128:2441-2448(1991).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC
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CC
CC EMBL; D17584; BAA04508.1; -
DR EMBL; M68908; AAA39969.1; -
DR EMBL; M68909; AAA39970.1; -
DR MGD; MGI:98474; Tac1.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR ProDom; PD005598; Protachykinin; 1.
DR SMART; SM00203; TK; 2.

DR PROSITE; PS00267; TACHYKININ; 2.
KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
KW Amidation; Alternative splicing; Signal; Neurotransmitter.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 56 SUBSTANCE P.
FT PEPTIDE 58 68 NEUROPEPTIDE K.
FT PEPTIDE 72 107 NEUROPEPTIDE GAMMA 1ST PART.
FT PEPTIDE 72 73 NEUROPEPTIDE GAMMA 2ND PART.
FT PEPTIDE 89 107 NEUROKININ A.
FT PEPTIDE 98 107 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
FT PEPTIDE 111 126 AMIDATION (G-69 PROVIDE AMIDE GROUP).
FT MOD_RES 68 68 AMIDATION (G-108 PROVIDE AMIDE GROUP).
FT MOD_RES 107 107 MISSING (IN ISOFORM GAMMA).
FT VARSPLIC 74 88 MISSING (IN ISOFORM GAMMA).
SQ SEQUENCE 130 AA; 15045 MW; 7BE8DA15FDE72FF8 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQQFFGLM 11
| | | | | | | | | |
DB 58 RPKPQQFFGLM 68

RESULT 7
TKNL_RAT STANDARD; PRT; 130 AA.
ID TKNL_RAT
AC P06767; P08856; P08857; P22356;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
GN TAC1 OR NKNA OR TAC2 OR NKA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).
RX MEDLINE=90331040; PubMed=1695945;
RA Carter M.S., Krause J.E.;
RT "Structure, expression, and some regulatory mechanisms of the rat
preprotachykinin gene encoding substance P, neurokinin A,
neuropeptide K, and neuropeptide gamma."
RL J. Neurosci. 10:2203-2214(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).
RX MEDLINE=87118268; PubMed=2433692;
RA Krause J.E., Chirgwin J.M., Carter M.S., Xu Z.S., Hershey A.D.;
RT "Three rat preprotachykinin mRNAs encode the neuropeptides substance
P and neurokinin A."
RL Proc. Natl. Acad. Sci. U.S.A. 84:881-885(1987).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
RX MEDLINE=87025808; PubMed=2429656;
RA Kawaguchi Y., Hoshimaru M., Nawa H., Nakanishi S.;
RT "Sequence analysis of cloned cDNA for rat substance P precursor:
existence of a third substance P precursor."
RL Biochem. Biophys. Res. Commun. 139:1040-1046(1986).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RC TISSUE=Dorsal root ganglion;
RX MEDLINE=91085565; PubMed=1702066;
RA Hamar A.J., Hyde V., Chapman K.E.;
RT "Identification and cDNA sequence of delta-preprotachykinin, a fourth
splicing variant of the rat substance P precursor."
RL FEBS Lett. 275:22-24(1990).
RN [5]
RP SEQUENCE OF 1-41 FROM N.A.

DR InterPro; IPR002040; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 82.0%; Score 50; DB 1; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.0015;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
 :1:1111111111
 Db 1 KPRPQQFFGLM 11

RESULT 10
 TKNA_GADMO STANDARD; PRT; 11 AA.
 AC P28498;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P.
 OS Gadus morhua (Atlantic cod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidei; Gadidae;
 OC Gadus.
 OX NCBI_TaxID=8049;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92298992; PubMed=1376687;
 RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 of the cod and trout."
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR InterPro; IPR003580; Protachykinin.
 DR InterPro; IPR002040; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 80.3%; Score 49; DB 1; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.0023;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
 :1:1111111111
 Db 1 KPRPQQFFGLM 11

RESULT 11
 TKNA_SCYCA STANDARD; PRT; 11 AA.
 AC P41333;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P.
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
 OC Scyliorhinidae; Scyliorhinus.
 OX NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=93292508; PubMed=7685693;
 RA Waugh D., Wang Y., Hazon N., Balmert R.J., Conlon J.M.;
 RT "Primary structures and biological activities of substance-P-related
 peptides from the brain of the dogfish, Scyliorhinus canicula.";
 RL Eur. J. Biochem. 214:469-474(1993).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR; S33300; S33300.
 DR InterPro; IPR003580; Protachykinin.
 DR InterPro; IPR002040; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

Query Match 78.7%; Score 48; DB 1; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.0036;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
 :1:1111111111
 Db 1 KPRPQQFFGLM 11

RESULT 12
 TKNA_PSEGU STANDARD; PRT; 11 AA.
 ID P42989;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P-LIKE PEPTIDE I (PG-SPI).
 OS Pseudophryne guentheri (Frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 the Australian frog Pseudophryne guentheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR; E60409; E60409.
 DR InterPro; IPR003580; Protachykinin.
 DR InterPro; IPR002040; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.

```
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CBIAB7 CRC64;

Query Match 72.1%; Score 44; DB 1; Length 11;
Best Local Similarity 63.6%; Pred. No. 0.02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGLM 11
   :|:|:|||||
Db 1 QPNPNEFFGLM 11

RESULT 13
TKN5_PSEGU STANDARD; PRT; 11 AA.
AC P42990;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P-LIKE PEPTIDE II (PG-SPII).
OS Pseudophryne guentheri (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=90287814; PubMed=2356157;
RA SImmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; F60409; F60409.
DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11
FT MOD_RES 11 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CBI457 CRC64;

Query Match 72.1%; Score 44; DB 1; Length 11;
Best Local Similarity 63.6%; Pred. No. 0.02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGLM 11
   :|:|:|||||
Db 1 QPNPNEFFGLM 11

RESULT 14
TKN1_KASMA STANDARD; PRT; 12 AA.
AC P08613;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HYLAMBATES KASSININ (GLU(2)-PRO(5) KASSININ).
OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC Kassina.
OX NCBI_TaxID=8414;
```

```
RN SEQUENCE.
RP Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;
RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and
RT hylambatin, in the skin of the African rhacophorid frog Hylambates
RT maculatus.";
RL Biomed. Res. 2:613-617(1981).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S10059; S10059.
DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Amphibian skin.
FT MOD_RES 12
FT MOD_RES 12 AMIDATION.
SQ SEQUENCE 12 AA; 1376 MW; 3E756D279DD6DAB7 CRC64;

Query Match 72.1%; Score 44; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 0.022;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPQQOFFGLM 11
   ||| || |||
Db 3 PKPDQFVGLM 12

RESULT 15
TKNA_RANRI STANDARD; PRT; 11 AA.
AC P29207;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE RANAKININ (SUBSTANCE-P-RELATED PEPTIDE).
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92044543; PubMed=1658233;
RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
RT neurokinin B from the brain of the frog Rana ridibunda.";
RL J. Neurochem. 57:2086-2091(1991).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11
FT MOD_RES 11 AMIDATION.
SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 70.5%; Score 43; DB 1; Length 11;
Best Local Similarity 54.5%; Pred. No. 0.03;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGLM 11
   :|:|:|||||
```



```
Db 1 KPNPERFYGLM 11
RESULT 16
TKNA_RANCA
ID TKNA_RANCA STANDARD; PRT; 11 AA.
AC P22688;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE RANATACHYKININ A (RUK A).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoides; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain, and Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
brain and intestine.";
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN [2]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=94023216; PubMed=8210506;
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
intestine.";
RL Regul. Pept. 46:81-88(1993).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; JEO426; JEO426.
DR PIR; A61033; A61033.
DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11
FT SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;

Query Match 67.2%; Score 41; DB 1; Length 11;
Best Local Similarity 54.5%; Pred. No. 0.071;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
:|:|:|:|
Db 1 KPSDRFYGLM 11

RESULT 17
TRX_DROVI
ID TRX_DROVI STANDARD; PRT; 3828 AA.
AC Q24742;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TRITHORAX PROTEIN.
GN TRX.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=96100387; PubMed=8555104;
RA Tillib S., Sedkov Y., Mizrokhi L., Mazo A.;
RT "Conservation of structure and expression of the trithorax gene
between Drosophila virilis and Drosophila melanogaster.";
RL Mech. Dev. 53:113-122(1995).
CC -!- FUNCTION: FUNCTIONS IN SEGMENT DETERMINATION THROUGH INTERACTION
WITH GENES OF BITHORAX (BX-C) AND ANTENNAPEDIA (ANT-X) COMPLEXES.
IT CAN BEHAVE AS AN ACTIVATOR OF BX-C.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: BELONGS TO THE TRITHORAX FAMILY OF TRANSCRIPTION
FACTORS.
CC -!- SIMILARITY: CONTAINS 1 'SET' DOMAIN.
CC -!- SIMILARITY: CONTAINS 5 PHD-TYPE ZINC FINGERS.
CC -!- SIMILARITY: CONTAINS 5 PHD-TYPE ZINC FINGERS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z50038; CAA90349.1; -
DR HSSP; P04002; IWFA.
DR Flybase; FBgn001484; Dvir\trix.
DR InterPro: IPR003889; Fyrich_C.
DR InterPro: IPR003888; Fyrich_N.
DR InterPro: IPR001965; PHD.
DR InterPro: IPR003616; PostSET.
DR InterPro: IPR001214; SET.
DR InterPro: IPR001841; Znf_ring.
DR Pfam; PF00628; PHD; 2.
DR Pfam; PF00856; SET; 1.
DR SMART; SM00542; FYR; 1.
DR SMART; SM00541; FYRN; 1.
DR SMART; SM00249; PHD; 4.
DR SMART; SM00508; PostSET; 1.
DR SMART; SM00184; RING; 2.
DR SMART; SM00317; SET; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS0280; SET; 1.
KW Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
Nuclear protein; Developmental protein; Activator.
FT ZN_FING 1251 1334 PHD-TYPE 1.
FT ZN_FING 1335 1380 PHD-TYPE 2.
FT ZN_FING 1408 1469 PHD-TYPE 3.
FT ZN_FING 1708 1767 PHD-TYPE 4 (ATYPICAL).
FT ZN_FING 1768 1818 PHD-TYPE 5 (ATYPICAL).
FT DOMAIN 3701 3810 SET.
FT DOMAIN 28 41 POLY-ALA.
FT DOMAIN 66 71 POLY-ASP.
FT DOMAIN 160 164 POLY-ASP.
FT DOMAIN 173 182 POLY-ALA.
FT DOMAIN 221 228 POLY-GLN.
FT DOMAIN 243 251 POLY-ALA.
FT DOMAIN 253 258 POLY-THR.
FT DOMAIN 292 296 POLY-ALA.
FT DOMAIN 538 546 POLY-ASP.
FT DOMAIN 1072 1075 POLY-GLU.
FT DOMAIN 2483 3271 GLN-RICH.
FT DOMAIN 3333 3339 POLY-ASP.
SQ SEQUENCE 3828 AA; 413721 MW; 32059CF303A3C504 CRC64;

Query Match 67.2%; Score 41; DB 1; Length 3828;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
:|:|:|:|
Db 618 KPKPKNYFGL 627
```

RESULT 18
TKN1_UPERU
ID TKN1_UPERU STANDARD; PRT; 11 AA.
AC P08612;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE UPEROLEIN.
OS Uperoleia rugosa (Australian leptodactylid frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Uperoleia.
OX NCBI_TaxID=8368;
RN [1]
RP SEQUENCE.
RX MEDLINE=75131227; PubMed=1120493;
RA Anastasi A., Erspamer V., Edean R.;
RT "Structure of uperolein, a physalaemin-like endecapeptide occurring
in the skin of Uperoleia rugosa and Uperoleia marmorata.";
RL Experientia 31:394-395(1975).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S07203; S07203.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 11 AMIDATION
FT MOD_RES 11 11 AMIDATION
SQ SEQUENCE 11 AA; 1252 MW; 32867C3E9CDD457 CRC64;

Query Match 60.7%; Score 37; DB 1; Length 11;
Best Local Similarity 54.5%; Pred. No. 0.39;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RPKPQQPFGLM 11
:| | | | |
DB 1 QPDNPFVGLM 11

RESULT 19
TKN2_PSEGU
ID TKN2_PSEGU STANDARD; PRT; 11 AA.
AC P42987;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE KASSININ-LIKE PEPTIDE K-II (PG-KII).
OS Pseudophryne guentheri (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RX TISSUE=Skin;
RA SImmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.

CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; C60409; C60409.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 1 11 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION
SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CBIAB7 CRC64;

Query Match 60.7%; Score 37; DB 1; Length 11;
Best Local Similarity 54.5%; Pred. No. 0.39;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQPFGLM 11
:| | | | |
DB 1 QPNPDEFVGLM 11

RESULT 20
TKN1_PSEGU
ID TKN1_PSEGU STANDARD; PRT; 11 AA.
AC P42986;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE KASSININ-LIKE PEPTIDE K-I (PG-KI).
OS Pseudophryne guentheri (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RX TISSUE=Skin;
RA SImmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.

CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

DR PIR; B60409; B60409.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 1 11 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION
SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CBIAB7 CRC64;

Query Match 59.0%; Score 36; DB 1; Length 11;
Best Local Similarity 54.5%; Pred. No. 0.6;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQPFGLM 11
:| | | | |
DB 1 QPNPDEFVGLM 11

RESULT 21
TKN3_PSEGU
ID TKN3_PSEGU STANDARD; PRT; 11 AA.

P42988;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE KASSININ-LIKE PEPTIDE K-III (PG-KIII).
OS Pseudophryne guentheri (Frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; D60409; D60409.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

Query Match 59.0%; Score 36; DB 1; Length 11;
Best Local Similarity 54.5%; Pred. No. 0.6;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKQQOFFGLM 11
: | : | | |
DB 1 QPHNPFVGLM 11

RESULT 22
TKN2_KASMA STANDARD; PRT; 12 AA.
AC P08614;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HYLAMBATIN.
OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC Kassina.
OX NCBI_TaxID=8414;
RN [1]
RP SEQUENCE.
RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;
RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and
hylambatin, in the skin of the African rhacophorid frog Hylambates
maculatus.";
RL Biomed. Res. 2:613-617(1981).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S07436; S07436.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.

Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Amphibian skin.
FT MOD_RES 12 12
SQ SEQUENCE 12 AA; 1441 MW; 3287CD2F0DD40AB7 CRC64;

Query Match 59.0%; Score 36; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 0.66;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPQQOFFGLM 11
: | : | | |
DB 3 PDPDRFVGLM 12

RESULT 23
TKN_KASSE STANDARD; PRT; 12 AA.
AC P08611;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE KASSININ.
OS Kassina senegalensis (Senegal running frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC Kassina.
OX NCBI_TaxID=8415;
RN [1]
RP SEQUENCE.
RX MEDLINE=77246385; PubMed=891753;
RA Anastasi A., Montecucci P.C., Erspamer V., Visser J.;
RT "Amino acid composition and sequence of kassinin, a tachykinin
dodecapeptide from the skin of the African frog Kassina
senegalensis.";
RL Experientia 33:857-858(1977).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S07206; S07206.
DR InterPro; IPR002040; Tachykinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Amphibian skin.
FT MOD_RES 12 12
SQ SEQUENCE 12 AA; 1336 MW; 91757AB89DD6DAB5 CRC64;

Query Match 59.0%; Score 36; DB 1; Length 12;
Best Local Similarity 70.0%; Pred. No. 0.66;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQQOFFGLM 11
: | : | | |
DB 3 PKSDQFVGLM 12

RESULT 24
SERO_GALME STANDARD; PRT; 167 AA.
AC O76192;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SEROIN PRECURSOR (SILK 23 KDA GLYCOPROTEIN).
OS Galleria mellonella (Wax moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Pyraloidea; Pyralidae; Galleriinae; Galleria.
OX NCBI_TaxID=7137;

RN SEQUENCE FROM N.A., AND SEQUENCE OF 18-31.
RP TISSUE-Silk gland;
RC MEDLINE-98288272; PubMed-9624126;
RA Zurovec M., Yang C., Kodrik D., Sehna F.;
RT "Identification of a novel type of silk protein and regulation of its
RL expression";
RL J. Biol. Chem. 273:15428-15428(1998).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- TISSUE SPECIFICITY: PRODUCED BY BOTH THE POSTERIOR (PSG) AND
CC MIDDLE (MSG) SECTIONS OF SILK GLANDS.
CC -1- DEVELOPMENTAL STAGE: SEROIN mRNA IS HIGH IN THE SILK GLANDS OF
CC FEEDING LARVAE, DECLINES AT ECDYSIS, REACHES A MAXIMUM DURING
CC COCOON SPINNING, AND THEREAFTER RAPIDLY DROPS TO AN UNDETECTABLE
CC LEVEL.
CC -----
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CC -----
DR EMBL; AF009828; AAC25171.1; -
KW Silk; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 17
FT CHAIN 18 167 SEROIN.
FT REPEAT 38 46 1-1.
FT REPEAT 56 64 1-2.
FT REPEAT 76 78 2-1.
FT REPEAT 79 81 2-2.
FT REPEAT 82 84 2-3.
FT CARBOHYD 26 26 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 167 AA; 18088 MW; 27AGABE862774EB9 CRC64;

Query Match 59.0%; Score 36; DB 1; Length 167;
Best Local Similarity 75.0%; Pred. No. 9.2;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQFF 8
: : : : :
Db 103 KPKPGQFF 110

RESULT 25
ISPE_HAEIN STANDARD; PRT; 313 AA.
ID ISPE_HAEIN STANDARD; PRT; 313 AA.
AC P45271;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE 4-DIPHOSPHOCYTIDYL-2-C-METHYL-D-ERYTHRITOL KINASE (EC 2.7.1.-) (CMK)
DE (4-(CYTIDINE-5'-DIPHOSPHO)-2-C-METHYL-D-ERYTHRITOL KINASE).
GN ISPE OR H11608.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RD / KW20 / ATCC 51907;
RA MEDLINE-95350630; PubMed-7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Frichman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: CATALYZES THE PHOSPHORYLATION OF THE POSITION 2 HYDROXY
CC GROUP OF 4-DIPHOSPHOCYTIDYL-2-C-METHYL-D-ERYTHRITOL (BY
CC SIMILARITY).
CC -1- PATHWAY: DEOXYXYLULOSE-5-PHOSPHATE PATHWAY (DXP) OF ISOPRENOID
CC BIOSYNTHESIS; FOURTH STEP.
CC -1- SIMILARITY: BELONGS TO THE ISPE FAMILY.
CC -----
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CC -----
DR EMBL; U32834; AAC23252.1; -
KW TIGR; H11608; -
KW Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
KW Complete proteome.
SQ NP_BIND 113 ATP (POTENTIAL).
SQ SEQUENCE 313 AA; 34657 MW; 7A84BAACA196821B CRC64;

Query Match 59.0%; Score 36; DB 1; Length 313;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
: : : : :
Db 273 RKPFAFFGV 283

RESULT 26
EF2_ARCFU STANDARD; PRT; 728 AA.
ID EF2_ARCFU STANDARD; PRT; 728 AA.
AC Q28385;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ELONGATION FACTOR 2 (EF-2).
GN FUSA OR FUS OR AF1894.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VQ-16 / DSM 4304 / ATCC 49558;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLLOCATION
CC OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
CC RIBOSOME.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.

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CC EMBL; AE000972; AAB89360.1; -
DR HSP; P1351; 1DAR.
DR TIGR; AF1894; -
DR InterPro; IPR000640; EFG_C.
DR InterPro; IPR000795; GTP_EFTU.
DR Pfam; PF00679; EFG_C; 1.
DR Pfam; PF00009; GTP_EFTU; 1.
DR PROSITE; PS00301; EFACOR_GTP; 1.
KW Elongation factor; Protein biosynthesis; GTP-binding;
KW Complete proteome.
FT NP_BIND 27 34 GTP (BY SIMILARITY).
FT NP_BIND 93 97 GTP (BY SIMILARITY).
FT NP_BIND 147 150 GTP (BY SIMILARITY).
FT MOD_RES 594 594 DIPHTAMIDE (BY SIMILARITY).
SQ SEQUENCE 728 AA; 81135 MW; 62BA963D6571AE9C CRC64;

Query Match 59.08; Score 36; DB 1; Length 728;
Best Local Similarity 66.78; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PKPQQFFGL 10
Db 720 KPPEFVGL 728

RESULT 27
SYK_VIBCH STANDARD; PRT; 512 AA.
AC Q9KU60;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE--TRNA LIGASE) (LYSRS).
GN LYS OR VC0664.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=686;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan T., Basso S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae".
RL Nature 406:477-483(2000).
CC -1- CATALYTIC ACTIVITY: ATP + L-LYSINE + TRNA(LYS) = AMP +
CC PYROPHOSPHATE + L-LYSYL-TRNA(LYS).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.

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CC EMBL; AE004152; AAF93829.1; -
DR TIGR; VC0664; -
DR InterPro; IPR002106; AA-trna_ligase_II.
DR InterPro; IPR002309; trna-synt_2.
DR InterPro; IPR002312; trna-synt_2.
DR InterPro; IPR002313; trna-synt_lys_2.
DR Pfam; PF00152; trna-synt_2; 1.
DR Pfam; PF01336; trna-anti; 1.
DR PROSITE; PS00179; AA-trna_ligase_II_1; 1.
DR PROSITE; PS00339; AA-trna_ligase_II_2; 1.
KW Aminoacyl-trna synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
SQ SEQUENCE 512 AA; 58336 MW; 3E0BAC911129554C CRC64;

Query Match 57.48; Score 35; DB 1; Length 512;
Best Local Similarity 60.08; Pred. No. 43;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGL 10
Db 152 RPLPEKPHGL 161

RESULT 28
CP3R_ONCMY STANDARD; PRT; 518 AA.
ID CP3R_ONCMY STANDARD; PRT; 518 AA.
AC O42563;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CYTOCHROME P450 3A27 (EC 1.14.14.1) (CYP11A27).
GN CYP3A27.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=SHASTA; TISSUE=Liver;
RX MEDLINE=99045386; PubMed=9826429;
RA Lee S.-J., Wang-Buhler J.-L., Cok I., Yu T.-S., Yang Y.H.,
RA Miranda C.L., Lech J., Buhler D.R.;
RT "Cloning, sequencing, and tissue expression of CYP3A27, a new member
RT of the CYP3A subfamily from embryonic and adult rainbow trout
RT livers".
RL Arch. Biochem. Biophys. 360:53-61(1998).
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -1- INDUCTION: P450 CAN BE INDUCED TO HIGH LEVELS IN LIVER AND OTHER
CC TISSUES BY VARIOUS FOREIGN COMPOUNDS, INCLUDING DRUGS, PESTICIDES,
CC AND CARCINOGENS.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

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CC EMBL; U96077; AAB82422.1; -
DR InterPro; IPR001128; Cyt_P450.

DR Pfam; PF00067; p450; 1.
 DR PRINTS; PR00359; BP450.
 DR PRINTS; PR00385; P450.
 DR PRINTS; PR00463; EP450I.
 DR PRINTS; PR00464; EP450II.
 DR PRINTS; PR00465; EP450IV.
 DR PROSITE; PS00086; CYTOCHROME_P450; 1.
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 KW Microsome; Endoplasmic reticulum.
 FT BINDING 447 447 HEME (BY SIMILARITY).
 SQ SEQUENCE 518 AA; 59210 MW; 9B93AA12E617D0DF CRC64;

Query Match 57.4%; Score 35; DB 1; Length 518;
 Best Local Similarity 60.0%; Pred. No. 43;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKQOFFGLM 11
 III:III
 DB 42 PKPLPYFGTM 51

RESULT 29
 ID RELA_MYXXA STANDARD; PRT; 757 AA.
 AC Q52177;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE GTP PYROPHOSPHOKINASE (EC 2.7.6.5) (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE)
 DE (PPGPP SYNTHETASE I) ((PPGPP SYNTHETASE)).
 GN RELA.
 OS Myxococcus xanthus
 OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
 OC Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
 ON NCBI_TaxID=34;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DK 101;
 RA Harris B.Z., Kaiser D., Singer M.H.;
 RT "The guanosine nucleotide (ppGpp) initiates development and A-factor
 production in Myxococcus xanthus";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IN EUBACTERIA PPGPP (GUANOSINE 3'-DIPHOSPHATE 5'-
 DIPHOSPHATE) IS A MEDIATOR OF THE STRINGENT RESPONSE THAT
 COORDINATES A VARIETY OF CELLULAR ACTIVITIES IN RESPONSE TO
 CHANGES IN NUTRITIONAL ABUNDANCE. THIS ENZYME CATALYSES THE
 FORMATION OF PPGPP WHICH IS THEN HYDROLYSED TO FORM PPAPP (BY
 SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + GTP = AMP + GUANOSINE 3'-DIPHOSPHATE
 5'-TRIPHOSPHATE.
 CC -1- PATHWAY: FIRST STEP IN THE METABOLISM OF PPGPP.
 CC -1- SIMILARITY: BELONGS TO THE RELA / SPOT FAMILY.

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 CC EMBL; AF025847; AAB97677.1; .
 DR InterPro; IPR002912; ACT.
 DR InterPro; IPR003607; HDC.
 DR Pfam; PF01842; ACT; 1.
 DR SMART; SM00471; HDC; 1.
 KW Transferase; Kinase.
 SQ SEQUENCE 757 AA; 84978 MW; D6CC1000A5F72A7B CRC64;

Query Match 57.4%; Score 35; DB 1; Length 757;
 Best Local Similarity 75.0%; Pred. No. 64;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KQOFFGL 10
 III:III
 DB 212 KQOFFGL 219

RESULT 30
 ID DP2L_METH STANDARD; PRT; 1092 AA.
 AC Q27579;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE DNA POLYMERASE II LARGE SUBUNIT (EC 2.7.7.7) (POL II).
 GN POLC OR MTH1536.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 OC Methanothermobacter.
 ON NCBI_TaxID=145262;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DELTA H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Ciu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 deltaH: functional analysis and comparative genomics";
 RL J. Bacteriol. 179:7135-7155(1997).
 CC -1- FUNCTION: POSSESSES TWO ACTIVITIES: A DNA SYNTHESIS (POLYMERASE)
 AND AN EXONUCLEOTIC ACTIVITY THAT DEGRADES SINGLE STRANDED DNA
 IN THE 3' TO 5' DIRECTION. HAS A TEMPLATE-PRIMER PREFERENCE WHICH
 IS CHARACTERISTIC OF A REPLICATIVE DNA POLYMERASE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE " N
 PYROPHOSPHATE + DNA(N).
 CC -1- CATALYTIC ACTIVITY: DEGRADATION OF SINGLE-STRANDED DNA. IT ACTS
 PROGRESSIVELY IN A 3' TO 5' DIRECTION, RELEASING 5'-
 PHOSPHONONUCLEOTIDES.
 CC -1- SUBUNIT: HETERODIMER OF A LARGE SUBUNIT AND A SMALL SUBUNIT (BY
 SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ARCHAEAL DNA POLYMERASE II FAMILY.

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 or send an email to license@isb-sib.ch).
 CC EMBL; AF000913; AAB86010.1; .
 DR Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
 KW Nuclease; Exonuclease; DNA-binding; Multifunctional enzyme;
 KW Complete proteome.
 SQ SEQUENCE 1092 AA; 123058 MW; AA6970F7A6F42DFF CRC64;

Query Match 57.4%; Score 35; DB 1; Length 1092;
 Best Local Similarity 66.7%; Pred. No. 92;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KQOFFGLM 11
 III:III
 DB 932 KPEQYTGML 940

RESULT 31
 Y130_MYCPN


```
PPOB_SOLTU          STANDARD;          PRT;          588 AA.
ID  PPOB_SOLTU
AC  Q06355;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  01-NOV-1995 (Rel. 32, Last annotation update)
DE  POLYPHENOL OXIDASE B PRECURSOR (EC 1.10.3.1) (PPO) (CATECHOL OXIDASE)
DE  (FRAGMENT).
OS  Solanum tuberosum (Potato).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC  Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX  NCBI_TaxID=4113;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CV, KATAHDIN; TISSUE=Leaf;
RX  MEDLINE=93144692; PubMed=7678763;
RA  Hunt M.D., Eannetta N.T., Yu H., Newman S.M., Steffens J.C.;
RT  "cDNA cloning and expression of potato polyphenol oxidase.";
RL  Plant Mol. Biol. 21:59-68(1993).
CC  -1- FUNCTION: CATALYZE THE OXIDATION OF MONO- AND O-DIPHENOLS TO O-
CC  DIQUINONES.
CC  -1- CATALYTIC ACTIVITY: 2 CATECHOL + O(2) = 2 1,2-BENZOQUINONE +
CC  2 H(2)O.
CC  -1- COFACTOR: BINDS TWO COPPER IONS (BY SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.
CC  -1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; M95197; AAA02879.1; -.
DR  InterPro; IPR002227; Tyrosinase.
DR  Pfam; PF00264; tyrosinase; 1.
DR  PROSITE; PS00497; TYROSINASE.1; 1.
DR  PROSITE; PS00498; TYROSINASE.2; 1.
KW  Oxidoreductase; Copper; Metal-binding; Chloroplast; Transit peptide;
KW  Multigene family.
FT  NON_TER 1
FT  TRANSIT <1 88 CHLOROPLAST (POTENTIAL).
FT  CHAIN 89 588 POLYPHENOL OXIDASE B.
FT  METAL 198 198 COPPER A (BY SIMILARITY).
FT  METAL 207 207 COPPER A (BY SIMILARITY).
FT  METAL 329 329 COPPER B (BY SIMILARITY).
FT  METAL 333 333 COPPER B (BY SIMILARITY).
FT  METAL 364 364 COPPER B (BY SIMILARITY).
SQ  SEQUENCE 588 AA; 66240 MW; A7E25383273428CC CRC64;

Query Match 55.7%; Score 34; DB 1; Length 588;
Best Local Similarity 75.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPQFFG 9
   | | | | |
DB 301 PCPSQFFG 308

RESULT 38
YJB0_YEAST          STANDARD;          PRT;          666 AA.
ID  YJB0_YEAST
AC  P47077;
DT  01-FEB-1996 (Rel. 33, Created)
DT  01-FEB-1996 (Rel. 33, Last sequence update)
DT  01-NOV-1997 (Rel. 35, Last annotation update)
DE  HYPOTHEICAL 77.7 KDA PROTEIN IN CCT3-CCT8 INTERGENIC REGION.
GN  YJL010C OR J1357.
OS  Saccharomyces cerevisiae (Baker's yeast).

Query Match 55.7%; Score 34; DB 1; Length 588;
Best Local Similarity 75.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPQFFG 9
   | | | | |
DB 301 PCPSQFFG 308

RESULT 38
YJB0_YEAST          STANDARD;          PRT;          666 AA.
ID  YJB0_YEAST
AC  P47077;
DT  01-FEB-1996 (Rel. 33, Created)
DT  01-FEB-1996 (Rel. 33, Last sequence update)
DT  01-NOV-1997 (Rel. 35, Last annotation update)
DE  HYPOTHEICAL 77.7 KDA PROTEIN IN CCT3-CCT8 INTERGENIC REGION.
GN  YJL010C OR J1357.
OS  Saccharomyces cerevisiae (Baker's yeast).

Query Match 55.7%; Score 34; DB 1; Length 666;
Best Local Similarity 55.6%; Pred. No. 86;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPQOFFGLM 11
   : | | | | |
DB 48 QPQMFFGVL 56

RESULT 39
YQ25_CAEEL          STANDARD;          PRT;          1799 AA.
ID  YQ25_CAEEL
AC  P34675;
DT  01-FEB-1994 (Rel. 28, Created)
DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  15-JUL-1998 (Rel. 36, Last annotation update)
DE  HYPOTHEICAL 202.6 KDA PROTEIN ZK688.5 IN CHROMOSOME III.
GN  ZK688.5.
OS  Caenorhabditis elegans.
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC  Rhabditidae; Peloderinae; Caenorhabditis.
OX  NCBI_TaxID=6239;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BRISTOL N2;
RX  MEDLINE=94150718; PubMed=7906398;
RA  Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA  Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA  Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA  Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA  Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA  Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA  Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
RA  Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
RA  Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA  Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA  Wohldman P.;
RT  *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT  elegans*.
RL  Nature 368:32-38(1994).
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; Z49285; CAA89301.1; -.
DR  SGD; S0003547; YJL010C.
DR  InterPro; IPR001313; PUM.
DR  Pfam; PF00806; PUF; 8.
DR  SMART; SM00025; Pumilio; 8.
KW  Hypothetical protein.
SQ  SEQUENCE 666 AA; 77722 MW; F6F8B3CD74DB2AB3 CRC64;

Query Match 55.7%; Score 34; DB 1; Length 666;
Best Local Similarity 55.6%; Pred. No. 86;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPQOFFGLM 11
   : | | | | |
DB 48 QPQMFFGVL 56

RESULT 39
YQ25_CAEEL          STANDARD;          PRT;          1799 AA.
ID  YQ25_CAEEL
AC  P34675;
DT  01-FEB-1994 (Rel. 28, Created)
DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  15-JUL-1998 (Rel. 36, Last annotation update)
DE  HYPOTHEICAL 202.6 KDA PROTEIN ZK688.5 IN CHROMOSOME III.
GN  ZK688.5.
OS  Caenorhabditis elegans.
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC  Rhabditidae; Peloderinae; Caenorhabditis.
OX  NCBI_TaxID=6239;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BRISTOL N2;
RX  MEDLINE=94150718; PubMed=7906398;
RA  Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA  Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA  Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA  Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA  Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA  Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA  Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
RA  Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
RA  Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA  Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA  Wohldman P.;
RT  *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT  elegans*.
RL  Nature 368:32-38(1994).
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; Z49285; CAA89301.1; -.
DR  SGD; S0003547; YJL010C.
DR  InterPro; IPR001313; PUM.
DR  Pfam; PF00806; PUF; 8.
DR  SMART; SM00025; Pumilio; 8.
KW  Hypothetical protein.
SQ  SEQUENCE 666 AA; 77722 MW; F6F8B3CD74DB2AB3 CRC64;
```



```
RP SEQUENCE FROM N.A. (CYP6B3V2).
RX MEDLINE=97057218; PubMed=8901557;
RA Hung C.F., Holznacher R., Connolly E., Berenbaum M.R., Schuler M.A.;
RT "Conserved promoter elements in the CYP6B gene family suggest common
an ancestry for cytochrome P450 monooxygenases mediating furanocoumarin
detoxification.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:12200-12205(1996).
CC -!- FUNCTION: ENABLES THE INSECT TO FEED ON FURANOCOUMARIN-PRODUCING
PLANTS AND EVOLVED AS AN ADAPTATION FOR DETOXIFICATION OF
XANTHOTOXIN AND OTHER FURANOCOUMARINS.
CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
OXIDIZED FLAVOPROTEIN + H(2)O.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- INDUCTION: BY XANTHOTOXIN AND BERGAPTEN (LINEAR FURANOCOUMARINS)
AS WELL AS BY ANGELICIN AND SPHONDIN (ANGULAR FURANOCOUMARINS).
CC -!- POLYMORPHISM: THE SEQUENCE SHOWN IS THAT OF 6B3-1, 6B3-2 SEEMS
TO DIFFER IN 17 POSITIONS AND IS PROBABLY AN ALLELE.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
-----
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-----
DR EMBL; U25819; AAR96255.1; -.
DR EMBL; U65488; AAB06741.1; -.
DR InterPro; IPR001128; Cyt_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PR00464; EP450II.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum; Polymorphism.
FT BINDING 443 443 HEME (BY SIMILARITY).
FT VARIANT 47 47 A -> V (IN 6B3-2).
FT VARIANT 52 52 P -> H (IN 6B3-2).
FT VARIANT 82 82 L -> I (IN 6B3-2).
FT VARIANT 92 93 PT -> LI (IN 6B3-2).
FT VARIANT 98 98 P -> S (IN 6B3-2).
FT VARIANT 108 108 L -> I (IN 6B3-2).
FT VARIANT 289 289 T -> I (IN 6B3-2).
FT VARIANT 350 350 G -> S (IN 6B3-2).
FT VARIANT 354 357 FLGR -> YLSK (IN 6B3-2).
FT VARIANT 395 397 IIV -> VII (IN 6B3-2).
FT VARIANT 401 401 G -> S (IN 6B3-2).
SQ SEQUENCE 498 AA; 57473 MW; 9BC760ACBEB657BC CRC64;

Query Match 54.1%; Score 33; DB 1; Length 498;
Best Local Similarity 75.0%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOOFFG 9
DB 34 PKPIFFG 41

RESULT 45
SYK_PASMU STANDARD; PRT; 501 AA.
AC P57822;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE--TRNA LIGASE) (LYSRS).
GN LYSS OR LYSU OR PM0189.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
```

```
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Faustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -!- CATALYTIC ACTIVITY: ATP + L-LYSINE + TRNA(LYS) = AMP +
PYROPHOSPHATE + L-LYSYL-TRNA(LYS).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
-----
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-----
DR EMBL; AE006053; AAK02273.1; -.
DR InterPro; IPR002106; AA_trna_ligase_II.
DR InterPro; IPR002309; trna-synt_2.
DR InterPro; IPR002313; trna-synt_lys_2.
DR Pfam; PF00152; trna-synt_2; 1.
DR Pfam; PF01336; trna-anti; 1.
DR PROSITE; PS00179; AA_trna_ligase_II_1; 1.
DR PROSITE; PS00339; AA_trna_ligase_II_2; 1.
KW Aminoacyl-trna synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
SQ SEQUENCE 501 AA; 56759 MW; 767E6F21AC85B240 CRC64;

Query Match 54.1%; Score 33; DB 1; Length 501;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOOFFGL 10
DB 146 RPLPKRFHGL 155

RESULT 46
SYK_HAEIN STANDARD; PRT; 502 AA.
ID SYK_HAEIN
AC P43825;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE--TRNA LIGASE) (LYSRS).
GN LYSS OR LYSU OR H11211.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Cocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Keiley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
influenzae Rd.";
RL Science 269:496-512(1995).
CC -!- CATALYTIC ACTIVITY: ATP + L-LYSINE + TRNA(LYS) = AMP +
```

```
CC PYROPHOSPHATE + L-LYSYL-TRNA(LYS).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; U32800; AAC22865.1; -.
DR HSSP; P14825; 1LYL.
DR TIGR; H11211; -.
DR InterPro; IPR002106; AA-trna_ligase_II.
DR InterPro; IPR002309; trna-synt_2.
DR Pfam; PF00152; trna-synt_2; 1.
DR Pfam; PF01336; trna-anti; 1.
DR PRINTS; PR00982; TRNASYNTHLYS.
DR PROSITE; PS00179; AA-TRNA-LIGASE_II_1; 1.
DR PROSITE; PS00339; AA-TRNA-LIGASE_II_2; 1.
DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
DR Complete proteome.
DR KW Complete proteome.
DR SQ SEQUENCE 502 AA; 56935 MW; DF281DF073A702B9 CRC64;

Query Match 54.1%; Score 33; DB 1; Length 502;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGL 10
Db 147 RPLPDKPHGL 156

RESULT 47
SYKL_ECOLI
ID SYKL_ECOLI STANDARD; PRT; 504 AA.
AC P13030;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE--TRNA LIGASE) (LYSRS).
GN LYSS OR HEC OR ASUD OR B2890.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88289768; PubMed=2456575;
RA Kawakami K., Joensson Y.H., Bjoerk G.R., Ikeda H., Nakamura Y.;
RT "Chromosomal location and structure of the operon encoding
RT peptide-chain-release factor 2 of Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:5620-5624(1988).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-27.
RX MEDLINE=90221811; PubMed=2183178;
RA Leveque F., Plateau P., Dessen P., Blanquet S.;
RT "Homology of lysyl and lysu, the two Escherichia coli genes encoding
RT distinct lysyl-tRNA synthetase species.";
RL Nucleic Acids Res. 18:305-312(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;

"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
[4]
RP STRUCTURE BY NMR.
RX MEDLINE=96028214; PubMed=7473706;
RA Commans S., Plateau P., Blanquet S., Dardel F.;
RT "Solution structure of the anticodon-binding domain of Escherichia
RT coli lysyl-tRNA synthetase and studies of its interaction with
RT tRNA(Lys).";
J. Mol. Biol. 253:100-113(1995).
CC -1- CATALYTIC ACTIVITY: ATP + L-LYSINE + TRNA(LYS) -> AMP +
CC PYROPHOSPHATE + L-LYSYL-TRNA(LYS).
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- MISCELLANEOUS: THERE ARE TWO LYSYL-TRNA LIGASES IN E. COLI: LYSS IS
CC EXPRESSED CONSTITUTIVELY, WHILE LYSU IS HEAT INDUCIBLE.
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; J03795; AAA23959.1; -.
DR EMBL; U28375; AAA83071.1; -.
DR PIR; JS0401; SYECKT.
DR PDB; 1KRS; 15-SEP-95.
DR PDB; 1KRT; 15-SEP-95.
DR SWISS-2DPAGE; P13030; COLI.
DR ECOBASE; D058.5; 6TH EDITION.
DR Ecogene; EG10552; lysS.
DR InterPro; IPR002106; AA-trna_ligase_II.
DR InterPro; IPR002309; trna-synt_2.
DR InterPro; IPR002313; trna-synt_lys_2.
DR Pfam; PF00152; trna-synt_2; 1.
DR Pfam; PF01336; trna-anti; 1.
DR PRINTS; PR00982; TRNASYNTHLYS.
DR PROSITE; PS00179; AA-TRNA-LIGASE_II_1; 1.
DR PROSITE; PS00339; AA-TRNA-LIGASE_II_2; 1.
DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
DR Multigene family; 3D-structure; Complete proteome.
DR INIT_MET 0
FT INIT_MET 0
SQ SEQUENCE 504 AA; 57472 MW; EE5F3D1FBA63CFEF CRC64;

Query Match 54.1%; Score 33; DB 1; Length 504;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGL 10
Db 150 RPLPDKPHGL 159

RESULT 48
SYK2_ECOLI
ID SYK2_ECOLI STANDARD; PRT; 504 AA.
AC P14825;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE LYSYL-TRNA SYNTHETASE, HEAT INDUCIBLE (EC 6.1.1.6) (LYSINE--TRNA
DE LIGASE) (LYSRS).
DE DE LYSU OR B4129.
GN LYSU OR B4129.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
[1]
```

RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
RX MEDLINE=90221811; PubMed=2183178;
RA Leveque F., Plateau P., Dessen P., Blanquet S.;
RT "Homology of lysS and lysU, the two Escherichia coli genes encoding
RL distinct lysyl-tRNA synthetase species";
RN Nucleic Acids Res. 18:305-312(1990).
RP [2]
RP REVISION TO 445.
RA Dessen P.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=90264318; PubMed=2188953;
RA Clark R.L., Neidhardt F.C.;
RT "Roles of the two lysyl-tRNA synthetases of Escherichia coli:
RL analysis of nucleotide sequences and mutant behavior";
RN J. Bacteriol. 172:3237-3243(1990).
RP [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RL region from 92.8 through 100 minutes";
RN Nucleic Acids Res. 23:2105-2119(1995).
RP [5]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=95253817; PubMed=7735833;
RA Onesti S., Miller A.D., Brick P.;
RT "The crystal structure of the lysyl-tRNA synthetase (LysU) from
RL Escherichia coli";
RN Structure 3:163-176(1995).
CC -!- FUNCTION: ALSO CAN SYNTHESIZE A NUMBER OF ADENYL DINUCLEOTIDES (IN
CC PARTICULAR APPRA). THESE DINUCLEOTIDES HAVE BEEN PROPOSED TO ACT
CC AS MODULATORS OF THE HEAT-SHOCK RESPONSE AND STRESS RESPONSE.
CC -!- CATALYTIC ACTIVITY: ATP + L-LYSINE + TRNA(LYS) = AMP +
CC PYROPHOSPHATE + L-LYSYL-TRNA(LYS).
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- MISCELLANEOUS: THERE ARE TWO LYSYL-TRNA LIGASES IN E. COLI: LYSY IS
CC EXPRESSED CONSTITUTIVELY, WHILE LYSU IS HEAT INDUCIBLE.
CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X16542; CAA34542.1; -;
DR EMBL; M30630; AAA24096.1; -;
DR EMBL; U14003; AAA97029.1; -;
DR EMBL; AE000485; AAC77090.1; -;
DR PIR; JS0400; SYECKU
DR PDB; 1LYL; 15-OCT-95.
DR ECODBASE; D060.5; 6TH EDITION.
DR EcoGene; EG10553; lysU.
DR InterPro; IPR002106; AA_trna_ligase_II.
DR InterPro; IPR002309; trna-synt_2.
DR InterPro; IPR002313; trna-synt_lys_2.
DR Pfam; PF00152; trna-synt_2; 1.
DR Pfam; PF01336; trna-anti; 1.
DR PRINTS; PR00982; TRNASYNTHYS.
DR PROSITE; PS00179; AA_TRNA_LIGASE_II_1; 1.
DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Multigene family; 3D-structure; Complete proteome.
FT INIT_MET 0
FT CONFLICT 124 124 MISSING (IN REF. 3).
FT CONFLICT 235 235 L -> A (IN REF. 3).
FT

FT CONFLICT 257 261 INRNF -> HVT (IN REF. 3).
FT CONFLICT 267 268 SV -> R (IN REF. 3).
FT CONFLICT 350 350 A -> R (IN REF. 3).
FT CONFLICT 370 370 I -> S (IN REF. 3).
FT CONFLICT 379 383 AEAHL -> VEGHV (IN REF. 3).
FT CONFLICT 387 387 T -> S (IN REF. 3).
SQ SEQUENCE 504 AA; 57695 MW; 48E1B8F5875396E0 CRC64;

Query Match 54.1%; Score 33; DB 1; Length 504;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQFFGL 10
DB 150 RPLPKFHGL 159
|| | : ||
- - - - -

RESULT 49
FRK_HUMAN
ID FRK_HUMAN STANDARD; PRT; 505 AA.
AC P42685; Q13128;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE TYROSINE-PROTEIN KINASE FRK (EC 2.7.1.112) (NUCLEAR TYROSINE PROTEIN
DE KINASE RAK).
GN FRK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=94171047; PubMed=7510261;
RA Lee J., Wang Z., Luoh S.-M., Wood W.I., Scadden D.T.;
RT "Cloning of FRK, a novel human intracellular SRC-like tyrosine
RT kinase-encoding gene";
RL Gene 138:247-251(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95210168; PubMed=7696183;
RA Cance W.G., Craven R.J., Bergman M., Xu L.H., Alitalo K., Liu E.T.;
RT "Rak, a novel nuclear tyrosine kinase expressed in epithelial cells";
RL Cell Growth Differ. 5:1347-1355(1994).
RN [3]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=93293373; PubMed=8099900;
RA Cance W.G., Craven R.J., Weiner T.M., Liu E.T.;
RT "Novel protein kinases expressed in human breast cancer";
RL Int. J. Cancer 54:571-577(1993).
CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
CC -!- TISSUE SPECIFICITY: RESTRICTED TO CELLS LINES DERIVED FROM TISSUES
CC OF LYMPHOID, BRAIN, BREAST, COLON AND BLADDER ORIGIN.
CC -!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U00803; AAA18284.1; -;
DR EMBL; U22322; AAC50116.1; -;
DR HSP; P00523; 2PTK.

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DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_Kin.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
DR Transferase; Tyrosine-protein kinase; ATP-binding; SH2 domain;
KW SH3 domain; Phosphorylation.
FT DOMAIN 42 110 SH3.
FT DOMAIN 116 208 SH2.
FT DOMAIN 234 491 PROTEIN KINASE.
FT NP_BIND 240 248 ATP (BY SIMILARITY).
FT BINDING 262 262 ATP (BY SIMILARITY).
FT ACT_SITE 354 354 BY SIMILARITY.
FT MOD_RES 387 387 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT VARIANT 122 122 G -> R.
FT CONFLICT 115 115 P -> A (IN REF. 2).
FT SEQUENCE 505 AA; 58254 MW; 06EC050DBDCD930B CRC64;

Query Match 54.1%; Score 33; DB 1; Length 505;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PQPFGLM 11
| | | | : |
Db 459 PQPFVNM 466

RESULT 50
SYK_ACICA
ID SYK_ACICA STANDARD; PRT; 509 AA.
AC Q43990;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE--TRNA LIGASE) (LYSRS).
GN LYSS.
OS Acinetobacter calcoaceticus.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OC Acinetobacter.
OX NCBI_TaxID=471;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BD413 / ADP1;
RC MEDLINE=97228433; PubMed=9074511;
RA Gelsdoerfer W., Ratajczak A., Hillen W.;
RT "Nucleotide sequence of a putative periplasmic Mn superoxide dismutase
from Acinetobacter calcoaceticus ADP1.";
RL Gene 186:305-308(1997).
CC -1- CATALYTIC ACTIVITY: ATP + L-LYSINE + TRNA(LYS) -> AMP +
PYROPHOSPHATE + L-LYSYL-TRNA(LYS).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; Z46863; CAA86924.1; -.
CC HSP; P14825; ILYL.
CC InterPro; IPR002106; AA_trna_ligase_II.
CC InterPro; IPR002309; trna-synt_2.
CC InterPro; IPR002313; trna-synt_lys_2.
CC Pfam; PF00152; trna-synt_2; 1.
CC Pfam; PF01336; trna-anti_1.
CC PRINTS; PR00982; TRNASYNTHLYS.
CC PROSITE; PS00179; AA-trna_ligase_II_1; 1.
CC PROSITE; PS00339; AA-trna_ligase_II_2; 1.
CC Aminoacyl-trna synthetase; Protein biosynthesis; Ligase; ATP-binding.
KW SEQUENCE 509 AA; 58079 MW; 95ED1AA43DC3D2F6 CRC64;

Query Match 54.1%; Score 33; DB 1; Length 509;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKPQPFGL 10
| | | | : | | |
Db 153 RLPDPKFHGL 162

RESULT 51
COX1_APILI
ID COX1_APILI STANDARD; PRT; 521 AA.
AC P20374;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).
GN COI.
OS Apis mellifera ligustica (Common honeybee).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Apis.
OX NCBI_TaxID=7469;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thorax;
RC MEDLINE=90136028; PubMed=2559293;
RA Crozier R.H., Crozier Y.C., Mackinlay A.G.;
RT "The CO-I and CO-II region of honeybee mitochondrial DNA: evidence
for variation in insect mitochondrial evolutionary rates.";
RL Mol. Biol. Evol. 6:399-411(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Thorax;
RC MEDLINE=93114603; PubMed=8417993;
RA Crozier R.H., Crozier Y.C.;
RT "The mitochondrial genome of the honeybee Apis mellifera: complete
sequence and genome organization.";
RL Genetics 133:97-117(1993).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B.
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O +
4 FERRICYTOCHROME C.
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE. CONTAINS 12 POTENTIAL TRANSMEMBRANE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
CC -----
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CC EMBL; M23409; AAL18476.1; -;
CC EMBL; L06178; AAB96799.1; -;
CC PIR; A32431; A32431.
CC HSP; P00396; 10CC.
CC InterPro; IPR000883; COX1.
CC Pfam; PF00115; COX1; 1.
CC PRINTS; PR01165; CYCOXIDASE1.
CC PROSITE; PS00077; COX1; 1.
CC Oxidoreductase; Heme; Copper; Mitochondrion; Transmembrane;
KW Respiratory chain; Inner membrane.
FT METAL 59 IRON (HEME A) (PROBABLE).
FT METAL 238 COPPER B (PROBABLE).
FT METAL 242 COPPER B (PROBABLE).
FT METAL 288 COPPER B (PROBABLE).
FT METAL 289 COPPER B (PROBABLE).
FT METAL 374 IRON (HEME A3) (PROBABLE).
FT METAL 376 IRON (HEME A) (PROBABLE).
SQ SEQUENCE 521 AA; 59293 MW; 2149417AC981CE64 CRC64;

Query Match 54.1%; Score 33; DB 1; Length 521;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
II I III
DB 425 PQHFLGLM 432

RESULT 52
ID IMALARATH STANDARD; PRT; 596 AA.
AC Q96321;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE IMPORTIN ALPHA-1 SUBUNIT (KARYOPHERIN ALPHA-1 SUBUNIT) (KAP ALPHA).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Ballas N., Citovsky V.;
RT "ATKAPalpha gene from Arabidopsis encodes a protein that mediates nuclear import of Agrobacterium VirD2 protein.";
RL (In) Plant Gene Register PGR97-129.
CC -!- FUNCTION: BINDS SPECIFICALLY AND DIRECTLY TO SUBSTRATES CONTAINING EITHER A SIMPLE OR BIPARTITE NLS MOTIF. PROMOTES DOCKING OF IMPORT SUBSTRATES TO THE NUCLEAR ENVELOPE. SEEMS TO ACT AS A CYTOSOLIC RECEPTOR FOR BOTH SIMPLE AND BIPARTITE NLS MOTIFS (BY SIMILARITY).
CC CELLULAR RECEPTOR FOR THE NUCLEAR IMPORT OF THE VIRD2 PROTEIN OF AGROBACTERIUM.
CC -!- SUBUNIT: FORMS A COMPLEX WITH IMPORTIN BETA-1 SUBUNIT (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE IMPORTIN ALPHA FAMILY.
CC -!- SIMILARITY: CONTAINS 8 ARM REPEATS.
CC -----
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CC EMBL; U69533; AAB72116.1; -;
CC HSP; Q02248; 2BCT.
CC InterPro; IPR000225; Armadillo.
CC InterPro; IPR002652; IBB.
CC Pfam; PF01749; IBB; 1.
CC SMART; SM00185; ARM; 8.
CC PROSITE; PS50176; ARM_REPEAT; 3.
KW Transport; Protein transport; Repeat.
FT DOMAIN 12. 51 IBB.
FT REPEAT 109 151 ARM 1.
FT REPEAT 152 196 ARM 2.
FT REPEAT 197 234 ARM 3.
FT REPEAT 235 279 ARM 4.
FT REPEAT 280 319 ARM 5.
FT REPEAT 320 362 ARM 6.
FT REPEAT 363 403 ARM 7.
FT REPEAT 403 445 ARM 8.
FT DOMAIN 446 596 ASP/GLU-RICH (ACIDIC).
SQ SEQUENCE 596 AA; 65606 MW; 2A2689E1C28F43E7 CRC64;

Query Match 54.1%; Score 33; DB 1; Length 596;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQFF 8
II III I
DB 231 RPKPOPHF 238

RESULT 53
TLD_DROME

ID TLD_DROME STANDARD; PRT; 1057 AA.
AC P25723; Q9VC46;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE DORSAL-VENTRAL PATTERNING TOLLID PROTEIN PRECURSOR (EC 3.4.24.-).
GN TLD OR CG6868.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RX MEDLINE=92034970; PubMed=1840509;
RA Shmell M.J., Ferguson E.L., Childs S.R., O'Connor M.B.;
RT "The Drosophila dorsal-ventral patterning gene tollid is related to human bone morphogenetic protein 1.";
RL Cell 67:469-481(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95324373; PubMed=7600963;
RA Finelli A.L., Bossie C.A., Xie T., Padgett R.W.;
RT "Mutational analysis of the Drosophila tollid gene, a human BMP-1 homolog.";
RN [3]
RP Development 120:861-870(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X., Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RX MEDLINE-90345939; PubMed-2200674;
RA Hawkins C.F., Borges A., Perham R.N.;
RT "Cloning and sequence analysis of the genes encoding the alpha and
RT beta subunits of the E1 component of the pyruvate dehydrogenase
RT multienzyme complex of Bacillus stearothermophilus.";
RL Eur. J. Biochem. 191:337-346(1990).
CC -!- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL
CC CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE
CC COPIES OF THREE ENZYMIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1),
CC DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE
CC (E3).
CC -!- CATALYTIC ACTIVITY: PYRUVATE + LIPOAMIDE = S-ACETYL-DIHYDRO-
CC LIPOAMIDE + CO(2).
CC -!- COFACTOR: THIAMINE PYRROPHOSPHATE.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC
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CC
CC
CC EMBL; X53560; CAA37629.1; -
DR PIR; S14230; S14230.
DR InterPro; IPR000360; Transketolase.
DR Pfam; PF00456; transketolase; 1.
KW Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate.
FT INIT_MET 0
SQ SEQUENCE 324 AA; 35328 MW; F7C6085E33371384 CRC64;

Query Match 53.3%; Score 32.5; DB 1; Length 324;
Best Local Similarity 58.3%; Pred. No. 79;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 RPQPO-QFFGLM 11
DB 75 RVPPEIQFGFV 86
11 1: 11111 :
75 RVPPEIQFGFV 86

RESULT 55
TKN_PHYFU STANDARD; PRT; 11 AA.
AC P08615;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PHYSALAEAMIN.
OS Physalaemus fuscumaculatus (Neotropical frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Leptodactylidae;
OC Physalaemus.
OX NCBI_TaxID=8378;
RN [1]
RP SEQUENCE.
RX MEDLINE-66076612; PubMed-5857249;
RA Ersamer V., Anastasi A., Bertaccini G., Cei J.M.;
RT "Structure and pharmacological actions of physalaemin, the main
RT active polypeptide of the skin of Physalaemus fuscumaculatus.";
RL Experientia 20:489-490(1964).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S07201; S07201.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.

KW Tachykinin; Neuropeptide; Amidation; Amphibian skin.
FT MOD_RES 1 1
FT MOD_RES 11 11
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

Query Match 52.5%; Score 32; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 3.3;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
DB 4 PNKFYGLM 11
1 1: 1111 :
4 PNKFYGLM 11

RESULT 56
IBPL_BOVIN STANDARD; PRT; 263 AA.
ID IBPL_BOVIN
AC P24591;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-1)
DE (IBP-1) (IGF-BINDING PROTEIN 1).
DE IGFBP1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HOLSTEIN-FRIESIAN; TISSUE=Liver;
RX MEDLINE-92119331; PubMed-1722724;
RA Sneyers M., Kettmann R., Massart S., Renaville R., Burny A.,
RA Portetelle D.;
RT "Cloning and characterization of a cDNA encoding the bovine
RT insulin-like growth factor binding protein 1 (biglycan-1).";
RL DNA Seq. 1:407-408(1991).
CC -!- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- MISCELLANEOUS: BINDS EQUALLY WELL IGF-I AND IGF-II.
CC -!- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
CC PROTEIN FAMILY.
CC
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CC
CC
CC EMBL; X54979; CAA38723.1; -
DR PIR; S23009; S23009.
DR InterPro; IPR000867; IGFBP.
DR InterPro; IPR000716; Thyroglobulin_1.
DR Pfam; PF00219; IGFBP; 1.
DR Pfam; PF00086; thyroglobulin_1; 1.
DR SMART; SM00121; IB; 1.
DR SMART; SM00211; TY; 1.
DR PROSITE; PS00222; IGF BINDING; 1.
DR PROSITE; PS00484; THYROGLOBULIN_1; 1.
KW Growth factor binding; Signal.
FT SIGNAL 1 25
FT CHAIN 26 263
FT DOMAIN 206 255
FT SITE 250 252
INSULIN-LIKE GROWTH FACTOR BINDING
PROTEIN 1.
THYROGLOBULIN TYPE I.
CELL ATTACHMENT SITE.

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FT DISULFID 73 86 BY SIMILARITY.
FT DISULFID 80 106 BY SIMILARITY.
FT DISULFID 180 210 BY SIMILARITY.
SQ SEQUENCE 263 AA; 28796 MW; 0403B642DDDC45B6 CRC64;

Query Match 52.5%; Score 32; DB 1; Length 263;
Best Local Similarity 66.7%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KPQOFFGL 10
| | | | |
Db 253 PKQQYFNL 261

RESULT 57
TRPA_THETH STANDARD; PRT; 271 AA.
AC P16608;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TRYPTOPHAN SYNTHASE ALPHA CHAIN (EC 4.2.1.20).
GN TRPA.
OS Thermus aquaticus (subsp. thermophilus).
OC Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB27;
RX MEDLINE=90264352; PubMed=2189962;
RA Koyama Y., Furukawa K.;
RT "Cloning and sequence analysis of tryptophan synthase genes of an
RT extreme thermophile, Thermus thermophilus HB27; plasmid transfer from
RT replica-plated Escherichia coli recombinant colonies to competent T.
RT thermophilus cells.";
RL J. Bacteriol. 172:3490-3495(1990).
CC -1- FUNCTION: THE ALPHA SUBUNIT IS RESPONSIBLE FOR THE ALDOL CLEAVAGE
CC OF INDOLGLYCEROL PHOSPHATE TO INDOL AND GLYCERALDEHYDE 3-
CC PHOSPHATE.
CC -1- CATALYTIC ACTIVITY: L-SERINE + 1-(INDOL-3-YL)GLYCEROL 3-PHOSPHATE
CC = L-TRYPTOPHAN + GLYCERALDEHYDE 3-PHOSPHATE + H(2)O.
CC -1- PATHWAY: LAST (FIFTH) STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (by
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE TRPA FAMILY.
CC
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CC
CC EMBL; M32108; AAA27509.1;
CC PIR; B35407; B35407.
CC HSSP; P00929; 1A5B.
CC InterPro; IPR002028; TRP_synthase_alpha.
CC Pfam; PF00290; trp_synta; 1.
CC ProDom; PD001535; TRP_synthase_alpha; 1.
CC PROSITE; PS00167; TRP_SYNTHASE_ALPHA; 1.
CC TrpTophan biosynthesis; Lysase.
SQ SEQUENCE 271 AA; 28924 MW; C9E2A86080224DA2 CRC64;

Query Match 52.5%; Score 32; DB 1; Length 271;
Best Local Similarity 71.4%; Pred. No. 82;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQQFFGL 10
| | | | |
Db 108 PERFFGL 114

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RESULT 58
YDHH_HAEIN STANDARD; PRT; 382 AA.
ID YDHH_HAEIN
AC P44861;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN HI0753.
GN HI0753.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uutterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:496-512(1995).
CC -1- SIMILARITY: BELONGS TO THE UPF0075 FAMILY.
CC
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CC
CC EMBL; U32759; AAC22412.1;
CC TIGR; HI0753;
CC Hypothetical protein; Complete proteome.
SQ SEQUENCE 382 AA; 42026 MW; D14E353287BC11A6 CRC64;

Query Match 52.5%; Score 32; DB 1; Length 382;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPQOFFGLM 11
| | | | |
Db 5 KPQYILGMM 13

RESULT 59
GCH2_CHLPN STANDARD; PRT; 418 AA.
ID GCH2_CHLPN
AC Q32734; Q9JQ68;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE RIBOFLAVIN BIOSYNTHESIS PROTEIN RIBA [INCLUDES: GTP CYCLOHYDROLASE II
DE (EC 3.5.4.25); 3,4-DIHYDROXY-2-BUTANONE 4-PHOSPHATE SYNTHASE (DHBP
DE SYNTHASE)].
GN RIBAB OR CPM0872 OR CP0997.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;

```

RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Reid T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher M., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA";
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -1- CATALYTIC ACTIVITY: GTP + 3 H(2)O = FORMATE + 2,5-DIAMINO-6-
CC HYDROXY-4-(5-PHOSPHORIBOSYLAMINO)PYRIMIDINE + PYROPHOSPHATE.
CC -1- PATHWAY: RIBOFLAVIN BIOSYNTHESIS.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE DHBP
CC SYNTHASE FAMILY.
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE GTP
CC CYCLOHYDROLASE II FAMILY.
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CC -----
DR EMBL; AE001667; AAD19010.1; -;
DR EMBL; AE002257; AAF38775.1; -;
DR EMBL; AP002548; BAA99080.1; -;
DR TIGR; CP0997; -;
DR InterPro; IPR000422; DHBP_synthase.
DR InterPro; IPR000926; GTP_cyclohydro2.
DR Pfam; PF00926; DHBP_synthase; 1.
DR Pfam; PF00925; GTP_cyclohydro2; 1.
DR ProDom; PD003034; DHBP_synthase; 1.
KW Multifunctional enzyme; Riboflavin biosynthesis; Hydrolase;
KW Complete proteome.
FT DOMAIN 1 211 DHBP SYNTHASE.
FT DOMAIN 212 418 GTP CYCLOHYDROLASE II.
SQ SEQUENCE 418 AA; 45845 MW; 7A5A214BB0EC0E32 CRC64;

Query Match 52.5%; Score 32; DB 1; Length 418;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 4 PQOFFGL 10
Db 366 PKIFGL 372

RESULT 60
RHO_BORBU STANDARD; PRT; 419 AA.
AC P33561; O51248;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TRANSCRIPTION TERMINATION FACTOR RHO.
GN RHO OR BB0230.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93197131; PubMed=8451174;
RA Tilly K., Campbell J.;
RT "A Borrelia burgdorferi homolog of the Escherichia coli rho gene";
RL Nucleic Acids Res. 21:1040-1040(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Utterback T., Wathley L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi";
RL Nature 390:580-586(1997).
RN [3]
RP SEQUENCE OF 46-235 FROM N.A.
RC STRAIN=212;
RX MEDLINE=95111614; PubMed=7812434;
RA Ojalimi C., Davidson B.E., Saint-Girons I., Old I.G.;
RT "Conservation of gene arrangement and an unusual organization of rRNA
RT genes in the linear chromosomes of the Lyme disease spirochaetes
RT Borrelia burgdorferi, B. garinii and B. afzelii";
RL Microbiology 140:2931-2940(1994).
CC -1- FUNCTION: FACILITATES TRANSCRIPTION TERMINATION BY A MECHANISM
CC THAT INVOLVES RHO BINDING TO THE NASCENT RNA. ACTIVATION OF RHO'S
CC RNA-DEPENDENT ATPASE ACTIVITY, AND RELEASE OF THE MRNA FROM THE
CC DNA TEMPLATE (BY SIMILARITY).
CC -1- SUBUNIT: HOMOHETEROMER (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
CC -----
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CC -----
DR EMBL; L07656; AAA71920.1; ALT_INIT.
DR EMBL; U35673; AAB41463.1; ALT_INIT.
DR EMBL; AE001133; AAC66619.1; ALT_INIT.
DR EMBL; L46347; AAA73991.1; -;
DR HSSP; P03002; 1A63.
DR TIGR; BB0230; -;
DR InterPro; IPR003593; AAA.
DR InterPro; IPR000194; ATPase_alpha_beta.
DR InterPro; IPR002059; Cold_shock.
DR Pfam; PF00006; ATP-synt_ab; 1.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00357; CSP; 1.
KW Transcription termination; Helicase; ATP-binding; RNA-binding;
KW Complete proteome.
FT DOMAIN 21 26 RNA-BINDING (RNP2) (BY SIMILARITY).
FT DOMAIN 63 66 RNA-BINDING (RNP1) (BY SIMILARITY).
FT NP_BIND 177 184 ATP (POTENTIAL).
FT CONFLICT 58 58 D -> H (IN REF. 3).
FT CONFLICT 210 210 E -> D (IN REF. 3).
SQ SEQUENCE 419 AA; 46950 MW; 38D0C354E6C00ABF CRC64;

Query Match 52.5%; Score 32; DB 1; Length 419;
 Best Local Similarity 71.4%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KPOOFFG 9
 ||::|||
 Db 295 KPKRFFG 301

RESULT 61
 RHO_PSEFL STANDARD; PRT; 419 AA.
 AC P52155;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE TRANSCRIPTION TERMINATION FACTOR RHO.
 GN RHO.
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 17400;
 RX MEDLINE=94327472; PubMed=8051015;
 RA Opperman T., Richardson J.P.;
 RT "Phylogenetic analysis of sequences from diverse bacteria with
 homology to the Escherichia coli rho gene.";
 RL J. Bacteriol. 176:5033-5043(1994).
 CC -1- FUNCTION: FACILITATES TRANSCRIPTION TERMINATION BY A MECHANISM
 THAT INVOLVES RHO BINDING TO THE NASCENT RNA, ACTIVATION OF RHO'S
 RNA-DEPENDENT ATPASE ACTIVITY, AND RELEASE OF THE MRNA FROM THE
 DNA TEMPLATE (BY SIMILARITY).
 CC -1- SUBUNIT: HOMOHXAMER (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
 CC -----
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 CC -----
 CC EMBL; L27278; AAA59209.1; -
 DR HSP; P03002; I463.
 DR InterPro; IPR003593; AAA.
 DR InterPro; IPR000194; ATPase_alpha_beta.
 DR Pfam; PF00006; ATP-synt_ab; 1.
 DR SMART; SM00382; AAA; 1.
 DR SMART; SM00357; CSP; 1.
 KW Transcription termination; Helicase; ATP-binding; RNA-binding.
 FT DOMAIN 21 26 RNA-BINDING (RNP2) (BY SIMILARITY).
 FT DOMAIN 61 64 RNA-BINDING (RNP1) (BY SIMILARITY).
 FT NP_BIND 178 185 ATP (POTENTIAL).
 SQ SEQUENCE 419 AA; 46954 MW; ED30BDE6ACE03253 CRC64;

Query Match 52.5%; Score 32; DB 1; Length 419;
 Best Local Similarity 71.4%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KPOOFFG 9
 ||::|||
 Db 296 KPKRFFG 302

RESULT 62
 RHO_THEMA STANDARD; PRT; 427 AA.
 ID RHO_THEMA
 AC P38527;

DT 01-OCT-1994 (Rel. 30, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE TRANSCRIPTION TERMINATION FACTOR RHO.
 GN RHO OR TMI470.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogales; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE OF 16-427 FROM N.A.
 RX MEDLINE=94327472; PubMed=8051015;
 RA Opperman T., Richardson J.P.;
 RT "Phylogenetic analysis of sequences from diverse bacteria with
 homology to the Escherichia coli rho gene.";
 RL J. Bacteriol. 176:5033-5043(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109;
 RX MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
 Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 McDonald L., Utterback T.R., Malek J.A., Linher R.D., Garrett M.M.,
 Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 genome sequence of Thermotoga maritima.";
 RL Nature 399:323-329(1999).
 CC -1- FUNCTION: FACILITATES TRANSCRIPTION TERMINATION BY A MECHANISM
 THAT INVOLVES RHO BINDING TO THE NASCENT RNA, ACTIVATION OF RHO'S
 RNA-DEPENDENT ATPASE ACTIVITY, AND RELEASE OF THE MRNA FROM THE
 DNA TEMPLATE (BY SIMILARITY).
 CC -1- SUBUNIT: HOMOHXAMER (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
 CC -----
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 CC -----
 CC EMBL; L27279; AAA59210.1; -
 DR EMBL; AE001798; AAD36538.1; -
 DR HSP; P03002; I462.
 DR TIGR; TMI470; -
 DR InterPro; IPR003593; AAA.
 DR InterPro; IPR000194; ATPase_alpha_beta.
 DR InterPro; IPR002059; Cold_shock.
 DR Pfam; PF00006; ATP-synt_ab; 1.
 DR SMART; SM00382; AAA; 1.
 DR SMART; SM00357; CSP; 1.
 KW Transcription termination; Helicase; ATP-binding; RNA-binding;
 Complete proteome.
 FT DOMAIN 28 33 RNA-BINDING (RNP2) (BY SIMILARITY).
 FT DOMAIN 68 71 RNA-BINDING (RNP1) (BY SIMILARITY).
 FT NP_BIND 182 189 ATP (POTENTIAL).
 SQ SEQUENCE 427 AA; 48301 MW; 37748653910AFC95 CRC64;

Query Match 52.5%; Score 32; DB 1; Length 427;
 Best Local Similarity 71.4%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KPOOFFG 9
 ||::|||
 Db 300 KPKRFFG 306

RESULT 63
 MM12_MOUSE STANDARD; PRT; 462 AA.
 ID MM12_MOUSE

P34960;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MACROPHAGE METALLOELASTASE PRECURSOR (EC 3.4.24.65) (MME) (MATRIX)
DE METALLOPROTEINASE-12) (MMP-12).
GN MMP12 OR MMEL OR MME.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 99-125.
RC TISSUE=Macrophage;
RX MEDLINE=92165826; PubMed=1537850;
RA Shapiro S.D., Griffin G.L., Gilbert D.J., Jenkins N.A.,
RA Copeland N.G., Welgus H.G., Senior R.M., Ley T.J.;
RT "Molecular cloning, chromosomal localization, and bacterial
expression of a murine macrophage metalloelastase";
RL J. Biol. Chem. 267:4664-4671(1992).
CC -!- FUNCTION: MAY BE INVOLVED IN TISSUE INJURY AND REMODELING. HAS
CC SIGNIFICANT ELASTOLYTIC ACTIVITY
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF SOLUBLE AND INSOLUBLE ELASTIN.
CC SPECIFIC CLEAVAGES ARE ALSO PRODUCED AT 14-ALA-|-LEU-15 AND 16-
CC TYR-|-LEU-17 IN THE B CHAIN OF INSULIN.
CC -!- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
CC -!- SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A (ZINC
CC METALLOPROTEASE) ALSO KNOWN AS MATRIXIN SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M82831; AAA39526.1; -
CC PIR; A42401; A42401.
CC HSP; P03956; ICGL.
CC MEROPS; M10.009; -
CC MGD; MGI:97005; Mmp12.
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR001818; Matrixin.
CC InterPro; IPR000130; Zn_MTPeptase.
CC Pfam; PF00045; hemopexin; 4.
CC PRINTS; PR00138; Peptidase_M10; 1.
CC SMART; SM00120; HX; 4.
CC SMART; SM00235; ZnMC; 1.
CC PROSITE; PS00024; HEMOPEXIN; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC PROSITE; PS00546; CYSTEINE_SWITCH; 1.
CC Hydrolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
CC Extracellular matrix; Signal.
FT SIGNAL 1 17 PROBABLE.
FT PROPEP 18 98 ACTIVATION PEPTIDE.
FT CHAIN 99 462 MACROPHAGE METALLOELASTASE.
FT DOMAIN 272 462 HEMOPEXIN-LIKE.
FT SITE 85 85 CYSTEINE SWITCH (BY SIMILARITY).
FT METAL 211 211 BY SIMILARITY.
FT ACT_SITE 212 212 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 215 215 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 221 221 ZINC (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 310 310 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 275 462 BY SIMILARITY.
SQ SEQUENCE 462 AA; 53841 MW; BB625906F1DBDF CRC64;

Query Match

52.5%; Score 32; DB 1; Length 462;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QOFFGL 10
DB 61 QOFFGL 66
RESULT 64
MM12_RAT STANDARD; PRT; 465 AA.
ID MM12_RAT
AC Q63341;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MACROPHAGE METALLOELASTASE PRECURSOR (EC 3.4.24.65) (MME) (MATRIX)
GN MMP12 OR MMEL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Cossins J., Clements J., Catlin G.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY BE INVOLVED IN TISSUE INJURY AND REMODELING. HAS
CC SIGNIFICANT ELASTOLYTIC ACTIVITY (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF SOLUBLE AND INSOLUBLE ELASTIN.
CC SPECIFIC CLEAVAGES ARE ALSO PRODUCED AT 14-ALA-|-LEU-15 AND 16-
CC TYR-|-LEU-17 IN THE B CHAIN OF INSULIN.
CC -!- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A (ZINC
CC METALLOPROTEASE) ALSO KNOWN AS MATRIXIN SUBFAMILY.
CC
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CC
CC EMBL; X98517; CAA67142.1; -
CC HSP; P03956; ICGL.
CC MEROPS; M10.009; -
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR001818; Matrixin.
CC InterPro; IPR000130; Zn_MTPeptase.
CC Pfam; PF00045; hemopexin; 4.
CC PRINTS; PR00138; Peptidase_M10; 1.
CC SMART; SM00120; HX; 4.
CC SMART; SM00235; ZnMC; 1.
CC PROSITE; PS00024; HEMOPEXIN; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC PROSITE; PS00546; CYSTEINE_SWITCH; 1.
CC Hydrolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
CC Extracellular matrix; Signal.
FT SIGNAL 1 21 PROBABLE.
FT PROPEP 22 101 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 102 465 MACROPHAGE METALLOELASTASE.
FT DOMAIN 275 465 HEMOPEXIN-LIKE.
FT SITE 88 88 CYSTEINE SWITCH (BY SIMILARITY).
FT METAL 214 214 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 215 215 BY SIMILARITY.
FT METAL 218 218 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 224 224 ZINC (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 278 465 BY SIMILARITY.
SQ SEQUENCE 465 AA; 53738 MW; E779B6Q14EC6FF68 CRC64;


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Query Match      52.5%; Score 32; DB 1; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QOFFGL 10
DB 64 QOFFGL 69

RESULT 65
MM01_PIG STANDARD; PRT; 469 AA.
AC P21692;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERSTITIAL COLLAGENASE PRECURSOR (BC 3.4.24.7) (MATRIX
DE METALLOPROTEINASE-1) (MMP-1).
GN MMP1.
OS Sus. scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91333421; PubMed=1651440;
RA Richards C.D., Rafferty J.A., Reynolds J.J., Saklatvala J.;
RT "Porcine collagenase from synovial fibroblasts: cDNA sequence and
RT modulation of expression of RNA in vitro by various cytokines.";
RL Matrix 11:161-167(1991).
RN [2]
RP SEQUENCE OF 25-469 FROM N.A.
RC TISSUE=Synovial cell;
RA Clarke N.J., O'Hare M.C., Cawston T.E., Harper G.P.;
RT "Nucleotide sequence of a cDNA for porcine type I collagenase,
RT obtained by PCR.";
RL Nucleic Acids Res. 18:6703-6703(1990).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-469.
RA MEDLINE=96173003; PubMed=8590015;
RA Li J., Brick P., O'Hare M.C., Skarzynski T., Lloyd L.F., Curry V.A.,
RA Clark I.M., Bigg H.F., Hazleman B.L., Cawston T.E., Blow D.M.;
RT "Structure of full-length porcine synovial collagenase reveals a C-
RT terminal domain containing a calcium-linked, four-bladed
RT beta-propeller.";
RL Structure 3:541-549(1995).
RN [4]
RP SEQUENCE OF 100-104 AND 248-282, AND AUTOLYTIC CLEAVAGE SITE.
RX MEDLINE=95142615; PubMed=7840605;
RA Clark I.M., Mitchell R.E., Powell L.K., Bigg H.F., Cawston T.E.,
RA O'Hare M.C.;
RT "Recombinant porcine collagenase: purification and autolysis.";
RL Arch. Biochem. Biophys. 316:123-127(1995).
CC -!- FUNCTION: CLEAVES COLLAGENS OF TYPES I, II, AND III AT ONE SITE IN
CC THE HELICAL DOMAIN. ALSO CLEAVES COLLAGENS OF TYPES VII AND X.
CC -!- COPACITOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
CC -!- ENZYME REGULATION: CAN BE ACTIVATED WITHOUT REMOVAL OF THE
CC ACTIVATION PEPTIDE.
CC -!- PTM: UNDERGOES AUTOLYTIC CLEAVAGE TO PRODUCE A N-TERMINAL
CC FRAGMENT HAVING REDUCED COLLAGENOLYTIC ACTIVITY.
CC -!- SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A (ZINC
CC METALLOPROTEASE) ALSO KNOWN AS MATRIXIN SUBFAMILY.
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EMBL; X54724; CAA38526.1; -.
PIR; S15986; KCFOI.
PDB; IFBL; 29-JAN-96.
MEROPS; M10.001; -.
DR InterPro; IPR000585; Hemoexin.
DR InterPro; IPR001818; Matrixin.
DR InterPro; IPR000130; Zn_Mtpeptdse.
DR Pfam; PF00045; Hemoexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Hydrolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
KW Collagen degradation; Extracellular matrix; Autocatalytic cleavage;
KW Signal; 3D-structure.
FT SIGNAL 1 19 ACTIVATION PEPTIDE.
FT PROPEP 20 99 INTERSTITIAL COLLAGENASE.
FT CHAIN 100 469 18 KDA INTERSTITIAL COLLAGENASE (WEAK
FT CHAIN 100 258 COLLAGENASE ACTIVITY).
FT DOMAIN 275 469 HEMOPEXIN-LIKE.
FT SITE 92 92 CYSTEINE SWITCH (POTENTIAL).
FT SITE 258 259 CLEAVAGE (AUTOLYTIC).
FT METAL 218 218 ZINC (CATALYTIC).
FT ACT_SITE 219 219 ZINC (CATALYTIC).
FT METAL 222 222 ZINC (CATALYTIC).
FT METAL 228 228 ZINC (CATALYTIC).
FT DISULFD 278 466 PROBABLE.
FT CARBOHYD 120 120 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 469 AA; 53666 MW; 7952D7B2753F682 CRC64;

Query Match      52.5%; Score 32; DB 1; Length 469;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QOFFGL 10
DB 68 QOFFGL 73

RESULT 66
SYK_BACST STANDARD; PRT; 494 AA.
AC Q9RHV9;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE--TRNA LIGASE) (LYSRS).
GN LYS5.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCA 1503;
RX MEDLINE=20199468; PubMed=10737207;
RA Takita T., Shimizu N., Sukata T., Hashimoto S., Akita E., Yokota T.,
RA Esaki N., Soda K., Inouye K., Tomomura B.;
RT "Lysyl-tRNA synthetase of Bacillus stearothermophilus molecular
RT cloning and expression of the gene.";
RL Biosci. Biotechnol. Biochem. 64:432-437(2000).
CC -!- CATALYTIC ACTIVITY: ATP + L-LYSINE + TRNA(LYS) -> AMP +
CC PYROPHOSPHATE + L-LYSYL-TRNA(LYS).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
```

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EMBL: AB012100; BAA88691.1; -
InterPro: IPR002106; AA_trna_ligase_II.
InterPro: IPR002309; trna-synt_2.
InterPro: IPR002312; trna-synt_2.
InterPro: IPR002313; trna-synt_lys_2.
Pfam: PF00152; trna-synt_2; 1.
Pfam: PF01336; trna-anti_1.
PRINTS: PRO0982; TRNASYNTHLYS.
PROSITE: PS01042; TRNASYNTHASP.
PROSITE: PS00179; AA_TRNA_LIGASE_II.1; 1.
PROSITE: PS00339; AA_TRNA_LIGASE_II.2; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
SQ SEQUENCE 494 AA; 57405 MW; 109D1A4FDD7F714C CRC64;

Query Match 52.5%; Score 32; DB 1; Length 494;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKQQQFFGL 10
|||::||
Db 142 RPLPKRYHGL 151

RESULT 67
RHO_TREPA
ID RHO_TREPA STANDARD; PRT; 519 AA.
AC O83281;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TRANSCRIPTION TERMINATION FACTOR RHO.
GN RHO OR TP0254.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NICHOLS;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis spirochete.";
RL Science 281:375-388(1998).
CC -!- FUNCTION: FACILITATES TRANSCRIPTION TERMINATION BY A MECHANISM THAT INVOLVES RHO BINDING TO THE NASCENT RNA, ACTIVATION OF RHO'S RNA-DEPENDENT ATPASE ACTIVITY, AND RELEASE OF THE MRNA FROM THE DNA TEMPLATE (BY SIMILARITY).
CC -!- SUBUNIT: HOMOHETEROMER (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).

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EMBL: AE001207; AAC65243.1; -
TIGR: TP0254; -
InterPro: IPR003593; AAA.
InterPro: IPR000194; ATPase_alpha_beta.
InterPro: IPR002059; Cold_shock.
Pfam: PF00006; ATP-synt_ab; 1.
SMART: SM00382; AAA; 1.
SMART: SM00357; CSP; 1.
KW Transcription termination; Helicase; ATP-binding; RNA-binding;
KW Complete Proteome.
FT DOMAIN 118 125 RNA-BINDING (RNP2) (BY SIMILARITY).
FT DOMAIN 160 163 RNA-BINDING (RNP1) (BY SIMILARITY).
FT NP_BIND 274 281 ATP (POTENTIAL).
SQ SEQUENCE 519 AA; 58265 MW; 321A637776025A10 CRC64;

Query Match 52.5%; Score 32; DB 1; Length 519;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KPOQFFG 9
|||::|||
Db 392 KPKRFFG 398

RESULT 68
RAI2_MOUSE
ID RAI2_MOUSE STANDARD; PRT; 529 AA.
AC Q9QVY8;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE RETINOIC ACID-INDUCED PROTEIN 2 (3F8).
GN RAI2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94148137; PubMed=8314004;
RA Jonk L.J.C., de Jonge M.E., Vervaaert J.M., Wissink S., Kruijer W.;
RT "Isolation and developmental expression of retinoic-acid-induced genes.";
RT genes.";
RL Dev. Biol. 161:604-614(1994).
CC -!- INDUCTION: BY RETINOIC ACID.

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EMBL: X76652; -; NOT_ANNOTATED_CDS.
DR MGD; MGI:1344378; RAI2.
FT DOMAIN 200 253 PRO-RICH.
SQ SEQUENCE 529 AA; 57178 MW; 10AA48B170FCDBD0 CRC64;

Query Match 52.5%; Score 32; DB 1; Length 529;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQQFFGL 10
|||::|||
Db 265 PKPPSSFFGL 273

RESULT 69
RAI2_HUMAN

```

ID RA12_HUMAN STANDARD; PRT; 530 AA.
AC Q9Y5P3;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE RETINOIC ACID-INDUCED PROTEIN 2.
GN RA12.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99168896; PubMed=10049581;
RA Walpole S.M., Hiriyana K.T., Nicolau A., Bingham E.L., Durham J.,
RA Vaudin M., Ross M.T., Yates J.R., Sieving P.A., Trump D.;
RT "Identification and characterization of the human homologue (RA12) of
RT a mouse retinoic acid-induced gene in Xp22.2."
RL Genomics 55:275-283(1999).
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-----
DR EMBL; AF136587; AAD33688.1; -.
DR MIM; 300217; -.
DR DOMAIN 200 253 PRO-RICH.
FT SEQUENCE 530 AA; 57148 MW; 9879BE869DC6188F CRC64;
SQ
Query Match 52.5%; Score 32; DB 1; Length 530;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 2 PKPQOFFGL 10
|||
Db 265 PKPPSSFGL 273
-----
RESULT 70
ID C4C3_DROME STANDARD; PRT; 535 AA.
AC Q9VA27; Q24121;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CYTOCHROME P450 4C3 (EC 1.14.-.-) (CYP1VC3).
GN CYP4C3 OR CG1438.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazer E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Llang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
[2]
RP SEQUENCE OF 347-472 FROM N.A.
RX STRAIN=HAAG-79;
RX MEDLINE=96262181; PubMed=8676871;
RA Dunkov B.C., Rodriguez-Arnaiz R., Pittendrigh B.,
RA french-Constant R.H., Feyerisen R.;
RT "Cytochrome P450 gene clusters in Drosophila melanogaster.";
RL Mol. Gen. Genet. 251:290-297(1996).
CC -!- FUNCTION: MAY BE INVOLVED IN THE METABOLISM OF INSECT HORMONES AND
CC IN THE BREAKDOWN OF SYNTHETIC INSECTICIDES (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) -> ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM
CC (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
-----
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-----
DR EMBL; AE003775; AAP57098.1; -.
DR EMBL; U34323; AAA80657.1; -.
DR FlyBase; FBgn0015032; Cyp4c3.
DR InterPro; IPR001128; Cyt_P450.
DR Pfam; PF00067; p450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
KW Endoplasmic reticulum.
FT BINDING 481 481 HEME (BY SIMILARITY).
SQ SEQUENCE 535 AA; 60757 MW; 0C78200AC2D35979 CRC64;
Query Match 52.5%; Score 32; DB 1; Length 535;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 2 PKPQOF 7
|||
Db 448 PKPEQF 453
-----
RESULT 71
```


SQ SEQUENCE 766 AA; 82363 MW; 1F3E9FD6DC84B100 CRC64;

Query Match 52.5%; Score 32; DB 1; Length 766;

Best Local Similarity 75.0%; Pred. No. 2.3e+02; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPQQFF 8

|||||

Db 267 RPKPQASF 274

RESULT 73

DSC3_BOVIN

ID DSC3_BOVIN STANDARD; PRT; 896 AA.

AC Q28060; Q28176;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE DESMOCOLLIN 3A/3B PRECURSOR.

GN DSC3.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=95403557; PubMed=7673337;

RA Yue K.K.M., Holton J.L., Clarke J.P., Hyam J.L.M., Hashimoto T.,

RA Chidgey M.A.J., Garrod D.R.;

RT "Characterisation of a desmocollin isoform (bovine DSC3) exclusively

RT expressed in lower layers of stratified epithelia.";

RL J. Cell Sci. 108:2163-2173(1995).

RN [2]

RN SEQUENCE OF 686-814 FROM N.A.

RP TISSUE=Epidermis;

RX MEDLINE=94308280; PubMed=8034749;

RA Legan P.K., Yue K.K.M., Chidgey M.A.J., Holton J.L., Wilkinson R.W.,

RA Garrod D.R.;

RT "The bovine desmocollin family: a new gene and expression patterns

RT reflecting epithelial cell proliferation and differentiation.";

RL J. Cell Biol. 126:507-518(1994).

CC -!- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED

CC IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS

CC MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERMAL CELL

CC POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL

CC ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 3A (SHOWN HERE) AND 3B; ARE

CC PRODUCED BY ALTERNATIVE SPLICING.

CC -!- TISSUE SPECIFICITY: STRATIFIED EPITHELIA ONLY (EPIDERMIS, TONGUE,

CC ESOPHAGUS AND RUMEN).

CC -!- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS

CC (POTENTIAL).

CC -!- SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.

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CC -----

CC EMBL; L33774; AAC41625.1; -

CC EMBL; L33774; AAC41626.1; -

CC EMBL; X75783; CAA53427.1; -

CC HSSP; P09803; 1SUH.

CC InterPro; IPR002126; Cadherin.

CC Pfam; PF00028; cadherin; 5.

CC PRINTS; PR00205; CADHERIN.

CC SMART; SM00112; CA; 5.

DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS0268; CADHERIN_2; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal;
KW Alternative splicing; Cytoskeleton; Calcium-binding.
FT SIGNAL 1 26 POTENTIAL.
FT PROPEP 27 134 POTENTIAL.
FT CHAIN 135 896 DESMOCOLLIN 3A/3B.
FT DOMAIN 135 690 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 691 711 POTENTIAL.
FT DOMAIN 712 896 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 135 242 CADHERIN 1.
FT DOMAIN 243 354 CADHERIN 2.
FT DOMAIN 355 471 CADHERIN 3.
FT DOMAIN 472 579 CADHERIN 4.
FT DOMAIN 580 690 CADHERIN 5.
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 546 546 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 832 839 KLHCNQD -> ESIRHTG (IN ISOFORM 3B).
FT VARSPLIC 840 896 MISSING (IN ISOFORM 3B).
FT CONFLICT 686 687 VI -> EF (IN REF. 2).
SQ SEQUENCE 896 AA; 99687 MW; 8CC0C30A63FB0BD4 CRC64;

Query Match 52.5%; Score 32; DB 1; Length 896;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QFFGLM 11

|||||

Db 330 QFFGLM 335

RESULT 74

STA2_MOUSE

ID STA2_MOUSE STANDARD; PRT; 923 AA.

AC Q9WVL2; Q64189; Q64250; Q64188;

DT 20-AUG-2001 (Rel. 40, Created)

DT 20-AUG-2001 (Rel. 40, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 2.

GN STAT2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RN SEQUENCE FROM N.A.

RP STRAIN=CD-1;

RA Paulson M.S., Mui A., Levy D.E.;

RT "Molecular cloning and characterization of murine Stat2.";

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RN SEQUENCE OF 595-658 FROM N.A. (ISOFORMS A AND B/C).

RX MEDLINE=96176320; PubMed=8601453;

RA Sugiyama T., Nishio Y., Kishimoto T., Akira S.;

RT "Identification of alternative splicing form of Stat2.";

RL FEBS Lett. 381:191-194(1996).

CC -!- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE IFN-STIMULATED

CC RESPONSE ELEMENT (ISRE) AND TO THE GAS ELEMENT. THIS MULTIPROTEIN

CC TRANSCRIPTION FACTOR IS TERMED ISGF3.

CC -!- SUBUNIT: IN RESPONSE TO IFN ALPHA/BETA, THREE SUBUNITS (STAT1-

CC ALPHA, STAT1-BETA, STAT2) OF ISGF3, BECOME PHOSPHORYLATED ON

CC TYROSINE, MIGRATE INTO THE NUCLEUS, AND ASSEMBLE INTO A COMPLEX

CC TOGETHER WITH ISGF3 GAMMA (P48), A DNA-BINDING PROTEIN THAT

CC SPECIFICALLY BINDS TO THE IFN-STIMULATED RESPONSE ELEMENT (BY

CC SIMILARITY).

CC -!- SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUCLEUS IN

CC RESPONSE TO PHOSPHORYLATION (BY SIMILARITY).

CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B/C; ARE

CC PRODUCED BY ALTERNATIVE SPLICING.

CC -!- TISSUE SPECIFICITY: FOUND IN THE BRAIN, LUNG, HEART, SPLEEN,

CC LIVER, KIDNEY, MUSCLE, AND THE TESTIS.
CC -!- PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IFN-ALPHA (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS.
CC -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -----
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CC -----
DR EMBL; AF088862; AAD38329.1; -;
DR EMBL; S81342; AAB36228.2; -;
DR EMBL; S81342; AAB36231.1; -;
DR EMBL; S81342; AAB36230.1; ALT_SEQ.
DR HSP; P42224; IBF5.
DR MGD; MGI:103039; Stat2.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS00001; SH2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein;
KW Phosphorylation; SH2 domain; Alternative splicing.
FT DOMAIN 571 666
FT MOD_RES 689 689
FT VARSPLIC 620 643
FT HKVEIYSQPTTKVQLSPLTEI -> GQHPVPVHSCSL
FT SARHPDRLTP (IN SHORT ISOFORM).
FT VARSPLIC 644 923
FT CONFLICT 596 596
FT CONFLICT 620 620
FT CONFLICT 620 620
SQ SEQUENCE 923 AA; 105416 MW; D50BB54C535B0774 CRC64;

Query Match 52.5%; Score 32; DB 1; Length 923;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRKPOQFF 8
DB 478 PRKPOQFF 484

RESULT 75
Y124.METJA
ID Y124.METJA STANDARD; PRT; 1075 AA.
AC Q57588;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN MJ0124.
GN MJ0124
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8680897;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrman J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii";
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: TO M.JANNASCHII MJ1214.
CC -!- SIMILARITY: SOME, TO TYPE I RESTRICTION ENZYMES.
CC -----
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CC -----
DR EMBL; U67469; AAB98104.1; -;
DR TIGR; MJ0124; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 1075 AA; 127796 MW; 4F765E19E0B52889 CRC64;

Query Match 52.5%; Score 32; DB 1; Length 1075;
Best Local Similarity 54.5%; Pred. No. 3.3e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
DB 690 RPKPOQFFGLI 700

RESULT 76
RPOB.HETCA
ID RPOB.HETCA STANDARD; PRT; 1116 AA.
AC P36440;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6).
GN RPOB.
OS Heterosigma carterae.
OG Chloroplast.
OC Eukaryota; Stramenopiles; Raphidophyceae; Heterosigma.
OX NCBI_TaxID=28465;
RN [1]
RP SEQUENCE FROM N.A.
RA Mangahas J.L., Cattolico R.A., Reynolds A.E.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
CC RNA(N).
CC -!- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".
CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
CC -----
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CC -----
DR EMBL; X75815; CAAS3450.1; -;
DR Mendel; 4095; HETCA; rpoB;1.
DR InterPro; IPR001572; RNA_pol_B.
DR Pfam; PF00562; RNA_pol_B; 1.
DR PROSITE; PS01166; RNA_POL_BETA; 1.
KW Transferase; DNA-directed RNA polymerase; Transcription; Chloroplast.
SQ SEQUENCE 1116 AA; 125818 MW; EC6C83C81234435B CRC64;

Query Match 52.5%; Score 32; DB 1; Length 1116;

```
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKQOFFGL 10
DB 775 RPKPGKVFVG 784

Query Match 52.5%; Score 32; DB 1; Length 1206;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

SQ SEQUENCE 1206 AA; 133464 MW; 4DFB38CB52BD8EE7 CRC64;

OY 2 PKPQOFF 8
DB 1037 PEQDFF 1043

RESULT 77
FM14_MOUSE STANDARD; PRT; 1206 AA.
AC Q05859;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE FORMIN 1 ISOFORM IV (LIMB DEFORMITY PROTEIN).
GN FMN OR LD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=92112033; PubMed=1339380;
RA Grusby-Jackson L., Kuo A., Leder P.;
RT "A variant limb deformity transcript expressed in the embryonic mouse
limb defines a novel formin";
RL Genes Dev. 6:29-37(1992).
CC -!- FUNCTION: IS IMPORTANT IN THE MORPHOGENESIS OF LIMB AND MAY HAVE A
CC FUNCTION IN DIFFERENTIATED CELLS OR BE INVOLVED IN MAINTAINING
CC SPECIFIC DIFFERENTIATED STATES.
CC -!- ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS: IA (AC Q05860), IB (AC
CC Q05860), II (AC Q05860), III (AC Q05860) AND IV (SHOWN HERE); ARE
CC PRODUCED BY ALTERNATIVE SPLICING. A VARIATION IN SPLICING IS SEEN
CC AMONG DIFFERENT TISSUES AND DIFFERENT SIZE TRANSCRIPTS EXIST
CC WITHIN ANY ONE TISSUE.
CC -!- TISSUE SPECIFICITY: IT IS FOUND THROUGHOUT THE EMBRYO BUT
CC HAS A FUNCTIONAL ROLE ONLY IN THE KIDNEY AND LIMB.
CC -!- DEVELOPMENTAL STAGE: THIS IS THE ISOFORM FOUND IN THE APICAL
CC ECTODERMAL RIDGE AND THE MESENCHYMAL COMPARTMENT OF THE DEVELOPING
CC LIMB BUD.
CC -!- PTM: PHOSPHORYLATED ON SERINE AND POSSIBLY THREONINE RESIDUES.
CC -!- SIMILARITY: CONTAINS 1 FORMIN HOMOMOLOGY 1 (FH1) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 FORMIN HOMOMOLOGY 2 (FH2) DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE FORMIN HOMOMOLOGY FAMILY. CAPPUCCINO
CC SUBFAMILY.
CC -----
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CC -----
CC EMBL; X62379; CAA44244.1; -.
CC PIR; S24407; S24407.
CC MGD; MGI:101815; Fmn.
CC InterPro; IPR003104; FH2.
CC Pfam; PF02181; FH2; 1.
CC PRINTS; PR00828; FORMIN.
CC SMART; SM00498; FH2; 1.
CC Nucleic protein; Developmental protein; Alternative splicing;
CC Phosphorylation; Coiled coil.
CC DOMAIN 418 443 COILED COIL (POTENTIAL).
CC DOMAIN 497 566 COILED COIL (POTENTIAL).
CC DOMAIN 644 744 FH1 (PRO-RICH).
CC DOMAIN 759 1164 FH2.
CC DOMAIN 1043 1116 COILED COIL (POTENTIAL).
CC DOMAIN 635 638 POLY-SER.
CC DOMAIN 751 755 POLY-SER.
CC -----
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CC -----
CC EMBL; X62379; CAA44244.1; -.
CC PIR; S24407; S24407.
CC MGD; MGI:101815; Fmn.
CC InterPro; IPR003104; FH2.
CC Pfam; PF02181; FH2; 1.
CC PRINTS; PR00828; FORMIN.
CC SMART; SM00498; FH2; 1.
CC Nucleic protein; Developmental protein; Alternative splicing;
CC Phosphorylation; Coiled coil.
CC DOMAIN 418 443 COILED COIL (POTENTIAL).
CC DOMAIN 497 566 COILED COIL (POTENTIAL).
CC DOMAIN 644 744 FH1 (PRO-RICH).
CC DOMAIN 759 1164 FH2.
CC DOMAIN 1043 1116 COILED COIL (POTENTIAL).
CC DOMAIN 635 638 POLY-SER.
CC DOMAIN 751 755 POLY-SER.
CC -----
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CC -----
CC EMBL; X62681; CAA44555.1; -.
CC InterPro; IPR003104; FH2.
CC InterPro; IPR001265; Formin.
CC Pfam; PF02181; FH2; 1.
CC PRINTS; PR00828; FORMIN.
CC SMART; SM00498; FH2; 1.
CC Nucleic protein; Developmental protein; Coiled coil;
CC Alternative splicing.
CC DOMAIN 428 450 COILED COIL (POTENTIAL).
```

FT DOMAIN 503 572 COILED COIL (POTENTIAL).
FT DOMAIN 652 751 FH1 (PRO-RICH).
FT DOMAIN 766 1171 FH2.
FT DOMAIN 1050 1125 COILED COIL (POTENTIAL).
SQ SEQUENCE 1213 AA; 135240 MW; ADE3EF0B3FB9D862 CRC64;

Query Match 52.5%; Score 32; DB 1; Length 1213;
Best Local Similarity 71.4%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPQOFF 8
Db 1044 PEQDFF 1050
I:|I|I|

RESULT 79
FMN1_MOUSE STANDARD; PRT; 1468 AA.
AC Q05860;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE FORMIN 1 ISOFORMS I/II/III (LIMB DEFORMITY PROTEIN).
GN FMN OR LD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Testis;
RX MEDLINE=90363291; PubMed=2392150;
RA Woychik R.P., Maas R.L., Zeller R., Vogt T.F., Leder P.;
RT "Formins": proteins deduced from the alternative transcripts of the
RT limb deformity gene.";
RL Nature 346:850-853(1990).
RN [2]
RP ALTERNATIVE SPLICING.
RX MEDLINE=97224459; PubMed=9119367;
RA Wang C.C., Chan D.C., Leder P.;
RT "The mouse formin (Fmn) gene: genomic structure, novel exons, and
RT genetic mapping.";
RL Genomics 39:303-311(1997).
RN [3]
RP PHOSPHORYLATION.
RX MEDLINE=93296176; PubMed=8516300;
RA Vogt T.F., Jackson-Grusby L., Rush J., Leder P.;
RT "Formins: phosphoprotein isoforms encoded by the mouse limb deformity
RT locus.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5554-5558(1993).
CC -!- FUNCTION: IS IMPORTANT FOR THE MORPHOGENESIS OF LIMB AND KIDNEY
CC AND MAY HAVE A FUNCTION IN DIFFERENTIATED CELLS OR MAY BE
CC INVOLVED IN MAINTAINING SPECIFIC DIFFERENTIATED STATES.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS: IA (SHOWN HERE), IB,
CC II, III AND IV (AC Q05860). ARE PRODUCED BY ALTERNATIVE SPLICING.
CC A VARIATION IN SPLICING IS SEEN AMONG DIFFERENT TISSUES AND
CC DIFFERENT SIZE TRANSCRIPTS EXIST WITHIN ANY ONE TISSUE.
CC -!- TISSUE SPECIFICITY: IT IS PRESENT IN THE ADULT KIDNEY, TESTIS,
CC LIMB, OVARY, BRAIN, SMALL INTESTINE, SALIVARY GLAND AND HARDERIAN
CC GLAND. IT IS PRESENT THROUGHOUT THE EMBRYO.
CC -!- DEVELOPMENTAL STAGE: IN THE DEVELOPING LIMB BUD, THE PROTEIN
CC IS EXPRESSED IN THE APICAL ECTODERMAL RIDGE AND THE MESENCHYMAL
CC COMPARTMENT, PREDOMINANTLY IN THE POSTERIOR REGION. DURING
CC KIDNEY MORPHOGENESIS, EXPRESSION IS INITIALLY RESTRICTED TO
CC THE EPITHELIAL COMPARTMENT OF THE PRONEPHROS AND MESONEPHROS.
CC -!- PTM: PHOSPHORYLATED ON SERINE AND POSSIBLY THREONINE RESIDUES.
CC -!- SIMILARITY: CONTAINS 1 FORMIN HOMOLGY 1 (FH1) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 FORMIN HOMOLGY 2 (FH2) DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE FORMIN HOMOLGY FAMILY. CAPPUPCINO
CC SUBFAMILY.

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DR EMBL; X53599; CAA37668.1; -
DR PIR; S11515; S11515.
DR MGD; MGI:101815; Fmn.
DR InterPro; IPR003104; FH2.
DR InterPro; IPR001265; Formin.
DR Pfam; PF02181; FH2; 1.
DR PRINTS; PR00828; FORMIN.
DR SMART; SM00498; FH2; 1.
KW Nuclear protein; Developmental protein; Alternative splicing;
KW Phosphorylation; Coiled coil.
FT DOMAIN 723 792 COILED COIL (POTENTIAL).
FT DOMAIN 870 970 FH1 (PRO-RICH).
FT DOMAIN 985 1426 FH2.
FT DOMAIN 1305 1378 COILED COIL (POTENTIAL).
FT DOMAIN 198 203 POLY-SER.
FT DOMAIN 861 864 POLY-SER.
FT DOMAIN 885 892 POLY-PRO.
FT DOMAIN 911 925 POLY-PRO.
FT DOMAIN 929 940 POLY-PRO.
FT DOMAIN 951 962 POLY-PRO.
FT DOMAIN 966 970 POLY-PRO.
FT DOMAIN 977 981 POLY-SER.
FT VARSPLIC 1252 1287 MISSING (IN ISOFORM IB).
FT VARSPLIC 625 722 MISSING (IN ISOFORM II).
FT VARSPLIC 626 627 IA -> SV (IN ISOFORM III).
FT VARSPLIC 628 1468 MISSING (IN ISOFORM III).
SQ SEQUENCE 1468 AA; 163809 MW; EF2FB1E9CA9DAF43 CRC64;

Query Match 52.5%; Score 32; DB 1; Length 1468;
Best Local Similarity 71.4%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 PKPQOFF 8
Db 1299 PEQDFF 1305
I:|I|I|

RESULT 80
VIT6_CAEEL STANDARD; PRT; 1651 AA.
AC P18948;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VITELLOGENIN 6 PRECURSOR.
GN VIT-6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=91251142; PubMed=1904098;
RA Spieth J., Nettleton M., Zucker-Aprison E., Lea K., Blumenthal T.;
RT "Vitellin motifs conserved in nematodes and vertebrates.";
RL J. Mol. Evol. 32:429-438(1991).
RN [2]
RP SEQUENCE OF 1-110 FROM N.A.
RX MEDLINE=86284606; PubMed=3841791;
RA Spieth J., Blumenthal T.;
RT "The Caenorhabditis elegans vitellogenin gene family includes a gene
RT encoding a distantly related protein.";
RL Mol. Cell. Biol. 5:2495-2501(1985).


```
Db 4 PRFTYGLM 11
|: |::|
|: |::|

RESULT 83
MOT2_MERUN
ID MOT2_MERUN STANDARD; PRT; 71 AA.
AC O35440;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MONOCARBOXYLATE TRANSPORTER 2 (MCT 2) (FRAGMENT).
GN SLC16A7 OR MCT2.
OS Meriones unguiculatus (Mongolian jird).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stria vascularis;
RX MEDLINE=98107623; PubMed=9447934;
RA Shinozono M., Scofield M.A., Wangemann P.;
RT "Functional evidence for a monocarboxylate transporter (MCT) in stria
RT marginal cells and molecular evidence for MCT1 and MCT2 in stria
RT vascularis."
RL Hear. Res. 114:213-222(1997).
CC -!- FUNCTION: PROTON-LINKED MONOCARBOXYLATE TRANSPORTER. CATALYZES THE
CC RAPID TRANSPORT ACROSS THE PLASMA MEMBRANE OF MANY
CC MONOCARBOXYLATES SUCH AS LACTATE, PYRUVATE, BRANCHED-CHAIN OXO
CC ACIDS DERIVED FROM LEUCINE, VALINE AND ISOLEUCINE, AND THE KETONE
CC BODIES ACETOACETATE, BETA-HYDROXYBUTYRATE AND ACETATE (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PLASMA MEMBRANE
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SLC16 FAMILY OF TRANSPORTERS.
CC
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CC
DR EMBL; AF029767; AAB84219.1;
FT TRANSPORT; Symptom; Transmembrane; Multigene family.
FT NON_TER 1
FT TRANSMEM <1 14 POTENTIAL.
FT TRANSMEM 24 44 POTENTIAL.
FT TRANSMEM 50 70 POTENTIAL.
FT NON_TER 71 71
SQ SEQUENCE 71 AA; 7864 MW; 25C82B27F22B61B1 CRC64;

Query Match 50.8%; Score 31; DB 1; Length 71;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
|: |::|
|: |::|
Db 21 RPRIQYFFSL 30

RESULT 84
FTRV_MAIZE
ID FTRV_MAIZE STANDARD; PRT; 97 AA.
AC P80680;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FERREDOXIN-THIOREDOXIN REDUCTASE, VARIABLE CHAIN (FTR-V) (FERREDOXIN-
DE THIOREDOXIN REDUCTASE SUBUNIT A) (FTR-A).

Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Leaf;
RX MEDLINE=97054599; PubMed=8898896;
RA Iwadata H., Tsugita A., Chow L.-P., Kizuki K., Stritt-Etter A.-L.,
RA Li J., Schuermann P.;
RT "Amino acid sequence of the maize ferredoxin:thioredoxin reductase
RT variable subunit."
RL Eur. J. Biochem. 241:121-125(1996).
CC -!- FUNCTION: FTR IS A [4FE-4S] PROTEIN PLAYING A CENTRAL ROLE IN THE
CC FERREDOXIN/THIOREDOXIN REGULATORY CHAIN. IT CONVERTS AN ELECTRON
CC SIGNAL (PHOTOREDOXED FERREDOXIN) TO A THIOL SIGNAL (REDUCED
CC THIOREDOXIN) IN THE REGULATION OF ENZYMES BY REDUCTION OF SPECIFIC
CC DISULFIDE GROUPS. CATALYZES THE LIGHT-DEPENDENT ACTIVATION OF
CC SEVERAL PHOTOSYNTHETIC ENZYMES.
CC -!- SUBUNIT: HETERODIMER OF SUBUNIT A (VARIABLE SUBUNIT) AND SUBUNIT
CC B (CATALYTIC SUBUNIT).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- SIMILARITY: TO SPINACH AND SYNECHOCOCCUS SP. FTR-V.
DR MaizedB; 134030;
KW Oxidoreductase; Chloroplast.
SQ SEQUENCE 97 AA; 10886 MW; DE1ED2AEE76B0FF5 CRC64;

Query Match 50.8%; Score 31; DB 1; Length 97;
Best Local Similarity 62.5%; Pred. No. 45;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQFF 8
|: |::|
|: |::|
Db 77 QPKPVRFF 84

RESULT 85
YD43_MYCLE
ID YD43_MYCLE STANDARD; PRT; 126 AA.
AC P54134;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 14.5 KDA PROTEIN ML1177.
GN ML1177 OR MLCB1701.03C OR B1549_F3_106.
OS Mycobacterium leprae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R., Robison K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eiglmeyer K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagers K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.-A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus."
RL Nature 409:1007-1011(2001).
CC -!- SIMILARITY: STRONG, TO M.TUBERCULOSIS RV1343C.
CC
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CC EMBL; U00014; AAA50903.1; -;
DR EMBL; AL049191; CAB39143.1; -;
DR EMBL; AL583921; CAC31558.1; -;
DR Leproma; MLI177; -;
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; UNKNOWN_1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 44 64 POTENTIAL.
SQ SEQUENCE 126 AA; 14479 MW; 6B7096956561908D CRC64;

Query Match 50.8%; Score 31; DB 1; Length 126;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQ 6
||||:|
Db 90 RPKPEQ 95

RESULT 86
RS16_YEAST
ID RS16_YEAST STANDARD; PRT; 142 AA.
AC P40213; P26787;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 40S RIBOSOMAL PROTEIN S16 (RP61R).
GN (RPS16A OR RP61R OR YMR143W OR YMR375.12) AND (RPS16B OR YDL083C).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A. (RPS16A).
RC STRAIN=S288C / AB972;
RA Badcock K., Churcher C., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RT [2]
RP SEQUENCE FROM N.A. (RPS16B).
RA Wambutt R., Wedler H., Wedler E., Scharfe M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RT [3]
RP PRELIMINARY PARTIAL SEQUENCE OF 1-25.
RX MEDLINE=92184799; PubMed=1544921;
RA Takakura H., Tsunasawa S., Miyagi M., Warner J.R.;
RT "NH2-terminal acetylation of ribosomal proteins of Saccharomyces
RT cerevisiae";
RL J. Biol. Chem. 267:5442-5445(1992).
CC -!- MISCELLANEOUS: THERE ARE TWO GENES FOR S16 IN YEAST.
CC -!- SIMILARITY: BELONGS TO THE SGP FAMILY OF RIBOSOMAL PROTEINS.

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CC EMBL; 247071; CAA87357.1; -;
DR EMBL; 274131; CAA98649.1; -;
DR SGD; S0004751; RPS16A.
DR SGD; S0002241; RPS16B.
DR InterPro; IPR000754; Ribosomal_S9.
DR Pfam; PF00380; Ribosomal_S9; 1.

DR ProDom; PD001627; Ribosomal_S9; 1.
DR PROSITE; PS00360; RIBOSOMAL_S9; 1.
KW Ribosomal protein; Acetylation; Multigene family.
FT INIT_MET 0
FT MOD_RES 1 1 ACETYLATION.
SQ SEQUENCE 142 AA; 15716 MW; 15873374B3262144 CRC64;

Query Match 50.8%; Score 31; DB 1; Length 142;
Best Local Similarity 55.6%; Pred. No. 66;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQFFG 9
||||:|
Db 122 RPEPKKEGG 130

RESULT 87
PR39_PIG
ID PR39_PIG STANDARD; PRT; 172 AA.
AC P80054; Q9TR84;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ANTIBACTERIAL PROTEIN PR-39 PRECURSOR.
GN PR39.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95350216; PubMed=7624374;
RA Gudmundsson G.H., Magnusson K.P., Chowdhary B.P., Johansson M.,
RA Andersson L., Boman H.G.;
RT "Structure of the gene for porcine peptide antibiotic PR-39, a
RT cathelin gene family member: comparative mapping of the locus for the
RT human peptide antibiotic FALL-39";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=94071853; PubMed=8250863;
RA Storici P., Zanetti M.;
RT "A cDNA derived from pig bone marrow cells predicts a sequence
RT identical to the intestinal antibacterial peptide PR-39";
RL Biochem. Biophys. Res. Commun. 196:1058-1065(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96105365; PubMed=7498526;
RA Zhao C., Ganz T., Lehrer R.I.;
RT "Structures of genes for two cathelin-associated antimicrobial
RT peptides: prophenin-2 and PR-39";
RL FEBS Lett. 376:130-134(1995).
RN [4]
RP SEQUENCE OF 131-169.
RC TISSUE=Intestine;
RX MEDLINE=92111534; PubMed=1765098;
RA Agerberth B., Lee J.-Y., Bergman T., Carlquist M., Boman H.G.,
RA Mutt V., Joernvall H.;
RT "Amino acid sequence of PR-39. Isolation from pig intestine of a new
RT member of the family of proline-arginine-rich antibacterial
RT peptides";
RL Eur. J. Biochem. 202:849-854(1991).
RN [5]
RP SEQUENCE OF 131-164, AND FUNCTION.
RC TISSUE=Neutrophils;
RX MEDLINE=95088504; PubMed=7996056;
RA Shi J., Ross C.R., Chengappa M.M., Blecha P.;
RT "Identification of a proline-arginine-rich antibacterial peptide from
RT neutrophils that is analogous to PR-39, an antibacterial peptide from
RT the small intestine";

RL J. Leukoc. Biol. 56:807-811(1994).
CC -1- FUNCTION: EXERTS A POTENT ANTIMICROBIAL ACTIVITY AGAINST BOTH
CC E. COLI AND B. MEGATERIUM.
CC -1- TISSUE SPECIFICITY: SMALL INTESTINE AND BONE MARROW.
CC -1- SIMILARITY: BELONGS TO THE CATHHELICIDIN FAMILY.
CC -----
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CC -----
CC EMBL; X87236; CAA60682.1; -;
CC EMBL; L23825; AAA31109.1; -;
CC EMBL; X89201; CAA61487.1; -;
CC PIR; S19563; S19563.
CC InterPro; IPR001894; Cathelicidin.
CC Pfam; PF00666; Cathelicidins; 1.
CC ProDom; PD001838; Cathelicidin; 1.
CC PROSITE; PS00946; CATHHELICIDINS_1; 1.
CC PROSITE; PS00947; CATHHELICIDINS_2; 1.
KW Antibiotic; Amidation; Signal.
FT SIGNAL 1 29
FT PROPEP 30 130
FT CHAIN 131 169
FT MOD_RES 30 30
FT -----
FT DISULFID 85 96
FT DISULFID 107 124
FT MOD_RES 169 169
FT CONFLICT 21 21
FT CONFLICT 29 29
FT CONFLICT 90 91
FT CONFLICT 117 119
FT CONFLICT 157 157
SQ SEQUENCE 172 AA; 994B792798C0E133 CRC64;

Query Match 50.8%; Score 31; DB 1; Length 172;
Best Local Similarity 62.5%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQFF 8
Db 141 RRPDPFF 148
||:|||||

RESULT 88
TBP_ARCFU
ID TBP_ARCFU STANDARD; PRT; 183 AA.
AC O29874;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TATA-BOX BINDING PROTEIN (TATA-BOX FACTOR) (TATA SEQUENCE-BINDING
DE PROTEIN) (TBP) (BOX A BINDING PROTEIN) (BAP).
GN TBP OR AF0373.

OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kierlavage A.R., Graham D.E., Kyripides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeill L.K., Badger J.H., Glodek A., Zhou L.,

RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -1- FUNCTION: GENERAL FACTOR THAT PLAYS A ROLE IN THE ACTIVATION OF
CC ARCHAEL GENES TRANSCRIBED BY RNA POLYMERASE. BINDS SPECIFICALLY
CC TO THE TATA BOX PROMOTER ELEMENT WHICH LIES CLOSE TO THE POSITION
CC OF TRANSCRIPTION INITIATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TBP FAMILY.
CC -----

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CC -----

CC EMBL; AE001078; AAB90862.1; -;
CC TIGR; AF0373; -;
CC InterPro; IPR000814; TFIID.
CC Pfam; PF00352; TBP; 2.
CC PRINTS; PR00686; TIFACTORIID.
CC PROSITE; PS00351; TFIID; 1.
KW Transcription regulation; DNA-binding; Repeat; Complete proteome.
FT REPEAT 8 84
FT REPEAT 99 177
SQ SEQUENCE 183 AA; 20135 MW; 255C5C05BBE3D8A3 CRC64;

Query Match 50.8%; Score 31; DB 1; Length 183;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQFFGLM 11
Db 36 RPKQFPGLV 44
||:|||||

RESULT 89
MOV_P_TOML
ID MOV_P_TOML STANDARD; PRT; 264 AA.
AC P03584;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MOVEMENT PROTEIN (CELL-TO-CELL TRANSPORT PROTEIN) (30 KDA PROTEIN).
GN MP.

OS Tomato mosaic virus (strain L) (TOMV) (TMV strain tomato),
OS Tomato mosaic virus (strain Kazakh K1) (TOMV) (TMV strain K1), and
OS Tomato mosaic virus (strain Kazakh K2) (TOMV) (TMV strain K2).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=12252, 138311, 138312;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L;
RX MEDLINE=83220776; PubMed=6304642;
RA Takamatsu N., Ohno T., Meshi T., Okada Y.;
RT "Molecular cloning and nucleotide sequence of the 30K and the coat
RT protein cistron of TMV (tomato strain) genome.";
RL Nucleic Acids Res. 11:3767-3778(1983).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=L;
RX MEDLINE=85157522; PubMed=6549393;
RA Ohno T., Aoyagi M., Yamanashi Y., Saito H., Ikawa S., Meshi T.,
RA Okada Y.;
RT "Nucleotide sequence of the tobacco mosaic virus (tomato strain)
RT genome and comparison with the common strain genome.";

```
RL J. Biochem. 96:1915-1923(1984).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-KAZAKH K1;
RA MEDLINE=20196905; PubMed=10732356;
RX Belenovich E.V., Novikov V.K., Zavriv S.K.;
RT "Biological properties and genome structure of the Kazakh isolate K1
of Tobacco mosaic virus.";
RL Mol. Biol. (Mosk) 34:172-176(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-KAZAKH K1;
RA Belenovich E.V., Novikov V.K., Zavriv S.K.;
RT "Kazakh isolates of tomato mosaic virus: possible connections of point
mutations in the coat protein gene with symptom formation.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-KAZAKH K2;
RX MEDLINE=98012318; PubMed=9454068;
RA Belenovich E.V., Genetozov E.V., Novikov V.K., Zavriv S.K.;
RT "Properties and structure of the tobacco mosaic virus strain K2
genome.";
RL Mol. Biol. (Mosk) 31:826-830(1997).
CC -|- FUNCTION: INVOLVED IN TRANSPORT OF THE VIRUS FROM THE INITIALLY
INFECTED CELLS TO ADJACENT CELLS, POSSIBLY BY MODIFYING THE
FUNCTION OF THE PLASMODESMATA. ALSO INFLUENCES LOCAL LESION
DEVELOPMENT. BINDS TO SINGLE-STRANDED NUCLEIC ACID.
CC -|- SIMILARITY: BELONGS TO THE TOBAMOVIRUSES MOVEMENT PROTEIN FAMILY.
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-----
DR EMBL; X02144; CAA36083.1; -
DR EMBL; AJ243571; CAB62913.1; -
DR EMBL; AF062519; AAD19281.1; -
DR EMBL; Z92909; CAB07440.1; -
DR PIR; A04182; WMBVT3.
DR InterPro: IPR001022; Tobamo_MP.
DR Pfam: PF01107; Tobamo_MP; 1.
DR PRINTS; PR00964; MOVEMENT.
KW DNA-binding; Transport.
SQ SEQUENCE 264 AA; 29291 MW; 3B01EB2359AF9C4E CRC64;

Query Match 50.8%; Score 31; DB 1; Length 264;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQF 7
| | | | |
DB 233 RPKPKSF 239

RESULT 90
MOV_P-TOML2 STANDARD; PRT; 264 AA.
ID MOV_P-TOML2
AC Q9YJQ9;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MOVEMENT PROTEIN (CELL-TO-CELL TRANSPORT PROTEIN) (30 KDA PROTEIN).
GN MP.
OS Tomato mosaic virus (strain S-1) (ToMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=138314;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou X., Xue C., Chen Q., Qi Y., Li D.;
RT "Complete nucleotide sequence of a Chinese isolate of tomato mosaic
virus.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-200 FROM N.A.
RA Zhou X., Xue C., Qi Y., Li D.;
RT "Isolation and nucleotide sequence of the 30k and the coat protein
cistron of a Chinese isolate of tomato mosaic virus.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: INVOLVED IN TRANSPORT OF THE VIRUS FROM THE INITIALLY
INFECTED CELLS TO ADJACENT CELLS, POSSIBLY BY MODIFYING THE
FUNCTION OF THE PLASMODESMATA. ALSO INFLUENCES LOCAL LESION
DEVELOPMENT. BINDS TO SINGLE-STRANDED NUCLEIC ACID.
CC -|- SIMILARITY: BELONGS TO THE TOBAMOVIRUSES MOVEMENT PROTEIN FAMILY.
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-----
DR EMBL; AJ132845; CAB36999.1; -
DR EMBL; AJ011934; CAA09878.1; -
DR InterPro: IPR001022; Tobamo_MP.
DR Pfam: PF01107; Tobamo_MP; 1.
DR PRINTS; PR00964; MOVEMENT.
KW DNA-binding; Transport.
SQ SEQUENCE 264 AA; 29261 MW; 018394057CA46FAB CRC64;
```

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RX MEDLINE=92113565; PubMed=1730937;
RA Calder V.L., Palukaitis P.;
RT "Nucleotide sequence analysis of the movement genes of resistance
breaking strains of tomato mosaic virus.";
RL J. Gen. Virol. 73:165-168(1992).
CC -|- FUNCTION: INVOLVED IN TRANSPORT OF THE VIRUS FROM THE INITIALLY
INFECTED CELLS TO ADJACENT CELLS, POSSIBLY BY MODIFYING THE
FUNCTION OF THE PLASMODESMATA. ALSO INFLUENCES LOCAL LESION
DEVELOPMENT. BINDS TO SINGLE-STRANDED NUCLEIC ACID.
CC -|- SIMILARITY: BELONGS TO THE TOBAMOVIRUSES MOVEMENT PROTEIN FAMILY.
DR PIR; JQ1457; WMBVL2.
DR InterPro: IPR001022; Tobamo_MP.
DR Pfam: PF01107; Tobamo_MP; 1.
DR PRINTS; PR00964; MOVEMENT.
KW DNA-binding; Transport.
SQ SEQUENCE 264 AA; 29396 MW; 4737590A4EB8903B CRC64;

Query Match 50.8%; Score 31; DB 1; Length 264;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQF 7
| | | | |
DB 233 RPKPKSF 239

RESULT 91
MOV_P-TOMS1 STANDARD; PRT; 264 AA.
ID MOV_P-TOMS1
AC Q9YJQ9;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MOVEMENT PROTEIN (CELL-TO-CELL TRANSPORT PROTEIN) (30 KDA PROTEIN).
GN MP.
OS Tomato mosaic virus (strain S-1) (ToMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=138314;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou X., Xue C., Chen Q., Qi Y., Li D.;
RT "Complete nucleotide sequence of a Chinese isolate of tomato mosaic
virus.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-200 FROM N.A.
RA Zhou X., Xue C., Qi Y., Li D.;
RT "Isolation and nucleotide sequence of the 30k and the coat protein
cistron of a Chinese isolate of tomato mosaic virus.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: INVOLVED IN TRANSPORT OF THE VIRUS FROM THE INITIALLY
INFECTED CELLS TO ADJACENT CELLS, POSSIBLY BY MODIFYING THE
FUNCTION OF THE PLASMODESMATA. ALSO INFLUENCES LOCAL LESION
DEVELOPMENT. BINDS TO SINGLE-STRANDED NUCLEIC ACID.
CC -|- SIMILARITY: BELONGS TO THE TOBAMOVIRUSES MOVEMENT PROTEIN FAMILY.
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-----
DR EMBL; AJ132845; CAB36999.1; -
DR EMBL; AJ011934; CAA09878.1; -
DR InterPro: IPR001022; Tobamo_MP.
DR Pfam: PF01107; Tobamo_MP; 1.
DR PRINTS; PR00964; MOVEMENT.
KW DNA-binding; Transport.
SQ SEQUENCE 264 AA; 29261 MW; 018394057CA46FAB CRC64;
```

Query Match 50.8%; Score 31; DB 1; Length 264;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQF 7
||||:|
DB 233 RPKPKSF 239

RESULT 92
ID YOTB_CAEEL STANDARD; PRT; 266 AA.
AC P34657;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 30.2 KDA PROTEIN ZK632.12 IN CHROMOSOME III.
GN ZK632.12.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
Bonfield J., Burton J., Connell M., Copey T., Cooper J., Fraser A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
Sims M., Smaldon N., Smith A., Smith K., Vaudin M., Vaughan K.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans";
RT Nature 368:32-38(1994).

CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 FYVE-TYPE ZINC FINGER.
CC
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CC
CC -----

DR EMBL; 222181; CAA80187.1; -;
DR WormPep; ZK632.12; CE01110.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000306; Znf_FYVE.
DR Pfam; PF01363; FYVE; 1.
DR Pfam; PF00169; PH; 1.
DR SMART; SM00064; FYVE; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; PS50178; ZF_FYVE; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
KW Hypothetical protein: Zinc-finger.
FT DOMAIN 35 131 PH.
FT ZN_FING 152 212 FYVE-TYPE.
SQ SEQUENCE 266 AA; 30187 MW; 91C2F62EDF13839E CRC64;

Query Match 50.8%; Score 31; DB 1; Length 266;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQFF 8

DB 49 KPKQKQFF 56
|||:|

RESULT 93
ID THIM_PASMU STANDARD; PRT; 267 AA.
AC P57931;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYDROXYETHYLTHIAZOLE KINASE (EC 2.7.1.50) (4-METHYL-5-BETA-
DE HYDROXYETHYLTHIAZOLE KINASE) (THZ KINASE) (TH KINASE).
GN THIM OR PML262.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Faustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- CATALYTIC ACTIVITY: ATP + 4-METHYL-5-(2-HYDROXYETHYL)-THIAZOLE =
CC ADP + 4-METHYL-5-(2-PHOSPHOETHYL)-THIAZOLE.
CC -1- COFACTOR: MAGNESIUM (BY SIMILARITY).
CC -1- PATHWAY: THIAMINE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE THZ KINASE FAMILY.
CC
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CC
CC -----

DR EMBL; AE006165; AAK03346.1; -;
DR InterPro; IPR000417; Hyethyz_kinase.
DR Pfam; PF02110; HK; 1.
KW Thiamine biosynthesis; Transferase; Kinase; ATP-binding; Magnesium;
KW Complete proteome.
FT METAL 91 91 MAGNESIUM (BY SIMILARITY).
FT METAL 123 123 MAGNESIUM (BY SIMILARITY).
FT ACT_SITE 194 194 BASE (BY SIMILARITY).
SQ SEQUENCE 267 AA; 28245 MW; C710B90C6BB5E971 CRC64;

Query Match 50.8%; Score 31; DB 1; Length 267;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQFFGLM 11
|||:|
DB 208 KPEQYFDM 216

RESULT 94
ID CCHL_YEAST STANDARD; PRT; 269 AA.
AC P06182;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOCHROME C HEME LYASE (EC 4.4.1.17) (CCHL) (HOLOCYTOCHROME-C
DE SYNTHASE).
GN CYC3 OR YAL039C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B-7034;
RX MEDLINE=87218469; PubMed=3034577;
RA Dumont M.E., Ernst J.F., Hampsey D.M., Sherman F.;
RT "Identification and sequence of the gene encoding cytochrome c heme
RL lyase in the yeast *Saccharomyces cerevisiae*.";
RL EMBO J. 6:235-241(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RX MEDLINE=95249563; PubMed=7731988;
RA Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.;
RA Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
RA Storms R.K.;
RT "The nucleotide sequence of chromosome I from *Saccharomyces
RT cerevisiae*.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
RN [3]
RP FUNCTION: LINKS COVALENTLY THE HEME GROUP TO THE APOPROTEIN
CC OF CYTOCHROME C.
CC -1- CATALYTIC ACTIVITY: HOLOCYTOCHROME C = APOCYTOCHROME C + HEME.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C-TYPE HEME LYASE FAMILY.
CC -1- SIMILARITY: CONTAINS 2 HEME REGULATORY MOTIFS (HRM).
CC -----
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CC -----
CC EMBL; X04776; CAA28470.1; -;
CC EMBL; U12980; AAC04992.1; -;
CC PIR; A26162; A26162.
CC SGD; S0000037; CYC3.
CC InterPro; IPR000511; Cyto_heme_lyase.
CC Pfam; PF01265; Cyto_heme_lyase.1.
CC PROSITE; PS00821; CYTO_HEME_LYASE_1; 1.
CC PROSITE; PS00822; CYTO_HEME_LYASE_2; 1.
CC Lyase; Heme; Mitochondrion; Repeat.
CC DOMAIN 25 30 HRM 1 (POTENTIAL).
CC FT DOMAIN 41 46 HRM 2 (POTENTIAL).
CC SQ SEQUENCE 269 AA; 30081 MW; A672A48BBD848AF CRC64;

Query Match 50.8%; Score 31; DB 1; Length 269;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 2 PKPOFFGLM 11
Db 95 PPOQMYNAM 104

RESULT 95
RRP1_YEAST
ID RRP1_YEAST STANDARD; PRT; 278 AA.
AC P35178;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE RIBOSOMAL RNA PROCESSING PROTEIN 1.
GN RRP1 OR YDR087C OR D4478.
OS *Saccharomyces cerevisiae* (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / FY1679;
RA Coster F., Jonniaux J.-L., Goffeau A.;

Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 146-278 FROM N.A.
RX MEDLINE=94038890; PubMed=8223425;
RA Esnault Y., Blondel M.-O., Deshaies R.J., Schekman R., Kepes F.;
RT "The yeast SSSI gene is essential for secretory protein translocation
RT and encodes a conserved protein of the endoplasmic reticulum.";
RL EMBO J. 12:4083-4093(1993).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=99276573; PubMed=10341208;
RA Savino T.M., Bastos R., Jansen E., Hernandez-Verdun D.;
RT "The nucleolar antigen Nop52, the human homologue of the yeast
RT ribosomal RNA processing RRP1, is recruited at late stages of
RT nucleogenesis.";
RL J. Cell Sci. 112:1889-1900(1999).
CC -1- FUNCTION: REQUIRED FOR 27S RNA PROCESSING TO 25S AND 5.8S.
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
CC -1- SIMILARITY: BELONGS TO THE NRP-1 FAMILY.
CC -----
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CC -----
CC EMBL; Z46796; CAA68809.1; -;
CC EMBL; Z74383; CAA98907.1; -;
CC EMBL; X82086; CAA57616.1; -;
CC EMBL; X74499; CAA52607.1; -;
CC PIR; S48776; S48776.
CC SGD; S0002494; RRP1.
CC KW Nuclear protein; rRNA processing; Coiled coil.
CC FT DOMAIN 266 274 POLY-GLU.
CC SQ SEQUENCE 278 AA; 33202 MW; 7E906A028ADA8A6 CRC64;

Query Match 50.8%; Score 31; DB 1; Length 278;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPKPQQ 6
Db 58 RPREQQ 63

RESULT 96
NUGM_NEUCR
ID NUGM_NEUCR STANDARD; PRT; 283 AA.
AC P23710;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE NADH-UBIQUINONE OXIDOREDUCTASE 30.4 KDA SUBUNIT, MITOCHONDRIAL
DE PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-30KD) (C1-31KD).
GN NUO-31.
OS *Neurospora crassa*.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91024977; PubMed=2145832;
RA Videla A., Tropschug W., Werner S.;
RT "Primary structure and expression of a nuclear-coded subunit of
RT complex I homologous to proteins specified by the chloroplast
RT genome.";
RL Biochem. Biophys. Res. Commun. 171:1168-1174(1990).
CC -1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC TO BE UBIQUINONE.

CC -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.
CC THIS IS A COMPONENT OF THE IRON-SULFUR PROTEIN FRACTION.
CC -!- SUBCELLULAR LOCATION: MATRIX AND CYTOPLASMIC SIDE OF THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE COMPLEX I 30 KDA SUBUNIT FAMILY.
CC PR; A35935; A35935.
CC DR InterPro: IPR001268; Complex1_30K.
CC DR Pfam: PF00329; complex1_30Kd; 1.
CC DR ProDom: PD001581; Complex1_30K; 1.
CC DR PROSITE; PS00542; COMPLEX1_30K; 1.
CC KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transit peptide.
CC FT TRANSIT 1 17 MITOCHONDRION (POTENTIAL).
CC FT CHAIN 18 283 NADH-UBIQUINONE OXIDOREDUCTASE 30.4 KDA
CC SUBUNIT.
CC SQ SEQUENCE 283 AA; 32283 MW; 3A2DCD32535986CA CRC64;

Query Match 50.8%; Score 31; DB 1; Length 283;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQF 7
DB 40 RPNRQF 46
| | | | |
| | | | |

RESULT 97
LST_HAEIN
ID LST_HAEIN STANDARD; PRT; 304 AA.
AC Q48211; Q05084;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE
DE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA
DE 2,3-ST) (LIPOLIGOSACCHARIDE SIALYLTRANSFERASE).
GN LST OR H11699.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
[1]
RP SEQUENCE FROM N.A.
RA McLaughlin R., Abu Kwaik Y., Young R., Spinola S., Apicella M.;
RT "Characterization and sequence of the *lsf* locus from *Haemophilus*
RT *influenzae*.";
RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-RD / KW20 / ATCC 51907;
RX MEDLINE-95350630; PubMed-7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kervilange A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of *Haemophilus influenzae*
RT Rd";
RL Science 269:496-512(1995).
CC -!- FUNCTION: TRANSFERS SIALIC ACID FROM THE SUBSTRATE CMP-SIALIC ACID
CC DONOR TO THE TERMINAL BETA-D-GALACTOSYL-1,4-ACETYL-BETA-D-
CC LIPOOLIGOSACCHARIDE.
CC -!- CATALYTIC ACTIVITY: CMP-N-ACETYLNEURAMINATE + BETA-D-GALACTOSYL-
CC 1,4-ACETYL-BETA-D-GLUCOSAMINE = CMP + ALPHA-N-ACETYLNEURAMINYL-
CC 2,3-BETA-D-GALACTOSYL-1,4-N-ACETYL-BETA-D-GLUCOSAMINE.
CC -!- PATHWAY: LIPOLIGOSACCHARIDE BIOSYNTHESIS.
CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 52.

CC -----
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CC -----
CC EMBL; M94855; AAA24979.1; -;
CC DR EMBL; U32842; AAC23345.1; -;
CC DR TIGR; H11699; -;
CC KW Transferase; Glycosyltransferase; Lipopolysaccharide biosynthesis;
CC Complete proteome.
CC FT CONFLICT 4 4 M -> I (IN REF. 1).
CC FT CONFLICT 68 68 F -> S (IN REF. 1).
CC FT CONFLICT 130 130 G -> D (IN REF. 1).
CC FT CONFLICT 220 220 Y -> C (IN REF. 1).
CC SQ SEQUENCE 304 AA; 35706 MW; B6D03890AC1CDD28 CRC64;

Query Match 50.8%; Score 31; DB 1; Length 304;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 QOFFGLM 11
DB 25 EQFFGVG 31
: | | | | :
: | | | | :

RESULT 98
RADA_METVO
ID RADA_METVO STANDARD; PRT; 322 AA.
AC O73948;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE DNA REPAIR AND RECOMBINATION PROTEIN RADA.
GN RADA.
OS Methanococcus voltae.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2188;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-PS / DSM 1537;
RA Reich C.I., Buldak G.L., McNeill L.K.;
RT "The Rada protein from the archaeon *Methanococcus voltae*: a functional
RT homolog of eukaryotic Rad51.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE OF 112-254 FROM N.A.
RX MEDLINE-99121030; PubMed-9922255;
RA Sandler S.J., Hugenholtz P., Schleper C., Delong E.F., Pace N.R.,
RA Clark A.J.;
RT "Diversity of rada genes from cultured and uncultured archaea:
RT comparative analysis of putative Rada proteins and their use as a
RT phylogenetic marker.";
RL J. Bacteriol. 181:907-915(1999).
CC -!- FUNCTION: INVOLVED IN DNA REPAIR AND IN HOMOLOGOUS RECOMBINATION.
CC BINDS AND ASSEMBLES ON SINGLE-STRANDED DNA TO FORM A NUCLEOPROTEIN
CC FILAMENT. HYDROLYSES ATP IN A SSDNA-DEPENDENT MANNER AND PROMOTES
CC DNA STRAND EXCHANGE BETWEEN HOMOLOGOUS DNA MOLECULES (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE EUKARYOTIC RECA-LIKE PROTEIN FAMILY.
CC -----
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```
CC -----
DR EMBL; AF008421; AAC23499.1; -.
DR EMBL; AF090200; AAD16066.1; -.
DR InterPro; IPR000445; HHH.
DR InterPro; IPR001583; RecA.
DR InterPro; IPR003583; HHH_1.
DR SMART; SM00278; HHH1; 2.
DR PROSITE; PS0162; RECA_2; 1.
DR PROSITE; PS0163; RECA_3; 1.
KW DNA damage; DNA recombination; ATP-binding; DNA-binding.
FT NP_BIND 105 112 ATP (POTENTIAL).
SQ SEQUENCE 322 AA; 35189 MW; 8A9F5EFB927344B6 CRC64;

Query Match 50.8%; Score 31; DB 1; Length 322;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPQOFFGL 10
DB 261 KPDAFFGM 268

RESULT 99
VPRT_SMRVH
ID VPRT_SMRVH STANDARD; PRT; 323 AA.
AC P21407;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PROTEASE (EC 3.4.23.-).
GN PRT.
OS Squirrel monkey retrovirus (SMRV-H) (SMRV-HLB).
OC Viruses; Retrov. viruses; Retroviridae; Betaretrovirus.
OX NCBI_TaxID=11856;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89073750; PubMed=3201749;
RA Oda T., Ikeda S., Watanabe S., Hatsushika M., Akiyama K.,
RA Mitsunobu F.;
RT "Molecular cloning, complete nucleotide sequence, and gene structure
RT of the provirus genome of a retrovirus produced in a human
RT lymphoblastoid cell line.";
RL Virology 167:468-476(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A2; ALSO KNOWN AS THE
CC RETROPEPSIN FAMILY.
CC -----
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CC -----
CC EMBL; M23385; AAA66452.1; ALT_INIT.
CC PIR; B31827; PRLJHD.
CC HSP; P03366; 9HVP.
DR InterPro; IPR001995; Asp_prot_retrov.
DR InterPro; IPR001969; Asp_protease.
DR InterPro; IPR000457; G_patch.
DR InterPro; IPR001428; dufPase.
DR Pfam; PF00692; dufPase; 1.
DR Pfam; PF01585; G_patch; 1.
DR Pfam; PF00077; rvp; 1.
DR ProDom; PD000946; dufPase; 1.
DR SMART; SM00443; G_patch; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS00175; ASP_PROT_RETROV; 1.
KW Hydrolase; Aspartyl protease.
FT ACT_SITE 193 193 BY SIMILARITY.
SQ SEQUENCE 323 AA; 35126 MW; 5D6CEA38BA932786 CRC64;
```

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Query Match 50.8%; Score 31; DB 1; Length 323;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KPQOFFGLM 11
DB 82 PLPPQTEGLI 91

RESULT 100
PUR5_METTH
ID PUR5_METTH STANDARD; PRT; 338 AA.
AC O27272;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROBABLE PHOSPHORIBOSYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
DE (AIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE).
GN PURM OR MTH1204.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanothermobacter.
OX NCBI_TaxID=145262;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DELTA H.
RX MEDLINE=98037514; PubMed=93711463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwanji N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -1- CATALYTIC ACTIVITY: ATP + 5'-PHOSPHORIBOSYL-5-AMINOIMIDAZOLE
CC ADP + ORTHOPHOSPHATE + 5'-PHOSPHORIBOSYL-FORMYLGLYCINAMIDINE -
CC (BY SIMILARITY).
CC -1- PATHWAY: FIFTH STEP IN DE NOVO PURINE BIOSYNTHESIS.
CC (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER AIRS FROM BACTERIA AND EUKARYOTES.
CC -----
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CC -----
CC EMBL; AE000888; AAB85693.1; -.
CC InterPro; IPR000728; AIRS_related.
CC Pfam; PF00586; AIRS; 1.
KW Purine biosynthesis; Ligase; Complete proteome.
SQ SEQUENCE 338 AA; 35983 MW; 5C6AA2B6562E0E17 CRC64;
```

```
Query Match 50.8%; Score 31; DB 1; Length 338;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KPQOFF 8
DB 264 PEQQIF 270

RESULT 101
PYRD_PASMU
ID PYRD_PASMU STANDARD; PRT; 339 AA.
AC P57858;
```


20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE DIHYDROOROTATE DEHYDROGENASE (EC 1.3.3.1) (DIHYDROOROTATE OXIDASE)
DE (DHODPHASE) (DHODASE) (DHOD).
GN PYRD OR PM0617.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida PM70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- CATALYTIC ACTIVITY: L-DIHYDROOROTATE + O(2) -> OROTATE + H(2)O(2).
CC -1- COFACTOR: FMN (BY SIMILARITY).
CC -1- PATHWAY: FOURTH STEP IN PYRIMIDINE BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INNER SIDE OF THE MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE DIHYDROOROTATE DEHYDROGENASE FAMILY.
CC SUBFAMILY 2.

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DR EMBL; AE006098; AK02701.1; -
DR InterPro; IPR001295; DHO_dh.
DR InterPro; IPR003009; FMN_enzyme.
DR Pfam; PF01180; DHODehase; 1.
DR PROSITE; PS00911; DHODPHASE_1; 1.
DR PROSITE; PS00912; DHODPHASE_2; 1.
KW Pyrimidine biosynthesis; Oxidoreductase; Flavoprotein; FMN;
FT Complete proteome.
FT NP_BIND 292 300 FMN (POTENTIAL).
SQ SEQUENCE 339 AA; 36919 MW; AEA5E07B29942D68 CRC64;

Query Match 50.8%; Score 31; DB 1; Length 339;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PKPOOF 7
Db |||||
98 PKPROF 103

RESULT 102
CPXE_STRGO STANDARD; PRT; 405 AA.
AC P18326;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOCHROME P450-SUL (EC 1.14.-.-) (P450-CVAL) (CYP105A1).
GN CYP105A1 OR SUAC.
OS Streptomyces griseolus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1909;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-31.
RC STRAIN=ATCC 11796;
RX MEDLINE=90264332; PubMed=2345149;
RA Omer C.A., Lenstra R., Little P.J., Dean C., Tepperman J.M.,
RA Leto K.J., Romesser J.A., O'Keefe D.P.;

"Genes for two herbicide-inducible cytochromes P-450 from
Streptomyces griseolus.";
J. Bacteriol. 172:3335-3345(1990).
CC -1- FUNCTION: METABOLISM OF A NUMBER OF SULFONYLUREA HERBICIDES.
CC -1- INDUCTION: BY HERBICIDE.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

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DR EMBL; M32238; AAA26823.1; -
DR PIR; A35401; A35401.
DR HSP; P23295; 2ROM.
DR InterPro; IPR001128; Cyt_P450.
DR Pfam; PF00067; p450; 1.
DR PRINTS; PF00359; BP450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Heme.
FT INIT_MET 0
FT BINDING 354 354 HEME (BY SIMILARITY).
SQ SEQUENCE 405 AA; 44081 MW; 92AB36E064FD0B3E CRC64;

Query Match 50.8%; Score 31; DB 1; Length 405;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPKPOQFGL 10
Db | | | | |
88 RESPOAFGL 97

RESULT 103
TIG_MYCTU STANDARD; PRT; 466 AA.
ID TIG_MYCTU
AC O53189;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TRIGGER FACTOR (TF).
GN TIG OR RV2462C OR MT2537 OR MTV008.18C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Horsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;

RT "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN PROTEIN EXPORT. ACTS AS A CHAPERONE BY MAINTAINING THE NEWLY SYNTHESIZED PROTEIN IN AN OPEN CONFORMATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. TIG SUBFAMILY.
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CC -----
DR EMBL: AL021246; CAA16039.1; -;
DR EMBL: AB007090; AAK46837.1; -;
DR TIGR: MT2537; -;
DR TubercuList; RV2462c; -;
DR InterPro: IPR001179; FKBP_PPIase.
DR PROSITE: PS00453; FKBP_PPIase_1; FALSE_NEG.
DR PROSITE: PS00454; FKBP_PPIase_2; FALSE_NEG.
DR PROSITE: PS00059; FKBP_PPIase_3; 1.
KW Cell division; Chaperone; Isomerase; Rotamase; Complete proteome.
FT DOMAIN 162 243 PPIASE, FKBP-TYPE.
SQ SEQUENCE 466 AA; 50616 MW; AFF5DC88976036D CRC64;

Query Match 50.8%; Score 31; DB 1; Length 466;
Best Local Similarity 55.8%; Pred. NO. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPQOFFGLM 11
:|:|:|:|:
DB 387 EPQOLFGL 395

RESULT 104
TRE2_SYNY3
ID TRE2_SYNY3 STANDARD; PRT; 485 AA.
AC P74130;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ANTHRANILATE SYNTHASE COMPONENT I-LIKE PROTEIN (EC 4.1.3.27).
GN TRPE2 OR SLR1979.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hiroseawa M., Sugliura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE + PYRUVATE + L-GLUTAMATE.
CC -1- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC -1- SUBUNIT: Tetramer of two components I and two components II (by similarity).
CC -1- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I FAMILY.
CC -1- CAUTION: THIS IS A DIVERGENT FORM OF TRPE. IT IS NOT OBVIOUS IF IT

CC IS ACTIVE IN TRP BIOSYNTHESIS.
CC -----
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CC -----
DR EMBL: D90912; BAA18216.1; -;
DR InterPro: IPR000350; Chorismate_bind.
DR Pfam: PF00425; Chorismate_bind; 1.
DR PRINTS: PR00095; ANTSINTHASE1.
DR ProDom: PD000779; Chorismate_bind; 1.
KW Tryptophan biosynthesis; Lyase; Complete proteome.
SQ SEQUENCE 485 AA; 54270 MW; 4F25ECCB3857BC7C CRC64;

Query Match 50.8%; Score 31; DB 1; Length 485;
Best Local Similarity 40.0%; Pred. NO. 2.2e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQQFFGLM 11
:|:|:|:|:
DB 98 KPPEEIFSFL 107

RESULT 105
EXON_HSV6U
ID EXON_HSV6U STANDARD; PRT; 488 AA.
AC P24447;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALKALINE EXONUCLEASE (EC 3.1.11.-).
GN U70 OR 16R.
OS Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=10370;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90080132; PubMed=2152817;
RA Lawrence G.L., Chee M., Craxton M.A., Gompels U.A., Honess R.W., Barrell B.G.;
RT "Human herpesvirus 6 is closely related to human cytomegalovirus.";
RL J. Virol. 64:287-299(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95266321; PubMed=7747482;
RA Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomscn B.J., Martin M.E., Efsthliou S., Craxton M., Macaulay H.A.;
RT "The DNA sequence of human herpesvirus-6: structure, coding content, and genome evolution.";
RL Virology 209:29-51(1995).
CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES ALKALINE EXONUCLEASE FAMILY.
CC -----
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CC -----
DR EMBL: X83413; CAA58362.1; -;
DR EMBL: M68963; AAA65578.1; -;
DR PIR: F36769; QOBEHS.
DR InterPro: IPR001616; Herpes_alk_exo.
DR Pfam: PF01771; Herpes_alk_exo; 1.
DR PRINTS: PR00924; ALKEXNUCLASE.

KW Hydrolase; Nuclease; Exonuclease.
SQ SEQUENCE 488 AA; 56644 MW; 0F38A10597366A5B CRC64;

Query Match 50.8%; Score 31; DB 1; Length 488;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQFFG 9
| | | | |
DB 161 KGQFFFG 167

RESULT 106

EXON_HSV6Z STANDARD; PRT; 488 AA.
AC P52448;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALKALINE EXONUCLEASE (EC 3.1.11.-).
GN U70 OR CH3R.
OS Human herpesvirus (type 6 / strain 229) (HHV6).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=36351;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96195263; PubMed=8634027;
RA Lindquester G.J., Inoue N., Allen R.D., Castelli J.W.,
RA Stamey F.R., Dambaugh T.R., O'Brian J.J., Danovich R.M.,
RA Frenkel N., Pellett P.E.;
RT "Restriction endonuclease mapping and molecular cloning of the human
herpesvirus 6 variant B strain 229 genome.";
RL Arch. Virol. 141:367-379(1996).
CC -!- SIMILARITY: BELONGS TO THE HERPESVIRUSES ALKALINE EXONUCLEASE
FAMILY.
CC
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DB EMBL: AF157706; AAB06353.1; -
DR InterPro: IPR001616; Herpes_alk_exo.
DR Pfam: PF01771; Herpes_alk_exo; 1.
DR PRINTS: PR00924; ALKEXNUCLASE.
KW Hydrolase; Nuclease; Exonuclease.
SQ SEQUENCE 488 AA; 56687 MW; AE2872028D4B3D90 CRC64;

Query Match 50.8%; Score 31; DB 1; Length 488;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQFFG 9
| | | | |
DB 161 KGQFFFG 167

RESULT 107

SYK_MYCHO STANDARD; PRT; 488 AA.
AC P46191;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE--TRNA LIGASE) (LYSRS).
GN LYS.
OS Mycoplasma hominis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2098;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG21;
RA MEDLINE=94237425; PubMed=8181699;
RA Ozkokmen D., Birkelund S., Christiansen G.;
RT "Characterization of a Mycoplasma hominis gene encoding lysyl-trna
synthetase (LYSRS).";
RL FEMS Microbiol. Lett. 116:277-282(1994).
CC -!- CATALYTIC ACTIVITY: ATP + L-LYSINE + TRNA(LYS) -> AMP +
PYROPHOSPHATE + L-LYSYL-TRNA(LYS).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.

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DR EMBL: X74912; CAA52877.1; -
DR HSP: P14825; LYL.
DR InterPro: IPR002106; AA_trna_ligase_II.
DR InterPro: IPR002309; trna-synt_2.
DR InterPro: IPR002313; trna-synt_lys_2.
DR Pfam: PF00152; trna-synt_2; 1.
DR Pfam: PF01336; trna-anti_1.
DR PRINTS: PR00982; TRNASYNTHLYS.
DR PROSITE: PS00179; AA_TRNA_LIGASE_II_1; 1.
DR PROSITE: PS00339; AA_TRNA_LIGASE_II_2; FALSE_NEG.
KW Aminoacyl-trna synthetase; Protein biosynthesis; Ligase; ATP-binding.
SQ SEQUENCE 488 AA; 56868 MW; 83D34BF37E21E32E CRC64;

Query Match 50.8%; Score 31; DB 1; Length 488;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RKPKQOQFFGLM 11
: | | : | | : | | :
DB 137 KPLPKDFHGLV 147

RESULT 108

CPVL_BRARE STANDARD; PRT; 509 AA.
ID CPVL_BRARE
AC O42145;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CYTOCHROME P450 19 (AROMATASE) (EC 1.14.14.1) (CYP19) (ESTROGEN
SYNTHETASE) (P-450AROM).
GN CYP19.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Bauer M.P., Goetz F.W.;
RT "Isolation and characterization of a zebrafish (Danio rerio) aromatase
cDNA.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CATALYZES THE FORMATION OF AROMATIC C18 ESTROGENS FROM
C19 ANDROGENS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) -> ROH +

CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
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CC -----
CC EMBL: AF004521; AAB65788.1; -
CC ZFIN: ZDB-GENE-990415-43; Cyp19.
CC InterPro: IPR001128; Cyt_P450.
CC Pfam: PF00067; P450; 1.
CC PRINTS: PR00385; P450.
CC PROSITE: PS00086; CYTOCHROME_P450; 1.
CC Electron transport; Oxidoreductase; Monooxygenase; Membrane;
CC Heme.
CC FT BINDING 456 456 HEME (BY SIMILARITY).
CC FT SEQUENCE 509 AA; 57354 MW; F04532DEA8FDB628 CRC64;
CC
CC Query Match 50.8%; Score 31; DB 1; Length 509;
CC Best Local Similarity 66.7%; Pred. No. 2.4e+02;
CC Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CC
CC QY 2 PKPQQFGL 10
CC | | | | |
CC Db 68.PGPSFFGL 76
CC
CC RESULT 109
CC DHAF_VIBHA STANDARD; PRT; 510 AA.
CC AC Q56694;
CC DT 20-AUG-2001 (Rel. 40, Created)
CC DT 20-AUG-2001 (Rel. 40, Last sequence update)
CC DT 20-AUG-2001 (Rel. 40, Last annotation update)
CC DE FATTY ALDEHYDE DEHYDROGENASE (EC 1.2.1.3).
CC GN ALDH.
CC OS Vibrio harveyi.
CC OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
CC OX NCBI_TaxID=669;
CC RN [1]
CC RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
CC RC STRAIN=B392;
CC RX MEDLINE=96118391; PubMed=8527447;
CC RA Vedadi M., Zittner R., Smillie L., Meighen E.;
CC RT "Involvement of cysteine 289 in the catalytic activity of an NADP(+)-
CC specific fatty aldehyde dehydrogenase from Vibrio harveyi.";
CC RL Biochemistry 34:16725-16732(1995).
CC [2]
CC RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
CC RC STRAIN=B392;
CC RX MEDLINE=20363527; PubMed=10903148;
CC RA Ahvazi B., Coulombe R., Delarge M., Vedadi M., Zhang L., Meighen E.,
CC RA Vrielink A.;
CC RT "Crystal structure of the NADP+-dependent aldehyde dehydrogenase from
CC Vibrio harveyi: structural implications for cofactor specificity and
CC affinity.";
CC RL Blochem. J. 349:853-861(2000).
CC -1- FUNCTION: CATALYZES THE OXIDATION OF LONG-CHAIN ALIPHATIC
CC ALDEHYDES TO ACIDS. MAY BE IMPLICATED IN CONTROLLING LUMINESCENCE
CC AS IT CATALYZES THE OXIDATION OF THE FATTY ALDEHYDE SUBSTRATE FOR
CC THE LIGHT-EMITTING REACTION.
CC -1- CATALYTIC ACTIVITY: ALDEHYDE + NADP(+) + H(2)O = ACID + NADPH.
CC -1- COFACTOR: HAS A HIGH SPECIFICITY FOR NADP.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
CC -----
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CC -----
CC EMBL: U39638; AAA89078.1; -
CC PDB: 1EYV; 24-MAY-00.
CC PDB: 1E20; 24-MAY-00.
CC InterPro: IPR002086; Aldehyde_dehydr.
CC Pfam: PF00171; aldehyd; 1.
CC PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; FALSE_NEG.
CC PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; FALSE_NEG.
CC KW Oxidoreductase; NADP; 3D-structure.
CC FT NE_BIND 229 234 NADP (ADP PART).
CC FT ACT_SITE 253 253
CC FT ACT_SITE 289 289
CC FT SEQUENCE 510 AA; 54459 MW; E132F2406AA3F47A CRC64;
CC
CC Query Match 50.8%; Score 31; DB 1; Length 510;
CC Best Local Similarity 55.8%; Pred. No. 2.4e+02;
CC Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
CC
CC QY 1 RPKPQQFFG 9
CC | | | | |
CC Db 244.RPEPIPYG 252
CC
CC RESULT 110
CC YTE4_CAEEL STANDARD; PRT; 546 AA.
CC AC Q17865;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 01-NOV-1997 (Rel. 35, Last annotation update)
CC DE HYPOTHETICAL 60.9 KDA PROTEIN C09G1.4 IN CHROMOSOME X.
CC GN C09G1.4.
CC OS Caenorhabditis elegans.
CC OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
CC Rhabditidae; Peloderinae; Caenorhabditis.
CC OX NCBI_TaxID=6239;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=BRISTOL N2;
CC RA McMurray A.;
CC RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC [2]
CC RN REVISIONS.
CC RA Jones S.J.M.;
CC RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
CC EMBL: Z50176; CAA90541.1; -
CC WormPep; C09G1.4; CE08042.
CC InterPro: IPR001478; PDZ.
CC SMART: SM00228; PDZ; 1.
CC PROSITE: PS50106; PDZ; 1.
CC KW Hypothetical protein.
CC FT SEQUENCE 546 AA; 60864 MW; 2764EBB62461E3C2 CRC64;
CC
CC Query Match 50.8%; Score 31; DB 1; Length 546;
CC Best Local Similarity 63.6%; Pred. No. 2.5e+02;
CC Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
QY 1 RPKPQQFFGLM 11
    |||||
Db 314 RPLPQQQTSLM 324

RESULT 111
GPCL_RAT
ID GPCL_RAT STANDARD; PRT; 558 AA.
AC P35053;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GLYPICAN-1 PRECURSOR (HSPG M12).
GN GPCL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 24-55 AND 424-445.
RC TISSUE=Brain.
RX MEDLINE=93038690; PubMed=14117860;
RA Karthikeyan L., Maurel P., Rauch U., Margolis R.K., Margolis R.U.;
RT "Cloning of a major heparan sulfate proteoglycan from brain and
RT identification as the rat form of glypican".
RL Biochem. Biophys. Res. Commun. 188:395-401(1992).
RN [2]
SEQUENCE FROM N.A., AND SEQUENCE OF 83-112; 196-207 AND 422-443.
RC STRAIN=NEW ENGLAND DECONESS HOSPITAL;
RX MEDLINE=94267529; PubMed=8207484;
RA Litwack E.D., Stipp C.S., Kumbasar A., Lander A.D.;
RT "Neuronal expression of glypican, a cell-surface
RT glycosylphosphatidylinositol-anchored heparan sulfate proteoglycan,
RT in the adult rat nervous system.".
RL J. Neurosci. 14:3713-3724(1994).
CC -1- FUNCTION: CELL SURFACE PROTEOGLYCAN THAT BEARS HEPARAN SULFATE.
CC MAY PLAY AN IMPORTANT ROLE IN THE TROPIC AND INJURY RESPONSES OF
CC NEURONS.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
CC -1- TISSUE SPECIFICITY: NERVOUS SYSTEM.
CC -1- PTM: THIS CELL-ASSOCIATED GLYPICAN IS FURTHER PROCESSED TO GIVE
CC RISE TO A MEDIUM-RELEASED SPECIES.
CC -1- SIMILARITY: BELONGS TO THE GLYPICAN FAMILY.
CC -----
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CC -----
DR EMBL; L02896; AAA86439.1; -
DR EMBL; L34067; AAA41251.1; -
DR PIR; JC1281; JC1281.
DR InterPro; IPR001863; Glypican.
DR Pfam; PF01153; Glypican; 1.
DR PROSITE; PS01207; GLYPICAN; 1.
KW Proteoglycan; Heparan sulfate; Glycoprotein; Signal; GPI-anchor;
KW Extracellular matrix.
FT SIGNAL 1 23
FT CHAIN 24 530
FT PROPEP 531 558
FT LIPID 530 530
FT CARBOHYD 79 79
FT CARBOHYD 116 116
FT CARBOHYD 55 55
FT CARBOHYD 486 486
FT CARBOHYD 488 488
FT CARBOHYD 490 490
FT CONFLICT 21 21
FT CONFLICT 312 312

GPCL_RAT
ID GPCL_RAT STANDARD; PRT; 558 AA.
AC P35053;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GLYPICAN-1 PRECURSOR (HSPG M12).
GN GPCL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 24-55 AND 424-445.
RC TISSUE=Brain.
RX MEDLINE=93038690; PubMed=14117860;
RA Karthikeyan L., Maurel P., Rauch U., Margolis R.K., Margolis R.U.;
RT "Cloning of a major heparan sulfate proteoglycan from brain and
RT identification as the rat form of glypican".
RL Biochem. Biophys. Res. Commun. 188:395-401(1992).
RN [2]
SEQUENCE FROM N.A., AND SEQUENCE OF 83-112; 196-207 AND 422-443.
RC STRAIN=NEW ENGLAND DECONESS HOSPITAL;
RX MEDLINE=94267529; PubMed=8207484;
RA Litwack E.D., Stipp C.S., Kumbasar A., Lander A.D.;
RT "Neuronal expression of glypican, a cell-surface
RT glycosylphosphatidylinositol-anchored heparan sulfate proteoglycan,
RT in the adult rat nervous system.".
RL J. Neurosci. 14:3713-3724(1994).
CC -1- FUNCTION: CELL SURFACE PROTEOGLYCAN THAT BEARS HEPARAN SULFATE.
CC MAY PLAY AN IMPORTANT ROLE IN THE TROPIC AND INJURY RESPONSES OF
CC NEURONS.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
CC -1- TISSUE SPECIFICITY: NERVOUS SYSTEM.
CC -1- PTM: THIS CELL-ASSOCIATED GLYPICAN IS FURTHER PROCESSED TO GIVE
CC RISE TO A MEDIUM-RELEASED SPECIES.
CC -1- SIMILARITY: BELONGS TO THE GLYPICAN FAMILY.
CC -----
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CC -----
DR EMBL; L02896; AAA86439.1; -
DR EMBL; L34067; AAA41251.1; -
DR PIR; JC1281; JC1281.
DR InterPro; IPR001863; Glypican.
DR Pfam; PF01153; Glypican; 1.
DR PROSITE; PS01207; GLYPICAN; 1.
KW Proteoglycan; Heparan sulfate; Glycoprotein; Signal; GPI-anchor;
KW Extracellular matrix.
FT SIGNAL 1 23
FT CHAIN 24 530
FT PROPEP 531 558
FT LIPID 530 530
FT CARBOHYD 79 79
FT CARBOHYD 116 116
FT CARBOHYD 55 55
FT CARBOHYD 486 486
FT CARBOHYD 488 488
FT CARBOHYD 490 490
FT CONFLICT 21 21
FT CONFLICT 312 312

Query Match 50.8%; Score 31; DB 1; Length 558;
Best Local Similarity 62.5%; Pred.No. 2.6e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 RPKPQQFF 8
    ||:| ||
Db 534 RPEPHYFF 541

RESULT 112
MM02_HUMAN
ID MM02_HUMAN STANDARD; PRT; 660 AA.
AC P08253;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE 72 KDA TYPE IV COLLAGENASE PRECURSOR (EC 3.4.24.24) (72 KDA
DE GELATINASE) (MATRIX METALLOPROTEINASE-2) (MMP-2) (GELATINASE A)
DE (TBE-1).
DE MMP2 OR CLG4A.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE OF 19-660 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=86198218; PubMed=2834383;
RA Collier I.E., Wilhelm S.M., Eisen A.Z., Marmer B.L., Grant G.A.,
RA Seltzer J.L., Kronberger A., He C., Bauer E.A., Goldberg G.I.;
RT "H-ras oncogene-transformed human bronchial epithelial cells (TBE-1)
RT secrete a single metalloprotease capable of degrading basement
RT membrane collagen.".
RL J. Biol. Chem. 263:6579-6587(1988).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=91236162; PubMed=1851724;
RA Collier I.E., Bruns G.A.P., Goldberg G.I., Gerhard D.S.;
RT "On the structure and chromosome location of the 72- and 92-kDa human
RT type IV collagenase genes.".
RL Genomics 9:429-434(1991).
RN [3]
SEQUENCE FROM N.A.
RX MEDLINE=90293047; PubMed=2162831;
RA Huhtala P., Chow L.T., Tryggvason K.;
RT "Structure of the human type IV collagenase gene.".
RL J. Biol. Chem. 265:11077-11082(1990).
RN [4]
SEQUENCE OF 1-51 FROM N.A.
RX MEDLINE=90228972; PubMed=2158484;
RA Huhtala P., Eddy R.L., Fan Y.S., Byers M.G., Shows T.B.;
RT "Completion of the primary structure of the human type IV collagenase
RT preproenzyme and assignment of the gene (CLG4) to the q21 region of
RT chromosome 16.".
RL Genomics 6:554-559(1990).
RN [5]
X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 443-660.
RX MEDLINE=96069777; PubMed=7583664;
RA Libson A.M., Gittis A.G., Collier I.E., Marmer B.L., Goldberg G.I.,
RA Lattman E.E.;
RT "Crystal structure of the haemopexin-like C-terminal domain of
RT gelatinase A.".
RL Nat. Struct. Biol. 2:938-942(1995).
RN [6]
X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 458-660.
RX MEDLINE=96140723; PubMed=8549817;
```

RA Gohlke U., Gomis-Ruth F.X., Crabbe T., Murphy G., Docherty A.J.,
RA Bode W.;
RT "The C-terminal (haemopexin-like) domain structure of human
RT gelatinase A (MMP2): structural implications for its function.";
RL FEBS Lett. 378:126-130(1996).
CC -1- CATALYTIC ACTIVITY: CLEAVAGE OF GELATIN TYPE I AND COLLAGEN TYPES
CC IV, V, VII, X. CLEAVES THE COLLAGEN-LIKE SEQUENCE PRO-GLN-GLY-|-
CC ILE-ALA-GLN.
CC -1- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
CC -1- SUBUNIT: LIGAND FOR INTEGRIN ALPHA-V/BETA-3.
CC -1- TISSUE SPECIFICITY: PRODUCED BY NORMAL SKIN FIBROBLASTS.
CC -1- SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE II-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A (ZINC
CC METALLOPROTEASE) ALSO KNOWN AS MATRININ SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J03210; AAA35701.1; -
DR EMBL; M33789; AAA52027.1; -
DR EMBL; M55593; AAA52028.1; -
DR EMBL; M58552; AAA52028.1; JOINED.
DR EMBL; M55582; AAA52028.1; JOINED.
DR EMBL; M55583; AAA52028.1; JOINED.
DR EMBL; M55584; AAA52028.1; JOINED.
DR EMBL; M55585; AAA52028.1; JOINED.
DR EMBL; M55586; AAA52028.1; JOINED.
DR EMBL; M55587; AAA52028.1; JOINED.
DR EMBL; M55588; AAA52028.1; JOINED.
DR EMBL; M55589; AAA52028.1; JOINED.
DR EMBL; M55590; AAA52028.1; JOINED.
DR EMBL; M55591; AAA52028.1; JOINED.
DR EMBL; M55592; AAA52028.1; JOINED.
DR PIR; A28153; A28153.
DR PDB; 1RG6; 10-JUN-96.
DR PDB; 1GEN; 17-AUG-96.
DR MEROPS; M10.003; -
DR MTM; 120360; -
DR InterPro: IPR000562; FN_Type_II.
DR InterPro: IPR000585; Hemopexin.
DR InterPro: IPR001818; Matrxin.
DR InterPro: IPR000130; Zn_MTPeptdse.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00138; MATRININ.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Hydrolyase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
KW Collagen degradation; Extracellular matrix; Repeat; Signal;
KW 3D-structure.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 109 ACTIVATION PEPTIDE.
FT CHAIN 110 660 72 KDA TYPE IV COLLAGENASE.
FT DOMAIN 110 221 COLLAGENASE-LIKE.
FT DOMAIN 222 396 COLLAGEN-BINDING.
FT DOMAIN 397 465 COLLAGENASE-LIKE.
FT DOMAIN 226 283 FIBRONECTIN TYPE-II 1.
FT DOMAIN 284 341 FIBRONECTIN TYPE-II 2.
FT DOMAIN 342 399 FIBRONECTIN TYPE-II 3.

FT DOMAIN 466 660 HEMOPEXIN-LIKE.
FT SITE 102 102 CYSTEINE SWITCH (POTENTIAL).
FT METAL 403 403 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 404 404 BY SIMILARITY.
FT METAL 407 407 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 413 413 ZINC (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 573 573 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 642 642 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 469 660
SQ SEQUENCE 660 AA; 73882 MW; BC7147DC8B49F289 CRC64;

Query Match 50.8%; Score 31; DB 1; Length 660;
Best Local Similarity 75.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQFFGL 10
| :|||
Db 76 KMQKFFGL 83

RESULT 113
MM02_MOUSE STANDARD; PRT; 662 AA.
ID MM02_MOUSE
AC P33434;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE 72 KDA TYPE IV COLLAGENASE PRECURSOR (EC 3.4.24.24) (72 KDA
DE GELATINASE) (MATRIX METALLOPROTEINASE-2) (MMP-2) (GELATINASE A).
GN MMP2.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=92218452; PubMed=1373140;
RA Reponen P., Sahlberg C., Huhtala P., Hurskainen T., Thesleff I.,
RA Tryggvason K.;
RT "Molecular cloning of murine 72-kDa type IV collagenase and its
RT expression during mouse development.";
RL J. Biol. Chem. 267:7856-7862(1992).
CC -1- CATALYTIC ACTIVITY: CLEAVAGE OF GELATIN TYPE I AND COLLAGEN TYPES
CC IV, V, VII, X. CLEAVES THE COLLAGEN-LIKE SEQUENCE PRO-GLN-GLY-|-
CC ILE-ALA-GLN.
CC -1- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
CC -1- SUBUNIT: LIGAND FOR INTEGRIN ALPHA-V/BETA-3.
CC -1- SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE II-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A (ZINC
CC METALLOPROTEASE) ALSO KNOWN AS MATRININ SUBFAMILY.
CC -----
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CC -----
DR EMBL; M84324; AAA39338.1; -
DR PIR; A42496; A42496.
DR HSP; P08253; 1RTG.
DR MEROPS; M10.003; -
DR MGD; MGI:97009; Mmp2.
DR InterPro: IPR000562; FN_Type_II.
DR InterPro: IPR000585; Hemopexin.
DR InterPro: IPR001818; Matrxin.
DR InterPro: IPR000130; Zn_MTPeptdse.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.


```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93249363; PubMed=7916617;
RA Marti H.P., McNeil L., Davies M., Martin J., Lovett D.H.;
RT "Homology cloning of rat 72 kDa type IV collagenase: cytokine and
second-messenger inducibility in glomerular mesangial cells.";
RL Biochem. J. 291:441-446(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Skin;
RA Okada A., Basset P.;
RT "The cloning of the cDNA encoding rat gelatinase A from a rat skin
round cDNA library.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: CLEAVAGE OF GELATIN TYPE I AND COLLAGEN TYPES
IV, V, VII, X. CLEAVES THE COLLAGEN-LIKE SEQUENCE PRO-GLN-GLY-|-
ILE-ALA-GLY-GLN.
CC -1- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
CC -1- SUBUNIT: LIGAND FOR INTEGRIN ALPHA-V/BETA-3.
CC -1- SIMILARITY: CONTAINS 1 HEMOPLEXIN-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE II-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A (ZINC
METALLOPROTEASE) ALSO KNOWN AS MATRIXIN SUBFAMILY.
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DR EMBL; X71466; CAA50583.1; -
DR EMBL; U65656; AAB41692.1; -
DR PIR; S34780; S34780.
DR HSSP; P08253; IRTG.
DR MEROPS; M10.003; -.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Matrixin.
DR InterPro; IPR000130; Zn_MTPeptidase.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00138; MATRIXIN.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Hydrolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
KW Collagen degradation; Extracellular matrix; Repeat; Signal.
FT SIGNAL
FT PROPEP 30 109
FT CHAIN 110 662
FT DOMAIN 110 221
FT DOMAIN 222 396
FT DOMAIN 397 467
FT DOMAIN 468 662
FT DOMAIN 284 341
FT DOMAIN 342 399
FT DOMAIN 468 662
FT SITE 102 102
FT METAL 403 403
FT ACT_SITE 404 404
FT METAL 407 407
FT METAL 413 413
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FT CARBOHYD 575 575 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 644 644 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 471 662 BY SIMILARITY.
FT CONFLICT 42 A -> S (IN REF. 2).
FT CONFLICT 286 A -> G (IN REF. 2).
FT CONFLICT 369 N -> S (IN REF. 2).
FT CONFLICT 435 H -> N (IN REF. 2).
FT CONFLICT 586 A -> S (IN REF. 2).
SQ SEQUENCE 662 AA; 7496B34B0A21884B CRC64;

Query Match 50.8%; Score 31; DB 1; Length 662;
Best Local Similarity 75.0%; Pred. NO. 3,1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KQQFFGL 10
DB 76 KMQKFFGL 83
| : ||||
| : ||||

RESULT 116
MM02_CHICK STANDARD; PRT; 663 AA.
AC Q90611;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE 72 KDA TYPE IV COLLAGENASE PRECURSOR (EC 3.4.24.24) (72 KDA
DE GELATINASE) (MATRIX METALLOPROTEINASE-2) (MMP-2) (GELATINASE A).
GN MMP2.
OC Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94280397; PubMed=8010954;
RA Almes R.T., French D.L., Quigley J.P.;
RT "Cloning of a 72 kDa matrix metalloproteinase (gelatinase) from
RT chicken embryo fibroblasts using gene family PCR: expression of the
RT gelatinase increases upon malignant transformation.";
RL Biochem. J. 300:729-736(1994).
RN [2]
RP SEQUENCE OF 27-41 AND 107-122.
RX MEDLINE=91161603; PubMed=1848240;
RA Chen J.-M., Almes R.T., Ward G.R., Youngleib G.L., Quigley J.P.;
RT "Isolation and characterization of a 70-kDa metalloprotease
RT (gelatinase) that is elevated in Rous sarcoma virus-transformed
RT chicken embryo fibroblasts.";
RL J. Biol. Chem. 266:5113-5121(1991).
CC -1- CATALYTIC ACTIVITY: CLEAVAGE OF GELATIN TYPE I AND COLLAGEN TYPES
IV, V, VII, X. CLEAVES THE COLLAGEN-LIKE SEQUENCE PRO-GLN-GLY-|-
ILE-ALA-GLY-GLN.
CC -1- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
CC -1- SUBUNIT: LIGAND FOR INTEGRIN ALPHA-V/BETA-3.
CC -1- TISSUE SPECIFICITY: PRODUCED BY NORMAL SKIN FIBROBLASTS.
CC -1- SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE II-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A (ZINC
METALLOPROTEASE) ALSO KNOWN AS MATRIXIN SUBFAMILY.
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DR EMBL; U07775; AAA19596.1; -
DR HSSP; P08253; IRTG.
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DR MEROPS; M10.003; --
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Matrixin.
DR InterPro; IPR000130; Zn_MTpeptdse.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00138; MATRPIXIN.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZNMG; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Hydrolase; Metalloprotease; Zinc; Zymogen; Calcium;
KW Collagen degradation; Extracellular matrix; Signal.
FT SIGNAL 1 26
FT PROPEP 27 106 ACTIVATION PEPTIDE.
FT CHAIN 107 663 72 KDA TYPE IV COLLAGENASE.
FT DOMAIN 107 218 COLLAGENASE-LIKE.
FT DOMAIN 219 393 COLLAGEN-BINDING.
FT DOMAIN 394 468 COLLAGENASE-LIKE.
FT DOMAIN 223 280 FIBRONECTIN TYPE-II 1.
FT DOMAIN 281 338 FIBRONECTIN TYPE-II 2.
FT DOMAIN 339 396 FIBRONECTIN TYPE-II 3.
FT DOMAIN 469 663 HEMOPEXIN-LIKE.
FT SITE 99 99 CYSTEINE SWITCH (POTENTIAL).
FT METAL 400 400 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 401 401 BY SIMILARITY.
FT METAL 404 404 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 410 410 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 472 663 BY SIMILARITY.
FT CONFLICT 40 40 P -> Q (IN REF. 2).
FT CONFLICT 116 116 W -> T (IN REF. 2).
FT CONFLICT 122 122 T -> I (IN REF. 2).
SQ SEQUENCE 663 AA; 74941 MW; 8D6FDA4E67C3EBCA CRC64;

Query Match 50.8%; Score 31; DB 1; Length 663;
Best Local Similarity 75.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPQPFGL 10
DB 73 KMQKFFGL 80

RESULT 117
SNWA_DICDI.
ID SNWA_DICDI STANDARD; PRT; 685 AA.
AC P54705;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SNWA PROTEIN.
OS Dictyostelium discoideum (Slime mold).
ON Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44669;
RN [1]
RX MEDLINE=97128797; PubMed=8973337;
RA Folk P., Puta P., Krpejskova L., Blahuskova A., Markos A.,
RA Rabino M., Dotti R.P.;
RT "The homolog of chromatin binding protein Bx42 identified in
RT Dictyostelium.";
RL Gene 181:229-231(1996).
CC -!- SIMILARITY: BELONGS TO THE SNW FAMILY.
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-----
DR EMBL; U43887; AAB40497.1; --
DR DictyDB; DD00074; SNWA.
FT DOMAIN 31 41 POLY-GLN.
FT DOMAIN 194 360 SNW.
FT DOMAIN 245 253 PRO-RICH.
FT DOMAIN 409 415 POLY-ASP.
FT DOMAIN 539 616 SH2-LIKE DOMAIN.
SQ SEQUENCE 685 AA; 78529 MW; 1DC8521E9997A583 CRC64;

Query Match 50.8%; Score 31; DB 1; Length 685;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQ 6
DB 27 KRPKQQ 32

RESULT 118
AKA8_RAT
ID AKA8_RAT STANDARD; PRT; 687 AA.
AC Q63014;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE A-KINASE ANCHOR PROTEIN 8 (A-KINASE ANCHOR PROTEIN 95 KDA) (AKAP 95).
GN AKAP8 OR AKAP95.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=94171800; PubMed=8125992;
RA Coghlan V.M., Langeberg L.K., Fernandez A., Lamb N.J., Scott J.D.;
RT "Cloning and characterization of AKAP 95, a nuclear protein that
RT associates with the regulatory subunit of type II cAMP-dependent
RT protein kinase.";
RL J. Biol. Chem. 269:7658-7665(1994).
CC -!- FUNCTION: ANCHORING PROTEIN THAT MEDIATES THE SUBCELLULAR
CC COMPARTMENTATION OF CAMP-DEPENDENT PROTEIN KINASE (PKA TYPE II).
CC -!- SUBUNIT: BINDS TO DIMERIC RII-ALPHA REGULATORY SUBUNIT OF PKA
CC DURING MITOSIS.
CC -!- SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX.
CC REDISTRIBUTED AND DETACHED FROM CONDENSED CHROMATIN DURING MITOSIS
CC (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED. THE PROTEIN HAS BEEN
CC DETECTED IN LIVER, FIBROBLASTS, GRANULOSA, MYOBLAST, LYMPHOMA AND
CC SERTOLI CELLS.
CC -!- PTM: PHOSPHORYLATED BY PKC.
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-----
DR EMBL; U01914; AAA95941.1; --
DR InterPro; IPR000822; Znf_C2H2.
DR SMART; SM00355; Znf_C2H2; 1.
KW Nuclear protein; Zinc-finger; DNA-binding; Phosphorylation.
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FT 2N_FING 390 412 C2H2-TYPE.
FT 2N_FING 479 502 C2H2-TYPE.
FT DOMAIN 366 375 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 568 585 RII-BINDING.
FT DOMAIN 654 657 POLY-ALA.
SQ SEQUENCE 687 AA; 76161 MW; 7535F30F18F1B9CB CRC64;

Query Match 50.8%; Score 31; DB 1; Length 687;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
:|||||
Db 456 KPKPDPFKGI 465

RESULT 119
AKA8_HUMAN STANDARD; PRT; 692 AA.
AC O43823;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE A-KINASE ANCHOR PROTEIN 8 (A-KINASE ANCHOR PROTEIN 95 KDA) (AKAP 95).
GN AKAP8 OR AKAP95.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RA Phan H., Vellaco N., Do L., Regala W., Terry A., Ganes J.,
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Attix C., Andreise T., Trantheim M., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ANCHORING PROTEIN THAT MEDIATES THE SUBCELLULAR
CC COMPARTMENTATION OF CAMP-DEPENDENT PROTEIN KINASE (PKA TYPE II).
CC -1- SUBUNIT: BINDS TO DIMERIC RII-ALPHA REGULATORY SUBUNIT OF PKA
CC DURING MITOSIS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX.
CC REDISTRIBUTED AND DETACHED FROM CONDENSED CHROMATIN DURING
CC MITOSIS.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LIVER, SKELETAL
CC MUSCLE, KIDNEY AND PANCREAS.

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CC EMBL; Y11997; CAA72722.1;
CC EMBL; AC005785; AAC62838.1;
CC MM; 604692;
CC InterPro; IPR000822; 2nf-C2H2.

DR SMART; SM00355; 2nF_C2H2; 1.
KW Nuclear protein; Zinc-finger; DNA-binding.
FT DOMAIN 107 118 POLY-GLY.
FT DOMAIN 368 377 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT ZN_FING 392 414 C2H2-TYPE.
FT ZN_FING 481 504 C2H2-TYPE.
FT DOMAIN 572 589 RII-BINDING (BY SIMILARITY).
SQ SEQUENCE 692 AA; 76108 MW; CBGD5F014FD94B66 CRC64;

Query Match 50.8%; Score 31; DB 1; Length 692;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
:|||||
Db 458 KPKPDPFKGI 467

RESULT 120
PNP_BACSU STANDARD; PRT; 704 AA.
AC P50849;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE POLYBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE
DE PHOSPHORYLASE) (PNPase) (VEGETATIVE PROTEIN 15) (VEG15).
GN PNP OR COMR.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA Luttinger A., Hahn J., Dubnau D.;
RX MEDLINE=96423178; PubMed=8825779;
RT "Polynucleotide phosphorylase is necessary for competence development
RT in Bacillus subtilis."
RL Mol. Microbiol. 19:343-356(1996).
RN [2]
RP SEQUENCE OF 1-8 FROM N.A.
RC STRAIN=168;
RA Coquard D., Huecas M., Ott M., van Dijk J., van Loon A., Hohmann H.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-20.
RC STRAIN=IS58;
RX MEDLINE=97443988; PubMed=9298659;
RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
RA Hecker M.;
RT "First steps from a two-dimensional protein index towards a response-
RT regulation map for Bacillus subtilis."
RL Electrophoresis 18:1451-1463(1997).
CC -1- FUNCTION: INVOLVED IN RNA DEGRADATION. HYDROLYSES SINGLE-STRANDED
CC POLYBONUCLEOTIDES PROGRESSIVELY IN THE 3' TO 5' DIRECTION.
CC NECESSARY FOR COMPETENCE DEVELOPMENT IN BACILLUS SUBTILIS. MAY BE
CC NECESSARY FOR MODIFICATION OF THE SREA TRANSCRIPT (STABILIZATION
CC OR TRANSLATION ACTIVATION).
CC -1- CATALYTIC ACTIVITY: RNA(N+1) + ORTHOPHOSPHATE = RNA(N) + A
CC NUCLEOSIDE DIPHOSPHATE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: CONTAINS 1 KH DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 'S1 MOTIF' DOMAIN.

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CC

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DR EMBL: U29668; AAC43595.1; -
DR EMBL: Z80835; CAB02561.1; -
DR EMBL: Z99112; CAB13542.1; -
DR HSSP: P05055; 1SR0.
DR Subtilist; BG11491; pnpA.
DR InterPro: IPR001247; 3_ExoNase.
DR InterPro: IPR000958; KH.
DR InterPro: IPR003029; S1.
DR Pfam: PF00013; KH-domain; 1.
DR Pfam: PF01138; RNase_PH; 2.
DR Pfam: PF00575; S1; 1.
DR SMART; SM00322; KH; 1.
DR SMART; SM00316; S1; 1.
DR PROSITE; PS0084; KH_TYPE_1; 1.
KW Transferase; Nucleotidyltransferase; RNA-binding; Complete proteome.
FT INIT_MET 0
FT DOMAIN 553 612 KH.
FT DOMAIN 622 690 S1 MOTIF.
SQ SEQUENCE 704 AA; 77332 MW; 0E305B6B9B0A7B07 CRC64;

Query Match 50.8%; Score 31; DB 1; Length 704;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQOFFGL 10
||| |||
Db 50 PKPLDFEPL 58
||| |||

RESULT 121
LIPS.RAT STANDARD; PRT; 768 AA.
ID LIPS.RAT STANDARD; PRT; 768 AA.
AC P15304;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HORMONE SENSITIVE LIPASE (EC 3.1.1.-) (HSL).
GN LIPE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=adipose tissue;
RX MEDLINE=89041594; PubMed=3186461;
RA Holm C., Kirchgessner T.G., Svenson K.L., Lusis A.J., Belfrage P.,
RA Schotz M.C.;
RT "Nucleotide sequence of rat adipose hormone sensitive lipase cDNA.";
RL Nucleic Acids Res. 16:9879-9879(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88336885; PubMed=3420405;
RA Holm C., Kirchgessner T.G., Svenson K.L., Fredrikson G., Nilsson S.,
RA Miller C.G., Shively J.E., Heinzmann C., Sparkes R.S., Mohandas T.,
RA Lusis A.J., Belfrage P., Schotz M.C.;
RT "Hormone-sensitive lipase: sequence, expression, and chromosomal
RT localization to 19 cent-q13.3.";
RL Science 241:1503-1506(1988).
RN [3]
RP REVISIONS TO 542-555 AND 746-768.
RC TISSUE=Adipose tissue;
RA Holm C.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IN ADIPOSE TISSUE AND HEART, IT PRIMARILY HYDROLYZES
CC STORED TRIGLYCERIDES TO FREE FATTY ACIDS, WHILE IN STEROIDOGENIC
CC TISSUES, IT PRINCIPALLY CONVERTS CHOLESTERYL ESTERS TO FREE
CC CHOLESTEROL FOR STEROID HORMONE PRODUCTION.
CC -!- ENZYME REGULATION: RAPIDLY ACTIVATED BY CAMP-DEPENDENT
CC PHOSPHORYLATION UNDER THE INFLUENCE OF CATECHOLAMINES.
CC DEPHOSPHORYLATION AND INACTIVATION ARE CONTROLLED BY INSULIN.
CC -!- PATHWAY: HORMONE SENSITIVE LIPASE CATALYZES THE RATE LIMITING
```

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CC STEP IN TRIGLYCERIDE LIPOLYSIS.
CC -!- SIMILARITY: BELONGS TO THE "GDXG" FAMILY OF LIPOLYTIC ENZYMES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X51415; CAA35777.1; -
DR PIR: S03672; LIRTH.
DR InterPro: IPR000379; Est_lip_thioest_actsite.
DR InterPro: IPR002168; Lipolytic_enzyme.
DR PROSITE; PS01173; LIPASE_GDXG_HIS; 1.
DR PROSITE; PS01174; LIPASE_GDXG_SER; 1.
KW Hydrolase; Lipid degradation; Phosphorylation.
FT ACT_SITE 349 349 POTENTIAL.
FT ACT_SITE 423 423 POTENTIAL.
FT MOD_RES 563 563 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 565 565 (BY SIMILARITY).
FT MOD_RES 565 565 PHOSPHORYLATION (BY AMPK)
FT MOD_RES 565 565 (BY SIMILARITY).
SQ SEQUENCE 768 AA; 84169 MW; 90A1F0432DAC8B4C CRC64;

Query Match 50.8%; Score 31; DB 1; Length 768;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQ 6
||| |||
Db 332 RRPQQ 337

RESULT 122
E78A.DROME STANDARD; PRT; 864 AA.
ID E78A.DROME STANDARD; PRT; 864 AA.
AC P45447;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ECDYSONE-INDUCIBLE PROTEIN E78-A (DR-78).
GN EIP78C OR E78A OR NR1E1.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RX MEDLINE=94006562; PubMed=8402914;
RA Stone B.L., Thummel C.S.;
RT "The Drosophila 78C early late puff contains E78, an ecdysone-
RT inducible gene that encodes a novel member of the nuclear hormone
RT receptor superfamily.";
RL Cell 75:307-320(1993).
RN [2]
RP SEQUENCE OF 321-433 FROM N.A.
RX MEDLINE=94060116; PubMed=8241283;
RA Martin-Blanco E., Kornberg T.B.;
RT "DR-78, a novel Drosophila melanogaster genomic DNA fragment highly
RT homologous to the DNA-binding domain of thyroid hormone-retinoid
RT acid-vitamin D receptor subfamily.";
RL Biochim. Biophys. Acta 1216:339-341(1993).
CC -!- FUNCTION: INDUCES THE EARLY LATE PUFF 78C WHICH TRIGGERS PUPARIUM
CC FORMATION AND DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC -!- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF PROTEIN E78 ARE
CC PROBABLY PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
CC -!- DEVELOPMENTAL STAGE: THE LONGER FORM, E78A, IS EXPRESSED ONLY
```

CC IN MID-PUPAL STAGES, WHILE THE SHORTER FORM, E78B, IS MAXIMALLY
CC EXPRESSED IN NEWLY FORMED PREPUPAE.
CC -|- INDUCTION: BOTH FORMS REQUIRE ECDYSONE FOR ACTIVITY. E78B ALSO
CC REQUIRES ECDYSONE-INDUCED PROTEINS FOR MAXIMAL EXPRESSION.
CC -|- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NRI SUBFAMILY.

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CC -----

DR EMBL; U01087; AAA19975.1; -
DR EMBL; U01088; AAA19976.2; -
DR EMBL; Y73045; CAA51523.1; -
DR HSP; P03372; IHQC.
DR FlyBase; FBgn004865; Eip78C.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Strdhormone_receptor.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STROIDFINGER.
DR PRINTS; PR00398; STRODHORMONER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; ZnF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Alternative splicing.
FT DNA_BIND 367 432 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 367 387 C4-TYPE.
FT ZN_FING 403 427 C4-TYPE.
FT DOMAIN 64 80 POLY-GLU.
FT DOMAIN 182 188 POLY-GLN.
FT DOMAIN 192 202 POLY-GLN.
FT DOMAIN 240 247 POLY-SER.
FT DOMAIN 271 279 POLY-SER.
FT DOMAIN 312 315 POLY-GLN.
FT DOMAIN 321 333 POLY-GLN.
FT DOMAIN 336 339 POLY-GLN.
FT DOMAIN 346 349 POLY-SER.
FT DOMAIN 354 357 POLY-ASN.
FT DOMAIN 481 486 POLY-GLN.
FT DOMAIN 490 500 POLY-GLN.
FT DOMAIN 546 554 POLY-ASN.
FT VARSPPLIC 1 474 MISSING (IN TRUNCATED E78B ISOFORM).
FT CONFLICT 321 331 OLQOOQOHOQO -> SCNSSSTSSR (IN REF. 2).
FT CONFLICT 430 433 AGMS -> VGKM (IN REF. 2).
SQ SEQUENCE 864 AA; 95865 MW; 1A5CE6C39F31E994 CRC64;

Query Match 50.8%; Score 31; DB 1; Length 864;
Best Local Similarity 66.7%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PKPQOFGFL 10
Db 335 PQOQOFGFL 343
1: || |||

RESULT 123

ID YB1C_SCHPO STANDARD; PRT; 922 AA.
AC PB7177;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 103.4 KDA TRP-ASP REPEATS CONTAINING PROTEIN C3D6.12 IN
DE CHROMOSOME II.
GN SPC3D6.12.

OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Hilbert H., Duesterhoeft A., Wood V., Rajandream M.A., Barrell B.G.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: TO YEAST DIP2.
CC -|- SIMILARITY: CONTAINS 13 WD REPEATS (TRP-ASP DOMAINS).
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DR EMBL; Z95620; CAB09121.1; -
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 11.
DR PRINTS; PR00320; GPROTEINRPT.
DR SMART; SM00320; WD40; 11.
DR PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
FT REPEAT 63 101
FT REPEAT 102 141 WD 1.
FT REPEAT 169 210 WD 2.
FT REPEAT 213 252 WD 3.
FT REPEAT 268 307 WD 4.
FT REPEAT 336 377 WD 5.
FT REPEAT 394 432 WD 6.
FT REPEAT 475 514 WD 7.
FT REPEAT 532 571 WD 8.
FT REPEAT 574 615 WD 9.
FT REPEAT 616 655 WD 10.
FT REPEAT 658 695 WD 11.
FT REPEAT 658 695 WD 12.
FT REPEAT 658 695 WD 13.
SQ SEQUENCE 922 AA; 103427 MW; 578C01A1D71162C9 CRC64;

Query Match 50.8%; Score 31; DB 1; Length 922;
Best Local Similarity 45.5%; Pred. No. 4.3e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOOFFGLM 11
Db 7 RYPTTEFGVI 17
1: -||-|||:-

RESULT 124

ID PMAB_ARATH STANDARD; PRT; 956 AA.
AC Q9LV11;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ATPASE 11, PLASMA MEMBRANE-TYPE (EC 3.6.3.6) (PROTON PUMP 11).
GN AH11 OR AT5G62670 OR MRC21.9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20181125; PubMed=10718197;

RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.,
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty PI and TAC
RL clones";
RL DNA Res. 7:31-63(2000).
CC -!- FUNCTION: THE PLASMA MEMBRANE H+ ATPASE OF PLANTS AND FUNGI
CC GENERATES A PROTON GRADIENT THAT DRIVES THE ACTIVE TRANSPORT OF
CC NUTRIENTS BY H+-SYMPORT. THE RESULTING EXTERNAL ACIDIFICATION
CC AND/OR INTERNAL ALKALIZATION MAY MEDIATE GROWTH RESPONSES (BY
CC SIMILARITY).
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(IN) = ADP + PHOSPHATE +
CC H(+)(OUT).
CC -!- SUBUNIT: BINDS TO 14-3-3 PROTEINS. THE BINDING IS INDUCED BY
CC PHOSPHORYLATION OF THR-955. BINDING TO 14-3-3 PROTEINS ACTIVATES
CC THE H+-ATPASE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
CC (E1-E2 ATPASES). SUBFAMILY IIIA.
CC -----
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CC -----
CC EMBL; AB020751; BAA97214.1; -;
DR InterPro; IPR001757; E1-E2-ATPase.
DR InterPro; IPR000695; HATPase.
DR InterPro; IPR001454; Hydrolase.
DR Pfam; PF00122; E1-E2-ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00120; HATPase.
DR PROSITE; PS00154; ATPase_E1_E2; 1.
KW Hydrolase; Hydrogen ion transport; Transmembrane; Phosphorylation;
KW ATP-binding; Metal-binding; Magnesium; Multigene family.
FT DOMAIN 1 65
FT TRANSMEM 66 85
FT DOMAIN 86 97
FT TRANSMEM 98 118
FT DOMAIN 119 247
FT TRANSMEM 248 268
FT DOMAIN 269 277
FT TRANSMEM 278 295
FT DOMAIN 296 647
FT TRANSMEM 648 669
FT DOMAIN 670 674
FT TRANSMEM 675 697
FT DOMAIN 698 713
FT TRANSMEM 714 734
FT DOMAIN 735 759
FT TRANSMEM 760 780
FT DOMAIN 781 792
FT TRANSMEM 793 813
FT DOMAIN 814 821
FT TRANSMEM 822 846
FT DOMAIN 843 956
FT MOD_RES 333 333
FT MOD_RES 955 955
FT METAL 592 592
FT METAL 596 596
FT SITE 954 956
SQ SEQUENCE 956 AA; 105122 MW; CA59212B16B9C5BD CRC64;

Query Match 50.8%; Score 31; DB 1; Length 956;
Best Local Similarity 75.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 PQOFFGLM 11

Db 480 PQOFFGLM 487
RESULT 125
ATS9 HUMAN
ID ATS9 HUMAN STANDARD; PRT; 1629 AA.
AC O9P2N4; O9NR29;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADAM-TS 9 PRECURSOR (EC 3.4.24.-) (A DISINTEGRIN AND METALLOPROTEINASE
DE WITH THROMBOSPONDIN MOTIFS 9) (ADAMTS-9) (ADAM-TS9).
GN ADAMTS9 OR KIAA1312.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eumalia; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RC TISSUE=Fetal;
RX MEDLINE=20396138; PubMed=10936055;
RA Clark M.E., Kelner G.S., Turbeville L.A., Boyer A., Arden K.A.,
RA Maki R.A.;
RT "ADAMTS 9, a novel member of the ADAM-TS/Metallopondin gene
RT family";
RL Genomics 67:343-350(2000).
RN [2]
RP SEQUENCE OF 159-1629 FROM N.A. (LONG ISOFORM).
RC TISSUE=Brain;
RX MEDLINE=20181126; PubMed=10718198;
RA Nagase T., Kikuno R., Ishikawa K.-I., Hirotsawa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVI.
RT The complete sequences of 150 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:65-73(2000).
CC -!- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED. ASSOCIATED WITH THE EXTRACELLULAR
CC MATRIX (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ALL FETAL TISSUES.
CC EXPRESSED SLIGHTLY IN ADULT OVARY, PANCREAS, HEART, KIDNEY, LUNG,
CC PLACENTA. ALSO DETECTED IN SPINAL CORD AND BRAIN. NOT DETECTED IN
CC COLON, SMALL INTESTINE, TESTIS, LIVER, SKELETAL MUSCLE, SPLEEN OR
CC THYMUS.
CC -!- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT
CC FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
CC SIMILARITY).
CC -!- PTM: THE PRECURSOR IS CLEAVED BY A URIN ENDOPEPTIDASE (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B (ZINC
CC METALLOPROTEASE); ALSO KNOWN AS THE REPROLYSIN SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
CC -!- SIMILARITY: CONTAINS 11 TSP TYPE-1 DOMAINS.
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CC -----
CC EMBL; AF261918; AAF89106.1; -;
DR EMBL; AB037733; BAA92550.1; -;
DR MM; 605421; -;
DR InterPro; IPR001590; Reprolysin.
DR InterPro; IPR000884; TSPI.
DR InterPro; IPR000130; Zn_Mtpeptdse.
DR Pfam; PF01421; Reprolysin; 1.
DR Pfam; PF00090; tsp.1; 11.
DR SMART; SM00209; TSPI; 13.

```
DR PROSITE; PS00215; ADAM_MEPRO; 1.  
DR PROSITE; PS00427; DISINTEGRINS; FALSE_NEG.  
DR PROSITE; PS00092; TSP1; 9.  
DR PROSITE; PS00142; ZINC_PROTEASE; 1.  
KW Hydrolase; Metalloprotease; zinc; Signal; Glycoprotein; Zymogen;  
FT SIGNAL 1 18  
FT PROPEP 19 287  
FT CHAIN 288 1629  
FT DOMAIN 508 587  
FT DOMAIN 589 642  
FT DOMAIN 645 752  
FT DOMAIN 753 880  
FT DOMAIN 999 1053  
FT DOMAIN 1056 1108  
FT DOMAIN 1111 1156  
FT DOMAIN 1184 1239  
FT DOMAIN 1240 1295  
FT DOMAIN 1332 1383  
FT DOMAIN 1386 1439  
FT DOMAIN 1445 1498  
FT DOMAIN 1501 1554  
FT DOMAIN 1562 1612  
FT DOMAIN 88 96  
FT SITE 223 223  
FT METAL 434 434  
FT ACT_SITE 435 435  
FT METAL 438 438  
FT METAL 444 444  
FT CARBOHYD 112 112  
FT CARBOHYD 135 135  
FT CARBOHYD 171 171  
FT CARBOHYD 749 749  
FT CARBOHYD 840 840  
FT CARBOHYD 1213 1213  
FT CARBOHYD 1267 1267  
FT VARSPPLIC 1064 1064  
FT VARSPPLIC 1073 1629  
FT - CONFLICT 367 367  
SQ SEQUENCE 1629 AA; 182649 MW; C1C4CEFF58B8941F CRC64;  
  
Query Match 50.8%; Score 31; DB 1; Length 1629;  
Best Local Similarity 83.3%; Pred. No. 7.5e+02;  
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|||||  
Db 875 KPQQFY 880  
  
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ID ACVS_CEPAC  
AC P25464;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE DELTA-(L-ALPHA-AMINOADIPYL)-L-CYSTEINYL-D-VALINE SYNTHETASE  
DE (EC 6.-.-.-) (ACV SYNTHETASE) (ACVS).  
GN PCBAB.  
OS Cephalosporium acremonium (Acremonium chrysogenum).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreales; Hypocreaceae; mitosporic Hypocreaceae; Acremonium.  
OX NCBI_TaxID=5044;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=91177827; PubMed=1706706;  
RX Gutierrez S., Diez B., Montenegro E., Martin J.F.;  
RT "Characterization of the Cephalosporium acremonium pcbab gene  
encoding alpha-aminoadipyl-cysteine-yl-valine synthetase, a large  
RT multidomain peptide synthetase: linkage to the pcbab gene as a cluster
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RT of early cephalosporin biosynthetic genes and evidence of multiple  
RT functional domains.";  
RL J. Bacteriol. 173:2354-2365(1991).  
RN [2]  
RP PARTIAL SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC STRAIN=ATCC 11550;  
RX MEDLINE=91168300; PubMed=2076552;  
RA Hoskins J.A., O'Callaghan N., Queener S.W., Cantwell C.A., Wood J.S.,  
RA Chen V.J., Skatrud P.L.;  
RT "Gene disruption of the pcbab gene encoding ACV synthetase in  
Cephalosporium acremonium.";  
RL Curr. Genet. 18:523-530(1990).  
CC -|- FUNCTION: EACH OF THE CONSTITUENT AMINO ACIDS OF THE TRIPEPTIDE  
CC ACV ARE ACTIVATED AS AMINOACYL-ADENYLATES WITH PEPTIDE BONDS  
CC FORMED THROUGH THE PARTICIPATION OF AMINO ACID THIOLESTER  
CC INTERMEDIATES.  
CC -|- COFACTOR: CONTAINS 3 COVALENTLY BOUND PHOSPHOPANTETHEINES  
CC (POTENTIAL).  
CC -|- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF PENICILLIN AND  
CC CEPHALOSPORIN.  
CC -|- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME  
CC FAMILY.  
CC PIR; A38531; YGCEVC.  
DR HSPP; P14687; IAMU.  
DR InterPro; IPR000873; AMP-bind.  
DR InterPro; IPR001242; DUF4.  
DR InterPro; IPR000379; Est_lip_thioest_actsite.  
DR InterPro; IPR003880; Phosphopant_attach.  
DR InterPro; IPR001031; Thioesterase.  
DR Pfam; PF00501; AMP-binding; 3.  
DR Pfam; PF00668; Condensation; 3.  
DR Pfam; PF00550; pp-binding; 3.  
DR Pfam; PF00975; Thioesterase; 1.  
DR PRINTS; PR00154; AMPBINDING.  
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 2.  
DR PROSITE; PS00455; AMP_BINDING; 3.  
DR PROSITE; PS00075; ACP_DOMAIN; 3.  
DR Repeat; Antibiotic biosynthesis; Multifunctional enzyme;  
KW Repeat; Phosphopantetheine.  
FT REPEAT 234 1062 DOMAIN 1 (ADIPATE-ACTIVATING).  
FT REPEAT 1335 2162 DOMAIN 2 (CYSTEINE-ACTIVATING).  
FT REPEAT 2409 3387 DOMAIN 3 (VALINE-ACTIVATING).  
FT DOMAIN 795 864 ACYL CARRIER (ACP) 1.  
FT DOMAIN 1880 1953 ACYL CARRIER (ACP) 2.  
FT DOMAIN 2960 3027 ACYL CARRIER (ACP) 3.  
FT BINDING 827 827 PHOSPHOPANTETHEINE (BY SIMILARITY).  
FT BINDING 1916 1916 PHOSPHOPANTETHEINE (BY SIMILARITY).  
FT BINDING 2990 2990 PHOSPHOPANTETHEINE (BY SIMILARITY).  
FT ACT_SITE 3568 3568 THIOESTERASE (BY SIMILARITY).  
SQ SEQUENCE 3712 AA; 414767 MW; 4EE3C1EB5EBEF9B7 CRC64;  
  
Query Match 50.8%; Score 31; DB 1; Length 3712;  
Best Local Similarity 71.4%; Pred. No. 1.7e+03;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 RPKPOQF 7  
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Db 2189 RRPQAQF 2195  
  
RESULT 127  
ABCL_MOUSE STANDARD; PRT; 2261 AA.  
ID ABCL_MOUSE  
AC P41233;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 20-AUG-2001 (Rel. 40, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE ATP-BINDING CASSETTE, SUB-FAMILY A, MEMBER 1 (ATP-BINDING CASSETTE  
DE TRANSPORTER 1) (ATP-BINDING CASSETTE 1) (ABC-1).  
GN ABCAL OR ABCL.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2; TISSUE=Macrophage;
RX MEDLINE=94375008; PubMed=8088782;
RA Luciani M.F., Denicot F., Savary S., Mattei M.-G., Chimini G.;
RT "Cloning of two novel ABC transporters mapping on human chromosome
9.";
RL Genomics 21:150-159(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Qiu Y., Cavellier L., Chiu S., Rubin E., Cheng J.-F.;
RT "Human and mouse ABCA1 comparative sequencing and transgenesis studies
identify potential regulatory sequences";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION
CC TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL
CC TRANSPORT (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT TISSUES. HIGHEST
CC LEVELS ARE FOUND IN PREGNANT UTERUS AND UTERUS.
CC -1- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,
CC EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN
CC ATP BINDING CASSETTE (ABC) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC (ABC TRANSPORTERS). MDR SUBFAMILY.

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CC or send an email to license@sib-sib.ch).

DR EMBL; X75926; CAA53530.1; ALT_INIT.
DR EMBL; AF287263; AAG39073.1; ALT_INIT.
DR MGD; MGI:99607; Abca1.
DR InterPro; IPR003593; AAA.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR001687; ATP_GTP_A.
DR InterPro; IPR003838; DUF214.
DR InterPro; IPR001865; Ribosomal_S2.
DR InterPro; IPR000897; SRP54.
DR Pfam; PF00005; ABC_tran; 2.
DR Pfam; PF02687; DUF214; 1.
DR Pfam; PF00318; Ribosomal_S2; 1.
DR Pfam; PF00448; SRP54; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Glycoprotein; Transmembrane; Transport.
FT TRANSMEM 26 42 POTENTIAL.
FT TRANSMEM 640 656 POTENTIAL.
FT TRANSMEM 690 706 POTENTIAL.
FT TRANSMEM 717 733 POTENTIAL.
FT TRANSMEM 749 765 POTENTIAL.
FT TRANSMEM 771 787 POTENTIAL.
FT TRANSMEM 1041 1057 POTENTIAL.
FT TRANSMEM 1351 1367 POTENTIAL.
FT TRANSMEM 1661 1677 POTENTIAL.
FT TRANSMEM 1708 1724 POTENTIAL.
FT TRANSMEM 1737 1753 POTENTIAL.
FT TRANSMEM 1775 1791 POTENTIAL.
FT TRANSMEM 1854 1870 POTENTIAL.
FT NP_BIND 933 940 ATP (POTENTIAL).
FT NP_BIND 1946 1953 ATP (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 349 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 521 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 820 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1294 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 1504 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2044 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 1567 1568 MISSING (IN REF. 2).
FT CONFLICT 2024 2024 MISSING (IN REF. 2).
SQ SEQUENCE 2261 AA; 254011 MW; FAEG2B21FD1D09F9 CRC64;

Query Match 50.0%; Score 30.5; DB 1; Length 2261;
Best Local Similarity 77.8%; Pred. NO. 1.3e+03;
Matches 7; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Oy 3 KP-QOFFGL 10
Db 2153 KPQVEFFGL 2161

Search completed: April 1, 2002, 16:20:17
Job time: 163 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 1, 2002, 16:18:20 ; Search time 38.86 Seconds

(without alignments)
20.968 Million cell updates/sec

Title: US-09-988-792-2

Perfect score: 71

Sequence: 1 RPKPQQWFWM 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 434

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 50%

Maximum Match 100%

Listing first 1000 summaries

Database :

A_Geneseq_1101.*

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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	71	100.0	11	4	Sequence of peptid
2	71	100.0	11	9	Sequence of neurop
3	71	100.0	11	19	Substance P analog
4	71	100.0	11	20	Human tachykinin a
5	71	100.0	11	22	Chimeric analgesic
6	71	100.0	11	22	Tachykinins peptid
7	71	100.0	12	22	Chimeric analgesic
8	68	95.8	11	5	Substance P analog
9	68	95.8	11	9	Sequence of neurop
10	68	95.8	11	9	Sequence of neurop
11	68	95.8	11	11	D-arginine 1, D-pr

12	68	95.8	11	12	Substance P analog
13	68	95.8	11	19	Substance P analog
14	68	95.8	11	19	Human tachykinin a
15	68	95.8	11	20	Tachykinins peptid
16	68	95.8	11	22	Galanin(1-12)-Pro-
17	68	95.8	24	13	Galanin peptide SE
18	68	95.8	24	22	Galanin peptide SE
19	68	95.8	24	22	Spantide analogue,
20	66	93.0	11	16	Substance P analog
21	66	93.0	11	20	Substance P analog
22	66	93.0	11	20	Substance P analog
23	61	85.9	11	9	Sequence of neurop
24	61	85.9	11	19	Chimeric analgesic
25	61	85.9	11	22	Tachykinins peptid
26	61	85.9	11	22	Chimeric analgesic
27	61	85.9	12	22	Substance P analog
28	60	84.5	11	5	Substance P analog
29	60	84.5	11	9	Substance P analog
30	60	84.5	11	19	Substance P analog
31	60	84.5	11	19	Substance P analog
32	60	84.5	11	19	Substance P analog
33	60	84.5	11	21	Amino acid sequenc
34	60	84.5	11	22	Tachykinins peptid
35	57	80.3	11	21	Amino acid sequenc
36	54	76.1	8	9	Sequence of neurop
37	54	76.1	8	19	Substance P analog
38	51	71.8	11	13	Bradykinin recepto
39	50	70.4	11	4	Sequence of peptid
40	49	69.0	11	13	Substance P [Tyr7]
41	49	69.0	11	13	Neurokinine 1 liga
42	49	69.0	11	20	Human tachykinin a
43	48	67.6	8	9	Sequence of neurop
44	48	67.6	8	12	Substance P analog
45	48	67.6	8	12	Substance P analog
46	48	67.6	11	7	Sequence of undeca
47	48	67.6	11	9	Sequence of neurop
48	48	67.6	11	9	Sialic acid-bonded
49	48	67.6	11	12	Undecapeptide subs
50	48	67.6	11	12	Substance P [Me-Le
51	48	67.6	11	13	Substance P [MeMet
52	48	67.6	11	13	Substance P [Me-Ph
53	48	67.6	11	13	Substance P [Me-Gl
54	48	67.6	11	13	Substance P [Me-Gl
55	48	67.6	11	13	Substance P [p-Chl
56	48	67.6	11	13	Substance P. Synt
57	48	67.6	11	13	Neurokinin 1 recep
58	48	67.6	11	14	Neurokinin 1 recep
59	48	67.6	11	14	Substance P peptid
60	48	67.6	11	16	Substance P report
61	48	67.6	11	20	Non-crosslinked pr
62	48	67.6	11	20	Substance P. Synt
63	48	67.6	11	20	Human tachykinin a
64	48	67.6	11	20	Human tachykinin a
65	48	67.6	11	20	Human tachykinin a
66	48	67.6	11	20	Human tachykinin a
67	48	67.6	11	20	Substance P deriva
68	48	67.6	11	21	Peptide substrate
69	48	67.6	11	21	Human/rat tachykin
70	48	67.6	11	21	Cell differentiat
71	48	67.6	11	22	Amino acid sequenc
72	48	67.6	11	22	Substance P peptid
73	48	67.6	11	22	Amino acid sequenc
74	48	67.6	11	22	Chimeric analgesic
75	48	67.6	11	22	Chimeric analgesic
76	48	67.6	11	22	Substance P analog
77	48	67.6	11	22	Sequence of neurop
78	48	67.6	11	22	Sequence of neurop
79	48	67.6	11	22	Sequence of neurop
80	48	67.6	11	22	Sequence of neurop
81	48	67.6	11	22	Sequence of neurop
82	48	67.6	11	22	Sequence of neurop
83	48	67.6	11	22	Sequence of neurop
84	48	67.6	11	22	Sequence of neurop

262 886 60

85	48	67.6	11	22	AAB82070	Substance P, Unid	158	43	60.6	10	6	AAP50633	Substance P-like P
86	48	67.6	11	22	AAB91411	Tachykinins peptid	159	43	60.6	10	13	AAR21933	Human tachykinin a
87	48	67.6	11	22	AAB91436	Tachykinins peptid	160	43	60.6	10	20	AAW92663	Tachykinins peptid
88	48	67.6	11	22	AAB91449	Tachykinins peptid	161	43	60.6	10	22	AAB91427	Tachykinins peptid
89	48	67.6	11	22	AAB91450	Tachykinins peptid	162	43	60.6	10	22	AAB91427	Tachykinins peptid
90	48	67.6	11	22	AAB50544	Prolyl endopeptida	163	43	60.6	10	22	AAB91445	Tachykinins peptid
91	48	67.6	11	22	AAB50306	Substance P, Unid	164	43	60.6	11	13	AAR21945	Substance P [pro 1
92	48	67.6	12	14	AAR32798	Tyr-1 substance P	165	43	60.6	11	13	AAR21936	Substance P or (-
93	48	67.6	12	16	AAW85244	Substance P analog	166	43	60.6	11	13	AAR21941	Substance P [pglu
94	48	67.6	12	20	AAW03157	Substance P-Glycin	167	43	60.6	11	13	AAR21944	Human tachykinin a
95	48	67.6	12	20	AAW94412	Cancer protease-se	168	43	60.6	11	20	AAW92709	Human tachykinin a
96	48	67.6	12	22	AAW62769	Amino acid sequenc	169	43	60.6	11	20	AAW92717	Human tachykinin a
97	48	67.6	12	22	AAW62772	Amino acid sequenc	170	43	60.6	11	20	AAW92718	Human tachykinin a
98	48	67.6	12	22	AAW62775	Amino acid sequenc	171	43	60.6	11	20	AAW92667	Human tachykinin a
99	48	67.6	12	22	AAW84528	Amino acid sequenc	172	43	60.6	11	20	AAW92668	Human tachykinin a
100	48	67.6	12	22	AAW98867	Chimeric analgesic	173	43	60.6	11	20	AAW92670	Human tachykinin a
101	48	67.6	12	22	AAW98870	Chimeric analgesic	174	43	60.6	11	20	AAW92672	Human tachykinin a
102	48	67.6	12	22	AAW98871	Chimeric analgesic	175	43	60.6	11	21	AAW08614	Peptide identified
103	48	67.6	13	20	AAW03158	Substance P-Glycin	176	43	60.6	11	22	AAW99350	Substance P tachy
104	48	67.6	13	22	AAW62770	Amino acid sequenc	177	43	60.6	898	18	AAW14777	Granulosis virus 1
105	48	67.6	13	22	AAW62773	Amino acid sequenc	178	43	60.6	902	18	AAW14285	H. armigera granu
106	48	67.6	13	22	AAW62776	Amino acid sequenc	179	43	60.6	7	4	AAP30469	Sequence of poly
107	48	67.6	13	22	AAW98868	Chimeric analgesic	180	42	59.2	11	13	AAR21960	Cyclic substance P
108	48	67.6	13	22	AAW98871	Chimeric analgesic	181	42	59.2	11	13	AAR21939	Substance P [ile 8
109	48	67.6	13	22	AAW98874	Chimeric analgesic	182	42	59.2	11	13	AAR21949	Substance P [pro 3
110	48	67.6	14	20	AAW03159	Substance P-Glycin	183	42	59.2	11	20	AAW92683	Human tachykinin a
111	48	67.6	14	22	AAW62771	Amino acid sequenc	184	42	59.2	11	20	AAW92669	Human tachykinin a
112	48	67.6	14	22	AAW62774	Amino acid sequenc	185	42	59.2	11	20	AAW92673	Human tachykinin a
113	48	67.6	14	22	AAW62777	Amino acid sequenc	186	42	59.2	11	22	AAW49755	Complex sugar bou
114	48	67.6	14	22	AAW98869	Chimeric analgesic	187	42	59.2	398	22	AAW04896	Human transporter
115	48	67.6	14	22	AAW98872	Chimeric analgesic	188	41	57.7	8	19	AAW50976	Substance P analog
116	48	67.6	14	22	AAW98875	Chimeric analgesic	189	41	57.7	8	20	AAW92711	Human tachykinin a
117	48	67.6	14	22	AAW91440	Tachykinins peptid	190	41	57.7	9	13	AAR21932	Substance P (1-9)
118	48	67.6	20	21	AAW06258	Substance P analog	191	41	57.7	9	20	AAW03162	Substance P [fragme
119	48	67.6	129	8	AAP70431	Human beta-preprot	192	41	57.7	9	20	AAW92665	Human tachykinin a
120	48	67.6	129	8	AAW99353	Human atypical tac	193	41	57.7	9	22	AAW62780	Amino acid sequenc
121	48	67.6	129	18	AAW16339	DAB389-SP-Gly fusi	194	41	57.7	9	22	AAW98878	Chimeric analgesic
122	48	67.6	129	18	AAW26510	Amyloid precursor	195	41	57.7	9	22	AAW91444	Tachykinins peptid
123	48	67.6	129	18	AAW26394	Amyloid precursor	196	41	57.7	10	22	AAW91410	Tachykinins peptid
124	48	67.6	129	19	AAW44745	APP-REP 751 protei	197	41	57.7	10	22	AAW91422	Tachykinins peptid
125	48	67.6	129	19	AAW42979	Amyloid precursor	198	41	57.7	10	22	AAW91432	Tachykinins peptid
126	48	67.6	129	14	AAW45229	APP-REP 751 amyloi	199	41	57.7	11	13	AAR21940	Substance P [pro 1
127	48	67.6	129	18	AAW26509	Amyloid precursor	200	41	57.7	11	20	AAW92716	Human tachykinin a
128	48	67.6	129	18	AAW26393	Amyloid precursor	201	41	57.7	11	20	AAW92721	Human tachykinin a
129	48	67.6	129	19	AAW44744	APP-REP 751 protei	202	41	57.7	17	21	AAW06257	Substance P analog
130	48	67.6	129	19	AAW42978	Amyloid precursor	203	41	57.7	163	20	AAV37658	Tachykinins peptid
131	47	66.2	11	13	AAR21958	Substance P [ala 9	204	40	56.3	10	22	AAW91451	Protein which is s
132	47	66.2	11	20	AAW92674	Human tachykinin a	205	40	56.3	11	13	AAR21965	Tachykinins peptid
133	47	66.2	11	20	AAW92675	Human tachykinin a	206	40	56.3	11	13	AAR21964	Cyclic substance P
134	46	64.8	11	13	AAR21935	Substance P [pro 9	207	40	56.3	11	20	AAW92682	Substance P [D-Ala
135	46	64.8	11	13	AAR21943	Substance P [Met 7	208	40	56.3	11	22	AAW50311	Human tachykinin a
136	46	64.8	11	18	AAW13611	Spantide II, a sub	209	40	56.3	155	20	AAW94272	Prevlin peptide #3
137	46	64.8	11	20	AAW92677	Human tachykinin a	210	40	56.3	155	20	AAW94272	Fat-derived eosino
138	46	64.8	11	20	AAW92678	Human tachykinin a	211	40	56.3	188	22	AAW81317	Human AFP protein
139	46	64.8	11	20	AAW92671	Human tachykinin a	212	40	56.3	285	21	AAG15373	Arabidopsis thalia
140	46	64.8	11	22	AAW91415	Tachykinins peptid	213	40	56.3	285	21	AAG31456	Arabidopsis thalia
141	46	64.8	11	22	AAW91429	Tachykinins peptid	214	40	56.3	289	21	AAW79683	Arabidopsis thalia
142	45	63.4	8	19	AAW50973	Substance P analog	215	40	56.3	293	21	AAW75337	Neisseria meningit
143	45	63.4	8	19	AAW50975	Substance P analog	216	40	56.3	293	21	AAW75338	Neisseria meningit
144	45	63.4	11	13	AAR21937	Substance P or (-	217	40	56.3	293	21	AAW75339	Neisseria meningit
145	45	63.4	11	13	AAR21951	Substance P [Glu 3	218	40	56.3	317	21	AAG15372	Arabidopsis thalia
146	45	63.4	11	13	AAR28445	Neurokinine 1 liga	219	40	56.3	317	21	AAG40241	Arabidopsis thalia
147	45	63.4	11	14	AAR42649	Neurokinin 1 recep	220	40	56.3	321	21	AAG31455	Arabidopsis thalia
148	45	63.4	11	16	AAW09003	Substance P analog	221	40	56.3	363	21	AAW19416	A prenyltransferas
149	45	63.4	11	18	AAW33181	Mono-DTPA-Lys1 Sub	222	40	56.3	367	21	AAG15371	Arabidopsis thalia
150	45	63.4	11	19	AAW79775	Substance P, Mamm	223	40	56.3	367	21	AAG40240	Arabidopsis thalia
151	45	63.4	11	20	AAW99689	Substance P analog	224	40	56.3	370	20	AAW30648	A mechanotically sen
152	45	63.4	11	20	AAW92679	Human tachykinin a	225	40	56.3	371	21	AAG31454	Arabidopsis thalia
153	45	63.4	11	22	AAW91402	Tachykinins peptid	226	40	56.3	411	20	AAV34133	Human potassium ch
154	45	63.4	11	22	AAW91409	Tachykinins peptid	227	40	56.3	411	20	AAV28496	h-TREK1 polypeptid
155	45	63.4	455	20	AAV37217	Amino acid sequenc	228	40	56.3	411	20	AAV28497	Mouse h-TREK1 poly
156	44	62.0	11	21	AAW92927	Spantide II peptid	229	40	56.3	411	22	AAW50044	Human TREK, Homo
157	43	60.6	7	4	AAP30468	Sequence of poly	230	40	56.3	429	22	AAU14300	Human novel protei

231	40	56.3	476	22	AAM23959	Human EST encoded	304	38	53.5	405	12	AAR14404	Protein 7.2 (1.3-f
232	40	56.3	620	21	AAG35791	Arabidopsis thalia	305	38	53.5	405	13	AAR28840	HeLa cell fucosylt
233	40	56.3	639	22	AAB95440	Human protein sequ	306	38	53.5	405	15	AAR45937	A glycosyltransfer
234	40	56.3	725	21	AAG35790	Arabidopsis thalia	307	38	53.5	405	18	AAM13641	Human alpha(1,3)-f
235	40	56.3	797	21	AAG35789	Arabidopsis thalia	308	38	53.5	405	18	AAM11821	Human myeloid leri
236	40	56.3	1333	15	AAR63224	Cobra partial CVF2	309	38	53.5	412	19	AAW98765	H. pylori GHP0 111
237	40	56.3	1333	20	AAV23730	Partial cobra veno	310	38	53.5	445	15	AAW24153	Bovine LOX-1 extra
238	39	54.9	7	5	AAP40480	Substance P analog	311	38	53.5	496	15	AAR45938	A glycosyltransfer
239	39	54.9	12	21	AAV76923	HIV-1 gp41 inhibit	312	38	53.5	530	12	AAR14405	Protein 1 (1.3-fuc
240	39	54.9	12	21	AAV76931	HIV-1 gp41 inhibit	313	38	53.5	789	19	AAW39927	Human Arnt recepto
241	39	54.9	16	21	AAV76945	HIV-1 gp41 inhibit	314	38	53.5	901	13	AAW26790	Viral enhancing fa
242	39	54.9	18	21	AAV76946	HIV-1 gp41 inhibit	315	38	53.5	901	15	AAW39633	VEF. Trichoplusia
243	39	54.9	20	21	AAV76947	HIV-1 gp41 inhibit	316	38	53.5	1184	20	AAW24445	Human nucleotide p
244	39	54.9	98	22	AAG76780	Human colon cancer	317	38	53.5	1184	21	AAV66657	Membrane-bound pro
245	39	54.9	350	18	AAW14532	Human chimeric fuc	318	38	53.5	1184	22	AAU12377	Human PRO1188 poly
246	39	54.9	359	18	AAW14524	Human chimeric fuc	319	38	53.5	1184	22	AAW65180	Human PRO1188 (UNQ
247	39	54.9	359	18	AAW14529	Human chimeric fuc	320	38	53.5	1528	17	AAW95333	Manduca sexta Bac1
248	39	54.9	359	18	AAW14531	Human chimeric fuc	321	38	53.5	1528	20	AAW90182	Manduca sexta Bt t
249	39	54.9	360	18	AAW14512	Human chimeric fuc	322	38	53.5	1721	19	AAW48299	Cryptosporidium pa
250	39	54.9	360	18	AAW14526	Human chimeric fuc	323	38	53.5	1721	21	AAW11727	Portion of Cryptos
251	39	54.9	360	18	AAW14513	Human chimeric fuc	324	38	53.5	1837	21	AAW11726	Cryptosporidium pa
252	39	54.9	360	18	AAW14516	Human chimeric fuc	325	37.5	52.8	220	21	AAW73464	Human secreted pro
253	39	54.9	361	12	AAR13749	GDP-Fuc:(beta-D-Ga	326	37.5	52.8	487	22	AAW73515	Human transferrase
254	39	54.9	361	15	AAW45934	A glycosyltransfer	327	37.5	52.8	543	19	AAW72196	HSV-2 strain SB5 C
255	39	54.9	361	18	AAW23806	Human alpha 1.3/4	328	37.5	52.8	1196	19	AAW72105	HSV-2 strain SB5 C
256	39	54.9	361	18	AAW13638	Human alpha(1.3/1,	329	37	52.1	5	20	AAW99687	Substance P analog
257	39	54.9	361	18	AAW14517	Human chimeric fuc	330	37	52.1	6	5	AAW40521	Sequence of substa
258	39	54.9	361	18	AAW14518	Human chimeric fuc	331	37	52.1	9	20	AAV28521	Beta-1 integrin ce
259	39	54.9	361	18	AAW14520	Human chimeric fuc	332	37	52.1	9	21	AAW19063	Anino acid sequenc
260	39	54.9	361	22	AAG64452	Human Lewis enzyme	333	37	52.1	11	13	AAW21969	Cyclic substance P
261	39	54.9	374	15	AAW45939	Human CLOCK protei	334	37	52.1	11	13	AAW21961	Cyclic substance P
262	39	54.9	374	18	AAW13642	A glycosyltransfer	335	37	52.1	11	20	AAW92684	Human tachykinin a
263	39	54.9	463	20	AAV34697	Chlamydia pneumoni	336	37	52.1	11	20	AAW92686	Human tachykinin a
264	39	54.9	626	20	AAV68292	Human transcrip tio	337	37	52.1	11	22	AAW92688	Tachykinins peptid
265	39	54.9	816	19	AAW68094	Mouse neuronal PAS	338	37	52.1	11	22	AAW91438	Galanin(1-12)-Pro-
266	39	54.9	824	19	AAW68093	Human neuronal PAS	339	37	52.1	130	19	AAW80717	S. pneumoniae prot
267	39	54.9	846	19	AAW79533	Human CLOCK protei	340	37	52.1	181	21	AAW15532	Arabidopsis thalia
268	39	54.9	846	21	AAW84565	Human HSCLOCK poly	341	37	52.1	196	21	AAW44853	Streptococcus pneu
269	39	54.9	855	19	AAW79529	Mouse CLOCK protei	342	37	52.1	248	21	AAW87087	Human secreted pro
270	39	54.9	855	19	AAW79529	Mouse CLOCK protei	343	37	52.1	248	21	AAW23892	Human EST encoded
271	39	54.9	855	21	AAV32214	Pinus radiata cell	344	37	52.1	248	22	AAW60604	Human gene 24 enco
272	39	54.9	998	21	AAW25556	Sequence of neurop	345	37	52.1	265	20	AAW02283	Secreted protein c
273	38	53.5	6	9	AAP80319	Substance P antago	346	37	52.1	272	19	AAW40215	Human macrophage a
274	38	53.5	6	12	AAR15360	Substance P analog	347	37	52.1	342	15	AAW63215	Human alpha-1,3-fu
275	38	53.5	6	19	AAW50977	Substance P analog	348	37	52.1	342	15	AAW63215	Human alpha-1,3-fu
276	38	53.5	6	19	AAW50971	Substance P analog	349	37	52.1	342	20	AAV27558	Murine alpha1,3-fuc
277	38	53.5	6	22	AAW91403	Tachykinins peptid	350	37	52.1	359	21	AAW80995	Murine alpha-1,3-f
278	38	53.5	6	22	AAW91406	Tachykinins peptid	351	37	52.1	359	21	AAW80996	Human alpha-1,3-fu
279	38	53.5	7	22	AAW91400	Tachykinins peptid	352	37	52.1	388	22	AAW75230	Drosophila gustato
280	38	53.5	11	18	AAV22688	Neurokinin recepto	353	37	52.1	530	21	AAW43300	Human ORFX ORF3064
281	38	53.5	11	19	AAW60208	Peptide NFF1, a su	354	37	52.1	565	21	AAW18569	Amino acid sequenc
282	38	53.5	11	21	AAV67965	Carboxyfluorescein	355	37	52.1	616	21	AAW56941	Human prostate can
283	38	53.5	64	22	AAW17253	Peptide #3687 enco	356	37	52.1	697	21	AAW27790	Arabidopsis thalia
284	38	53.5	64	22	AAW29748	Peptide #3785 enco	357	37	52.1	717	21	AAW18609	Arabidopsis thalia
285	38	53.5	64	22	AAW04944	Peptide #3626 enco	358	37	52.1	717	21	AAW53129	Arabidopsis thalia
286	38	53.5	91	21	AAW11745	C. parvum Iowa iso	359	37	52.1	735	21	AAW27789	Arabidopsis thalia
287	38	53.5	124	21	AAW11742	C. parvum Iowa iso	360	37	52.1	745	21	AAW27788	Arabidopsis thalia
288	38	53.5	128	21	AAW11738	C. parvum Iowa iso	361	37	52.1	755	21	AAW18608	Arabidopsis thalia
289	38	53.5	130	21	AAW11739	C. parvum Iowa iso	362	37	52.1	755	21	AAW53128	Arabidopsis thalia
290	38	53.5	130	21	AAW11740	C. parvum Iowa iso	363	37	52.1	765	21	AAW18607	Arabidopsis thalia
291	38	53.5	138	21	AAW11741	C. parvum Iowa iso	364	37	52.1	765	21	AAW53127	Arabidopsis thalia
292	38	53.5	150	21	AAW11744	C. parvum Iowa iso	365	37	52.1	874	22	AAW72287	Murine ADAMTS-9 am
293	38	53.5	159	21	AAW11730	Cryptosporidium pa	366	37	52.1	958	21	AAW21255	Human metalloprote
294	38	53.5	159	21	AAW11735	Cryptosporidium pa	367	37	52.1	1073	21	AAW21264	Human metalloprote
295	38	53.5	175	21	AAW11743	C. parvum Iowa iso	368	37	52.1	1081	22	AAW95514	Human protein sequ
296	38	53.5	249	21	AAW11746	C. parvum NINC iso	369	37	52.1	1241	21	AAW42626	Human ORFX ORF2390
297	38	53.5	270	17	AAW99586	Low density lipopr	370	37	52.1	1306	21	AAW41456	Human ORFX ORF1220
298	38	53.5	270	20	AAV24152	Bovine LDL recepto	371	37	52.1	1882	22	AAW72286	Human ADAMTS-9 am
299	38	53.5	273	17	AAW99587	Low density lipopr	372	37	52.1	1934	22	AAW72301	Human ADAMTS-9 alt
300	38	53.5	273	17	AAW99588	Low density lipopr	373	37	52.1	3025	22	AAW99684	HIV-1 subtype C pr
301	38	53.5	273	20	AAV24151	Human LDL receptor	374	36.5	51.4	10	20	AAW99684	Substance P analog
302	38	53.5	405	11	AAW08119	CDX, a MILA involy	375	36.5	51.4	10	22	AAW66675	Tachykinin peptide
303	38	53.5	405	12	AAW13752	GDP-Fuc:beta-D-Gal	376	36.5	51.4	147	22	AAW75739	Human colon cancer

377 36.5 51.4 332 21 AAY71125 Human mitogenic re
378 36.5 51.4 364 21 AAY71119 Human mitogenic re
379 36 50.7 9 6 AAP50634 Substance P-like p
380 36 50.7 9 20 AAW92714 Human tachykinin a
381 36 50.7 9 22 AAB91435 Tachykinins peptid
382 36 50.7 9 22 AAB91446 Tachykinins peptid
383 36 50.7 11 22 AAB91437 Tachykinins peptid
384 36 50.7 12 19 AAW50967 Substance P analog
385 36 50.7 12 13 AAY76928 HIV-1 gp41 inhibit
386 36 50.7 12 13 AAR25993 Vertebrate Stromel
387 36 50.7 16 21 AAY76932 HIV-1 gp41 inhibit
388 36 50.7 16 21 AAY76943 HIV-1 gp41 inhibit
389 36 50.7 20 21 AAY76944 HIV-1 gp41 inhibit
390 36 50.7 39 22 AAM21536 Peptide #7970 enco
391 36 50.7 39 22 AAM37805 Peptide #11842 enc
392 36 50.7 46 21 AAG04268 Arabidopsis thalia
393 36 50.7 51 21 AAB44870 Human secreted pro
394 36 50.7 51 21 AAG04267 Arabidopsis thalia
395 36 50.7 83 21 AAG02778 Human secreted pro
396 36 50.7 89 21 AAG17699 Arabidopsis thalia
397 36 50.7 108 21 AAG04030 Human secreted pro
398 36 50.7 110 21 AAG01279 Human secreted pro
399 36 50.7 163 21 AAY54324 Amino acid sequenc
400 36 50.7 183 21 AAB08448 A human prostate s
401 36 50.7 200 21 AAB25378 Pinus radiata cell
402 36 50.7 218 21 AAB08446 A human prostate s
403 36 50.7 218 21 AAB08447 A human prostate s
404 36 50.7 318 22 AAB88540 Haemophilus influe
405 36 50.7 318 22 AAB60654 Haemophilus influe
406 36 50.7 359 20 AAY04133 Human Wnt-5b prote
407 36 50.7 359 21 AAY57271 Wnt-4AF and Wnt-5c
408 36 50.7 363 20 AAY04134 Human Wnt-5b prote
409 36 50.7 365 21 AAY70739 Human Wnt-5a prote
410 36 50.7 365 21 AAY57600 Human Wnt-5a prote
411 36 50.7 365 22 AAB73619 Wnt-5a tumour supp
412 36 50.7 372 20 AAY04132 Human Wnt-5b prote
413 36 50.7 375 21 AAB08449 A human prostate s
414 36 50.7 388 22 AAG91530 C glutamicum prote
415 36 50.7 393 21 AAY94425 Human h-TAAK poly
416 36 50.7 393 21 AAY94426 Human h-TAAK poly
417 36 50.7 398 20 AAY30647 A mechanically sen
418 36 50.7 414 21 AAB54295 Human pancreatic c
419 36 50.7 424 22 AAG90605 C glutamicum prote
420 36 50.7 472 22 AAM00914 Human bone marrow
421 36 50.7 534 22 AAB98644 Human UDP-glucose:
422 36 50.7 550 22 AAB80066 Corynebacterium gl
423 36 50.7 572 22 AAB03506 Human protein kina
424 36 50.7 611 20 AAW73924 Nucleobase permeas
425 36 50.7 661 22 AAG89960 C glutamicum prote
426 36 50.7 729 22 AAM00020 Human Plectin prote
427 36 50.7 817 22 AAB95492 Human protein sequ
428 36 50.7 1045 22 AAM00933 Human bone marrow
429 36 50.7 1493 22 AAB72444 UGGT. Caenorhabdi
430 36 50.7 1527 22 AAB72436 Rat UGGT. Rattus
431 36 50.7 2135 22 AAM00019 Human Plectin prote
432 36 50.7 2594 22 AAM00984 Human bone marrow
433 35.5 50.0 80 21 AAB51983 Gene 19 human secr
434 35.5 50.0 80 21 AAB51984 Human secreted pro

ALIGNMENTS

RESULT 1
AAP30142
ID AAP30142 standard; Protein; 11 AA.
AC AAP30142;
XX

14-JUN-1992 (first entry)

Sequence of peptides with substance P inhibiting activity.

XX

KW Substance P antagonist; pain therapy; hypertension.
XX
FH Key Location/Qualifiers
FT Modified-site 2
FT /label= D-P
FT Modified-site 7
FT /label= D-W
FT Misc-difference 8
FT /label= F,I
FT Modified-site 9
FT /label= D-W
FT Modified-site 11
FT /label= M,I
FT /note= "bonded to NH2"
XX
PN W08301251-A.
XX
PD 14-APR-1983.
XX
XX 09-OCT-1981; 81WO-DE00171.
XX
XX 09-OCT-1981; 81WO-DE00171.
PR 09-OCT-1981; 81EP-0902802.
PR 09-OCT-1981; 81EP-0902802.
XX
PA (FERR) FERRING ARZNEIMITTE.
PA (HORI/) HORIG J.
XX
PI Horig J;
XX
XX WPI; 1983-39155K/16 (39155K).
DR Undeca:peptide derivs. with substance P inhibiting activity -
XX useful for treating pain and hypertension
XX
XX Claim 2; Page 18; 25pp; German.
XX
XX The peptides of the invention are powerful antagonists of Substance
CC P and so are useful in human and veterinary medicine, for treating
CC pain and hypertension (esp.) chronic conditions. A 10 microm concn.
CC of the peptide produced about 50% inhibition at a Substance P concn. of
CC 7.5-20 nanom.
XX
XX Sequence 11 AA;
SQ
Query Match 100.0%; Score 71; DB 4; Length 11;
Best Local Similarity 100.0%; Pred No. 8.5e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPKPQQFWLM 11
|||||||
Db 1 rpkkqqqfwlm 11
RESULT 2
AAP80317
ID AAP80317 standard; protein; 11 AA.
XX
XX AAP80317;
XX
XX 14-SEP-1990 (first entry)
XX
XX Sequence of neuropeptide antagonist E which binds with polypeptide
DE receptor for bombesin type polypeptides.
XX
XX Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 373 cells; bombesin type polypeptides;
KW antagonist E.
XX
XX Swiss 373 cells.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 2
FT

KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiopathy.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FH Misc-difference 2 /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"

FT US5876948-A.
XX
XX
XX 02-MAR-1999.

XX 27-JUL-1991; 91US-0737371.
XX
XX 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.
PA Yankner BA;
PI WPI; 1999-189630/16.

XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Disclosure; Column 11-12; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX beta-amyloid peptide fragments.

XX Sequence 11 AA;
SQ

Query Match 100.0%; Score 71; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||
Db 1 rpkpqqwfwlm 11

RESULT 5

AAB98881
ID AAB98881 standard; Peptide; 11 AA.

XX AAB98881;

XX 14-AUG-2001 (first entry)

XX Chimeric analgesic peptide #37.

DE Opioid receptor binding; nociceptive receptor binding; analgesic;
XX pain; chimeric peptide.
XX Synthetic.

XX Key Location/Qualifiers

FH Misc-difference 2

FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 11 /label= OTHER
FT /note= "C-terminal amide"

XX WO200130371-A2.

XX 03-MAY-2001.

XX 27-OCT-2000; 2000WO-US29789.

XX 28-OCT-1999; 99US-0428692.

XX (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

XX Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

XX WPI; 2001-397593/42.

XX New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group

XX Claim 10; Page 16; 34pp; English.

XX The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.

XX Sequence 11 AA;
SQ

Query Match 100.0%; Score 71; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||
Db 1 rpkpqqwfwlm 11

RESULT 6

AAB91413
ID AAB91413 standard; Peptide; 11 AA.

XX AAB91413;

XX 22-JUN-2001 (first entry)

XX Tachykinins peptide SEQ ID NO:589.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimide; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

XX Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

XX 10-SEP-1999; 99US-0153406.

XX 15-OCT-1999; 99US-0159783.

XX PA (CONJ-) CONJUCHEM INC.
 XX BRIDON DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX WPI; 2001-112059/12.
 XX
 XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT
 XX
 XX Disclosure; Page 392; 733pp; English.
 XX
 XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 11 AA;
 SQ

Query Match 100.0%; Score 71; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.5e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
 |||||
 Db 1 rpkpqwfwm 11

RESULT 7
 AAB98882
 ID AAB98882 standard; Peptide; 12 AA.
 XX
 AC AAB98882;
 XX
 DT 14-AUG-2001 (first entry)
 XX
 DE Chimeric analgesic peptide #38.
 XX
 KW Opioid receptor binding; nociceptive receptor binding; analgesic;
 KW pain; chimeric peptide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2 /note= "D-form residue"
 FT FT
 FT Misc-difference 7 /note= "D-form residue"
 FT FT
 FT Misc-difference 9 /note= "D-form residue"
 FT FT
 FT Modified-site 12 /label= OTHER
 FT FT /note= "C-terminal amide"
 XX
 XX W0200130371-A2.
 XX
 PD 03-MAY-2001.
 XX
 PD

PF 27-OCT-2000; 2000WO-US29789.
 XX
 PR 28-OCT-1999; 99US-0428692.
 XX
 PA (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
 XX
 PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
 XX
 DR WPI; 2001-397593/42.
 XX
 PT New chimeric peptides used for treating pain comprise opioid receptor
 PT binding group and nociceptive receptor binding group
 XX
 PS Claim 10; Page 16; 34pp; English.
 XX
 CC The present invention describes a number of chimeric peptides comprising
 CC an opioid receptor binding moiety and a nociceptive receptor binding
 CC moiety. These can be used as analgesics for the treatment of pain. Unlike
 CC opioid receptor based peptides alone, tolerance does not result from
 CC their long-term use. The present sequence is one of the peptides of the
 CC invention.
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 71; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
 |||||
 Db 1 rpkpqwfwm 11

RESULT 8
 AAP40479
 ID AAP40479 standard; peptide; 11 AA.
 XX
 AC AAP40479;
 XX
 DT 27-NOV-1991 (first entry)
 XX
 DE Substance P analogue.
 XX
 KW Substance P; analogue; antiinflammatory agent; analgesic.
 XX
 PN US4481139-A.
 XX
 PD 06-NOV-1984.
 XX
 PF 13-APR-1983; 83US-0484646.
 XX
 PR 13-APR-1983; 83US-0484646.
 XX
 PA (UYTE-) UNIVERSITY OF TEXAS SYSTEM.
 XX
 PI Folkers K, Ji-cheng X;
 XX
 DR WPI; 1984-294258/47.
 XX
 PT Peptide analogues of substance P - useful as antagonists, e.g. as
 PT antiinflammatory agents and analgesics.
 XX
 PS Claim 1; page 5; 5pp; English.
 XX
 CC The peptide is a D-Arg1, D-Trp7, D-Trp9, Leu11 analogue of substance
 CC P. The peptide is a substance P antagonist with higher activity than
 CC known substance P analogues. It may be used as a biological
 CC research tool, ophthalmological antiinflammatory agent and analgesic.
 XX
 XX Sequence 11 AA;
 SQ

Query Match 95.8%; Score 68; DB 5; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | | | | | | | |
Db 1 rpkpqwfwll 11

RESULT 9
AAP80313
ID AAP80313 standard; protein; 11 AA.
XX AC AAP80313;
XX DT 14-SEP-1990 (first entry)
XX DE Sequence of neuropeptide antagonist A which binds with polypeptide
DE receptor for bombesin type polypeptides.
XX Spantide; neuropeptide; polypeptide receptor; bombesin; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist A.
XX Swiss 3T3 cells.
XX OS
XX FH Key Location/Qualifiers
FT Misc-difference 1 /label=OTHER
FT /note="DArg"
FT Misc-difference 2 /label=OTHER
FT /note="DPro"
FT Misc-difference 7 /label=OTHER
FT /note="DTrp"
FT Misc-difference 9 /label=OTHER
FT /note="DTrp"
FT Misc-difference 11 /label=OTHER
FT /note="Leu-NH2"
XX WO8807551-A.
XX PN
XX PD 06-OCT-1988.
XX PF 31-MAR-1988; 88WO-GB00255.
XX PR 25-NOV-1987; 87GB-0027638.
XX PA (IMCR) IMPERIAL CANCER RES.
XX PI Rosengurt E, Zachary I, Woll P;
XX DR WPI; 1988-292842/41.
XX PT New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation
PS Disclosure; Table 2; 42pp; English.
XX CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue

CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.
XX
XX SQ Sequence 11 AA;

Query Match 95.8%; Score 68; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | | | | | | | |
Db 1 rpkpqwfwll 11

RESULT 10
AAP80314
ID AAP80314 standard; protein; 11 AA.
XX AC AAP80314;
XX DT 14-SEP-1990 (first entry)
XX DE Sequence of neuropeptide antagonist B which binds with polypeptide
DE receptor for bombesin type polypeptides.
XX Spantide; neuropeptide; polypeptide receptor; bombesin; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist B.
XX Swiss 3T3 cells.
XX OS
XX FH Key Location/Qualifiers
FT Misc-difference 1 /label=OTHER
FT /note="DArg"
FT Misc-difference 7 /label=OTHER
FT /note="DTrp"
FT Misc-difference 1 /label=OTHER
FT /note="DTrp"
FT Misc-difference 14 /label=OTHER
FT /note="Leu-NH2"
XX WO8807551-A.
XX PN
XX PD 06-OCT-1988.
XX PF 31-MAR-1988; 88WO-GB00255.
XX PR 25-NOV-1987; 87GB-0027638.
XX PA (IMCR) IMPERIAL CANCER RES.
XX PI Rosengurt E, Zachary I, Woll P;
XX DR WPI; 1988-292842/41.
XX PT New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation
PS Disclosure; Table 2; 42pp; English.
XX CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a

CC commercially available structural variant of substance P, known as
CC [D-Ar¹, D-Pro², D-Trp^{7,9}, Leu¹¹] substance P. It is also known as
CC [D-Pro²] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe⁵] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 nM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.

XX Sequence 11 AA;

Query Match 95.8%; Score 68; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQOQFWLM 11
|||||
Db 1 rpkpqgfwll 11

RESULT 11

AAR05856
ID AAR05856 standard; protein; 11 AA.

XX

AC AAR05856;

XX

DT 07-SEP-1990 (first entry)

XX

DE D-arginine 1, D-proline 2, D-tryptophan 7,9, Leucine 11,
DE -substance P angiotensin antagonist.

XX

XX Angiotensin; ectopic hormone; mas oncogene; cancer;
XX neuroblastoma; neuroendocrine.

XX

OS Synthetic.

XX

Key Location/Qualifiers

FT Modified-site 1

FT /label=Dextrorotatory form.

FT Modified-site 2

FT /label=Dextrorotatory form.

FT Modified-site 7

FT /label=Dextrorotatory form.

FT Modified-site 9

FT /label=Dextrorotatory form.

XX

XX WO9003181-A.

PN

XX

PD 05-APR-1990.

XX

PF 22-SEP-1989; 89WO-0001121.

XX

PR 24-SEP-1988; 88GB-0022483.

XX

XX (MEDI-) MED RES COUNCIL.

XX

PI Hanley MR, Goedert M;

XX

DR WPI; 1990-132106/17.

XX

XX Use of substances which block the activity of angiotensin -
XX for the treatment or prevention of tumour development or ectopic
XX hormone prodn.

PT

PS Claim 8; Page 19; 23pp; English.

XX

XX Peptide blocks biological activity of angiotensin and is active

CC against the mas oncogene, retarding tumour growth, esp
CC neuroendocrine and neuroblastoma tumours.

XX

SQ Sequence 11 AA;

Query Match 95.8%; Score 68; DB 11; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQOQFWLM 11

|||||

Db 1 rpkpqgfwll 11

RESULT 12

AAR11144

ID AAR11144 standard; Protein; 11 AA.

XX

AC AAR11144;

XX

DT 21-MAY-1991 (first entry)

XX

DE Substance P analogue.

XX

XX Anti-proliferation agent; neurogenetic inflammation; fibroblasts;
XX agonist.

KW

XX

OS Synthetic.

XX

Key Location/Qualifiers

FT Modified-site 1

FT /label= D-Arg

FT Modified-site 7

FT /label= D-Trp

FT Modified-site 9

FT /label= D-Trp

FT Modified-site 9..10

FT /label= non-peptide bond

FT /note= "Trp-L[CH2NH]-Trp"

FT Modified-site 11

FT /label= Nle

XX

XX WO9102745-A.

PN

XX

PD 07-MAR-1991.

XX

PF 16-AUG-1990; 90WO-US04633.

XX

PR 16-AUG-1989; 89US-0394727.

XX

XX (TULA) TULANE E FUND ADMINISTRA.

PA

XX Coy DH, Moreau JP;

XX

XX WPI; 1991-087240/12.

DR

XX

XX Modified linear peptide analogue of natural substance P - acts as
XX competitive inhibitor of substance P and is used for treating
XX neuro genetic inflammation and as anti-proliferative agent.

PT

XX

PS Claim 11; Page 34; 40pp; English.

XX

XX The peptide has a non-peptide bond introduced between Trp⁹ and
XX Leu¹⁰. This may alternatively be positioned between Leu¹⁰ and
XX Nle¹¹. For prepn., a benzhydrylamine resin was coupled to Boc-Leu.
XX Boc-Leu aldehyde was dissolved in 5 ml DMF and added to the resin
XX TFA salt suspension followed by addn. of NaCNBH₃ and stirring for
XX one hour. The remaining amino acids were then coupled successively.
XX In tests the peptide inhibited P-stimulated amylase release from
XX pancreatic acini.
XX See also AAR11143.

XX

SQ Sequence 11 AA;

Query Match 95.8%; Score 68; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | | | | | | | |
Db 1 rpkpqgfwll 11

RESULT 13
AAW50966
ID AAW50966 standard; peptide; 11 AA.
XX AC AAW50966;
XX DT 31-JUL-1998 (first entry)
XX DE Substance P analogue, spantide I.
XX KW Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
KW Substance P; cancer; inhibition; growth hormone releasing factor;
KW spantide.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Misc-difference 11 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
XX EP835662-A2.
XX PN 15-APR-1998.
XX PD 11-DEC-1996; 96EP-0309012.
XX PF 08-OCT-1996; 96US-0727679.
XX PR 16-AUG-1996; 96IN-0001822.
XX PA (NAIM-) NAT INST IMMUNOLOGY.
XX PI Jaggi M, Mukherjee R;
XX PI WPI; 1998-208959/19.
XX DR Composition containing analogues of vasoactive intestinal peptide,
XX PT somatostatin - bombesin and substance P, for treatment of tumours
XX PT and for inhibiting over-expression of these peptide(s)
XX PS Disclosure; Page 13; 49pp; English.
XX XX

The invention relates to a new composition which comprises: (1) the somatostatin analogue SOM2 AGCKNFFQWKPTSDC (3-14 disulphide bridge), and (1i) at least 4 of the peptides: antagonist of vasoactive intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin antagonist (BOM1) and substance P antagonist (SP1). Also claimed are more general compositions containing peptide analogues of somatostatin, VIP, bombesin and substance P. The compositions are used in human or veterinary medicine: (a) to kill (or inhibit multiplication of) tumour or cancer cells, particularly for treatment of leukaemia, lymphoma, adenocarcinoma of stomach, pancreas or prostate, or cancer of lung, breast, kidney or particularly rectum and colon, and (b) to prevent, inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer cells express receptors for VIP, somatostatin, bombesin and/or substance

CC P. The present sequence represents a substance P analogue, spantide I.
XX
SQ Sequence 11 AA;

Query Match 95.8%; Score 68; DB 19; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | | | | | | | |
Db 1 rpkpqgfwll 11

RESULT 14
AAW50958
ID AAW50958 standard; peptide; 11 AA.
XX AC AAW50958;
XX DT 31-JUL-1998 (first entry)
XX DE Substance P analogue, [D-Arg1,D-Pro2,D-Trp7,9,Leu11]-Substance P.
XX KW Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
KW Substance P; cancer; inhibition; growth hormone releasing factor.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Misc-difference 2 /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Misc-difference 11 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
XX EP835662-A2.
XX PN 15-APR-1998.
XX PD 11-DEC-1996; 96EP-0309012.
XX PF 08-OCT-1996; 96US-0727679.
XX PR 16-AUG-1996; 96IN-0001822.
XX PA (NAIM-) NAT INST IMMUNOLOGY.
XX PI Jaggi M, Mukherjee R;
XX PI WPI; 1998-208959/19.
XX DR Composition containing analogues of vasoactive intestinal peptide,
XX PT somatostatin - bombesin and substance P, for treatment of tumours
XX PT and for inhibiting over-expression of these peptide(s)
XX PS Disclosure; Page 12; 49pp; English.
XX XX

The invention relates to a new composition which comprises: (1) the somatostatin analogue SOM2 AGCKNFFQWKPTSDC (3-14 disulphide bridge), and (1i) at least 4 of the peptides: antagonist of vasoactive intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin antagonist (BOM1) and substance P antagonist (SP1). Also claimed are more general compositions containing peptide analogues of somatostatin, VIP, bombesin and substance P. The compositions are used in human or veterinary medicine: (a) to kill (or inhibit multiplication of) tumour or cancer cells, particularly for treatment of leukaemia, lymphoma, adenocarcinoma of stomach, pancreas or prostate, or cancer of lung, breast, kidney or particularly rectum and colon, and (b) to prevent, inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer cells express receptors for VIP, somatostatin, bombesin and/or substance

CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.
XX
SQ Sequence 11 AA;

Query Match 95.8%; Score 68; DB 19; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RPKPOQWFWM 11
|||||
Db 1 rpkpqgfwll 11

RESULT 15

AAW92657
ID AAW92657 standard; peptide; 11 AA.

AC AAW92657;

DT 30-APR-1999 (first entry)

XX Human tachykinin agonist beta-amyloid peptide fragment #3.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX
OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

XX US5876948-A.

XX 02-MAR-1999.

XX 27-JUL-1991; 91US-0737371.

XX 29-JUL-1991; 91US-0737371.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Yankner BA;

XX WPI; 1999-189630/16.

XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX

PS Disclosure: Column 11-12; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

XX Sequence 11 AA;

Query Match 95.8%; Score 68; DB 22; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match 95.8%; Score 68; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RPKPOQWFWM 11
|||||
Db 1 rpkpqgfwll 11

RESULT 16

AAAB91434
ID AAB91434 standard; Peptide; 11 AA.

XX AAB91434;

XX 22-JUN-2001 (first entry)

XX Tachykinins peptide SEQ ID NO:610.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

XX Synthetic.

XX WO2000069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

XX 10-SEP-1999; 99US-0153406.

XX 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
PI WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT

PS Disclosure; Page 398; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 11 AA;

QY 1 RPKPQQWFWM 11
Db 1 rpkpqgfwll 11

RESULT 17
AAR28680
ID AAR28680 standard; Protein; 24 AA.
XX AC AAR28680;
XX DT 22-MAR-1993 (first entry)
XX DE Galanin(1-12)-Pro-Spantide amide (C7).
XX KW Receptor; Substance P; insulin; growth hormone;
KW acetylcholine; dopamine; somatostatin; noradrenaline;
KW endocrinology; food intake; neurology; psychiatry;
KW Alzheimer-type senile dementia; schizophrenia;
KW intestinal diseases.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 14 /note= "D-form residue"
FT Misc-difference 20 /note= "D-form residue"
FT Misc-difference 22 /note= "D-form residue"
FT Peptide 1..12 /label= galanin(1-12)
FT Peptide 14..24 /label= spantide
XX EP514361-A.
XX 19-NOV-1992.
XX 14-MAY-1992; 92EP-0850108.
XX 15-MAY-1991; 91SE-0001472.
XX (ASTR) ASTRA AB.
XX Ahren B, Bartfai T, Consolo S, Hoekfelt T, Land T;
XX Langel U, Lindskog S, Wiesenfeld-Hallin Z;
XX WPI: 1992-384184/47.
XX New galanin antagonist peptide(s) - used for treating
XX Alzheimer's-type senile dementia, schizophrenia, analgesia and
XX intestinal diseases
XX Disclosure; Page 7; 21pp; English.
XX The C-terminal of this peptide is amidated. MW= 2827; IC50= 0.2nM.
XX The peptides given in AAR28679-90 are used to treat disorders in
XX mammals caused by the function of galanin at its receptor. The
XX peptides may be useful in the regulation of insulin release, growth
XX hormone release, acetylcholine release, dopamine release, substance
XX P release, somatostatin release and noradrenaline release. They are
XX useful in endocrinology, food intake, neurology and psychiatry, and
XX to treat Alzheimer-type senile dementia, schizophrenia, intestinal
XX diseases, and in analgesia. Dosage is 0.01-1000, pref. 0.1-1000
XX microg/kg body wt.
XX Sequence 24 AA;
XX Query Match 95.8%; Score 68; DB 13; Length 24;
XX Best Local Similarity 90.9%; Pred. No. 0.00051;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPKPQQWFWM 11
Db 14 rpkpqgfwll 24

RESULT 18
AAB92023
ID AAB92023 standard; Peptide; 24 AA.
XX AC AAB92023;
XX DT 22-JUN-2001 (first entry)
XX DE Galanin peptide SEQ ID NO:1199.
XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimide; maleimide group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX OS Homo sapiens.
XX OS Synthetic.
XX WO200069900-A2.
XX 23-NOV-2000.
XX 17-MAY-2000; 2000WO-US13576.
XX 17-MAY-1999; 99US-0134406.
XX 10-SEP-1999; 99US-0153406.
XX 15-OCT-1999; 99US-0159783.
XX (CONJ-) CONJUCHEM INC.
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX WPI: 2001-112059/12.
XX Modifying and attaching therapeutic peptides to albumin prevents
XX peptidase degradation, useful for increasing length of in vivo activity
XX Disclosure; Page 586; 733pp; English.
XX The present invention describes a modified therapeutic peptide (I)
XX comprising a therapeutically active amino acid region (III) and a
XX reactive group (II) (e.g. succinimide and maleimide groups) attached to
XX a less therapeutically active amino acid region (IV), which covalently
XX bonds with amino/hydroxyl/thiol groups on blood components to form a
XX peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX factors and neurotransmitters, to protect them from peptidase activity
XX in vivo for the treatment of various disorders. Endogenous therapeutic
XX peptides are not suitable as drug candidates as they require frequent
XX administration due to rapid degradation by peptidases in the body.
XX Modifying and attaching therapeutic peptides to albumin prevents or
XX reduces the action of peptidases to increase length of activity (half
XX life) and specificity as bonding to large molecules decreases
XX intracellular uptake and interference with physiological processes.
XX AAB90829 to AAB92441 represent peptides which can be used in the
XX exemplification of the present invention.
XX Sequence 24 AA;
XX Query Match 95.8%; Score 68; DB 22; Length 24;
XX Best Local Similarity 90.9%; Pred. No. 0.00051;
XX Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
Db 1 rpkpqgfwll 11

Query Match 95.8%; Score 68; DB 13; Length 24;
Best Local Similarity 90.9%; Pred. No. 0.00051;

Db 14 rpkpqgfwl1 24

RESULT 19

AAB92031
ID AAB92031 standard; Peptide; 24 AA.XX AC AAB92031;
XX DT 22-JUN-2001 (first entry)

XX DE Galanin peptide SEQ ID NO:1207.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX KW blood component; modification; succinimidyl; maleimido group; amino;
XX KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.XX OS Homo sapiens.
XX OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US13576.

XX PR 17-MAY-1999; 99US-0134406.

XX PR 10-SEP-1999; 99US-0153406.

XX PR 15-OCT-1999; 99US-0159783.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX DR WPI; 2001-112059/12.

XX PT Modifying and attaching therapeutic peptides to albumin prevents
XX PT peptidase degradation, useful for increasing length of in vivo activity

XX PS Disclosure; Page 589; 733pp; English.

XX CC The present invention describes a modified therapeutic peptide (I)
XX CC comprising a therapeutically active amino acid region (III) and a
XX CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
XX CC a less therapeutically active amino acid region (IV), which covalently
XX CC bonds with amino/hydroxyl/thiol groups on blood components to form a
XX CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
XX CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX CC factors and neurotransmitters, to protect them from peptidase activity
XX CC in vivo for the treatment of various disorders. Endogenous therapeutic
XX CC peptides are not suitable as drug candidates as they require frequent
XX CC administration due to rapid degradation by peptidases in the body.
XX CC Modifying and attaching therapeutic peptides to albumin prevents or
XX CC reduces the action of peptidases to increase length of activity (half
XX CC life) and specificity as bonding to large molecules decreases
XX CC intracellular uptake and interference with physiological processes.
XX CC AAB90829 to AAB92441 represent peptides which can be used in the
XX CC exemplification of the present invention.

XX SQ Sequence 24 AA;

Query Match 95.8%; Score 68; DB 22; Length 24;
Best Local Similarity 90.9%; Pred. No. 0.00051;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQGFWM 11

Db 14 rpkpqgfwl1 24

RESULT 20

AAW09004

ID AAW09004 standard; peptide; 11 AA.

XX AC AAW09004;

XX DT 03-MAR-1997 (first entry)

XX DE Spantide analogue, acts as substance P antagonist.

XX KW Analogue; substance P; spantide; non-peptide bond;
XX KW competitive inhibitor; receptor; neurogenic inflammation;
XX KW rheumatoid arthritis; ulcerative colitis; eczema; Crohn's disease;
XX KW anti-proliferative agent; small cell lung carcinoma; fibroblast.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT FT Misc-difference 1 /note= "D-form residue"

FT FT Modified-site 6..7

FT FT /label= Gln-psi[CH2-NH]-Trp

FT FT /note= "Opt. non-peptide bond, Claim 7"

FT FT Misc-difference 7 /note= "D-form residue"

FT FT Modified-site 7..8

FT FT /label= Trp-psi[CH2-NH]-Phe

FT FT /note= "Opt. non-peptide bond, Claim 6"

FT FT Modified-site 8..9

FT FT /label= Phe-psi[CH2-NH]-Trp

FT FT /note= "Opt. non-peptide bond"

FT FT Misc-difference 9 /note= "D-form residue"

FT FT Modified-site 9..10

FT FT /label= Trp-psi[CH2-NH]-Leu

FT FT /note= "Opt. non-peptide bond, Claim 4"

FT FT Modified-site 10..11

FT FT /label= Leu-psi[CH2-NH]-Nle

FT FT /note= "Opt. non-peptide bond, Claim 5"

FT FT Modified-site 11 /label= Nle

FT FT /note= "Amidated C-terminal"

XX US5410019-A.

XX 25-APR-1995.

XX PF 24-SEP-1987; 87US-0100571.

XX PR 30-MAR-1992; 92US-0860675.

XX PR 24-SEP-1987; 87US-0100571.

XX PR 25-MAR-1988; 88US-0173311.

XX PR 08-JUN-1988; 88US-0204171.

XX PR 16-JUN-1988; 88US-0207759.

XX PR 23-SEP-1988; 88US-0248771.

XX PR 14-OCT-1988; 88US-0257998.

XX PR 09-DEC-1988; 88US-0282328.

XX PR 02-MAR-1989; 89US-0317941.

XX PR 16-AUG-1989; 89US-0394727.

XX (TULA) TULANE EDUCATIONAL FUND.

XX COY DH, Moreau J;

XX WPI; 1995-169633/22.

XX PT Novel linear peptide substance P analogues - useful as substance P
XX PT antagonists, for treating neurogenic inflammation
XX PS Claim 4-7; Column 20; 16pp; English.

XX CC The sequences given in AAW09003-04 represent analogues of substance P
XX CC and spantide, respectively. These analogues comprise a non-peptide
XX CC bond between an amino acid residue of the active site, which occurs

CC in the C-terminal half of the peptide, and an adjacent amino acid
CC residue. They act as competitive inhibitors of the naturally
CC occurring peptide by binding to its receptor. These peptides may be
CC used in the treatment of diseases involving neurogenic inflammation,
CC e.g. rheumatoid arthritis, ulcerative colitis, eczema and Crohn's
CC disease. They are also useful as anti-proliferative agents, in
CC the treatment of small cell lung carcinoma or disorders involving the
CC proliferation of fibroblasts.

XX Sequence 11 AA;

Query Match 93.0%; Score 66; DB 16; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00048;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFwl 10
| | | | | | | | | |
Db 1 rpkpqgqfwl 10

RESULT 21

AAW99690

ID AAW99690 standard; peptide; 11 AA.

XX AC AAW99690;

DT 03-JUN-1999 (first entry)

DE Substance P analogue #7.

XX Substance P receptor antagonist; analgesic; inhibitor; NMDA blocker;
KW nontoxic N-methyl-D-aspartate receptor antagonist; muscular pain;
KW musculoskeletal pain; chronic pain; neuropathic pain; migraine.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 9..10 /note= "D-form residue"

FT Modified-site 11 /note= "Trp-psi(CH2-NH)-Leu"

FT /label= Nle

FT /note= "Norleucine, amidated"

XX WO9907413-A1.

XX 18-FEB-1999.

XX 26-MAY-1998; 98WO-US10707.

XX 11-AUG-1997; 97US-0055233.

XX (ALGO-) ALGOS PHARM CORP.

XX Caruso FS;

XX WPI; 1999-167216/14.

XX New analgesic composition comprises - a substance P receptor

XX antagonist with a substance P receptor antagonist potentiator, used

XX for the treatment of pain

XX Claim 3; Page 29; 54pp; English.

XX A method has been developed for treating pain with: (a) a substance P

XX receptor antagonist; and (b) a substance P receptor antagonist

XX potentiator, i.e. N-methyl-D-aspartate (NMDA) receptor antagonist or

CC substance that blocks at least 1 major intracellular consequence of
CC NMDA receptor activation. The method can be used for treating muscular,
CC musculoskeletal, chronic or neuropathic pain, or migraine. The present
CC sequence represents a substance P analogue for use in the method.

XX Sequence 11 AA;

Query Match 93.0%; Score 66; DB 20; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00048;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFwl 10
| | | | | | | | | |
Db 1 rpkpqgqfwl 10

RESULT 22

AAW99691

ID AAW99691 standard; peptide; 11 AA.

XX AC AAW99691;

DT 03-JUN-1999 (first entry)

DE Substance P analogue #8.

XX Substance P receptor antagonist; analgesic; inhibitor; NMDA blocker;
KW nontoxic N-methyl-D-aspartate receptor antagonist; muscular pain;
KW musculoskeletal pain; chronic pain; neuropathic pain; migraine.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Modified-site 7..8 /note= "D-form residue"

FT Misc-difference 9 /note= "Trp-psi(CH2-NH)-Phe"

FT Misc-difference 11 /note= "D-form residue"

FT /label= Nle

FT /note= "Norleucine, amidated"

XX WO9907413-A1.

XX 18-FEB-1999.

XX 26-MAY-1998; 98WO-US10707.

XX 11-AUG-1997; 97US-0055233.

XX (ALGO-) ALGOS PHARM CORP.

XX Caruso FS;

XX WPI; 1999-167216/14.

XX New analgesic composition comprises - a substance P receptor

XX antagonist with a substance P receptor antagonist potentiator, used

XX for the treatment of pain

XX Claim 3; Page 29; 54pp; English.

XX A method has been developed for treating pain with: (a) a substance P

XX receptor antagonist; and (b) a substance P receptor antagonist

XX potentiator, i.e. N-methyl-D-aspartate (NMDA) receptor antagonist or

XX substance that blocks at least 1 major intracellular consequence of

XX NMDA receptor activation. The method can be used for treating muscular,

XX musculoskeletal, chronic or neuropathic pain, or migraine. The present

XX sequence represents a substance P analogue for use in the method.

XX
SQ Sequence 11 AA;

Query Match 93.0%; Score 66; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFWL 10
Db 1 rpkpqfwl 10
|||||

RESULT 23
AAP80315
ID AAP80315 standard; protein; 11 AA.
XX
AC AAP80315;
XX
DT 14-SEP-1990 (first entry)
XX
DE Sequence of neuropeptide antagonist C which binds with polypeptide
DE receptor for bombesin type polypeptides.
XX
KW Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist C.
XX
OS Swiss 3T3 cells.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /label=OTHER
FT /label=OTHER
FT /note="DPro"
FT Misc-difference 7 /label=OTHER
FT /label=OTHER
FT /note="DPhe"
FT Misc-difference 1 /label=OTHER
FT /label=OTHER
FT /note="DTrp"
FT Misc-difference 11 /label=OTHER
FT /note="Met-NH2"
XX WO8807551-A.
XX
XX
PD 06-OCT-1988.
XX
XX 31-MAR-1988; 88WO-GB00255.
XX
XX 25-NOV-1987; 87GB-0027638.
XX
XX (IMCR) IMPERIAL CANCER RES.
XX
XX Rosengurt E, Zachary I, Woll P;
XX WPI; 1988-292842/41.
XX
XX New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation
XX
XX Disclosure; Table 2; 42pp; English.

XX The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their

ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
potent than either A or D. Spantide (B) had no antagonist activity even
at 100 uM. Polypeptide antagonists A and D and novel variants are useful
for diagnosis and therapy, esp. of cancers where uncontrolled cell
growth is associated with disorders of proteins of the bombesin family.

XX
SQ Sequence 11 AA;

Query Match 85.9%; Score 61; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0028;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFWL 11
Db 1 rpkpqfwl 11
|||||

RESULT 24
AAW50968
ID AAW50968 standard; peptide; 11 AA.
XX
AC AAW50968;
XX
DT 31-JUL-1998 (first entry)
XX
DE Substance P analogue, [D-Pro2,D-Phe7,D-Trp9].
XX
KW Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
KW Substance P; cancer; inhibition; growth hormone releasing factor;
KW spantide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /note="D-form residue"
FT Misc-difference 7 /note="D-form residue"
FT Misc-difference 9 /note="D-form residue"
FT Modified-site 11 /note="C-terminal amide"
XX
XX EP835662-A2.
XX
XX 15-APR-1998.
XX
XX 11-DEC-1996; 96EP-0309012.
XX
XX 08-OCT-1996; 96US-0727679.
XX
XX 16-AUG-1996; 96IN-0001822.
XX
XX (NATM-) NAT INST IMMUNOLOGY.
XX
XX Jaggi M, Mukherjee R;
XX WPI; 1998-208959/19.
XX
XX Composition containing analogues of vasoactive intestinal peptide,
PT somatostatin - bombesin and substance P, for treatment of tumours
PT and for inhibiting over-expression of these peptide(s)
XX
XX Disclosure; Page 13; 49pp; English.

XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 AGCNFpDWTPTSDC (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are

CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.
XX
SQ Sequence 11 AA;

Query Match 85.9%; Score 61; DB 19; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0028;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | : | | | |
Db 1 rpkpqgffwlm 11

RESULT 25

AAB98879
ID AAB98879 standard; Peptide; 11 AA.

XX AAB98879;

DT 14-AUG-2001 (first entry)

DE Chimeric analgesic peptide #35.

KW Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX Synthetic.

XX Key Location/Qualifiers
FH Misc-difference 2 /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 11 /note= "D-form residue"
FT /label= OTHER
FT /note= "C-terminal amide"

XX WO200130371-A2.

XX 03-MAY-2001.

XX 27-OCT-2000; 2000WO-US29789.

XX 28-OCT-1999; 99US-0428692.

XX (NEWEL) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

XX Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

XX WPI; 2001-397593/42.

XX New chimeric peptides used for treating pain comprise opioid receptor
XX binding group and nociceptive receptor binding group

PS Claim 10; Page 15; 34pp; English.

XX The present invention describes a number of chimeric peptides comprising
XX an opioid receptor binding moiety and a nociceptive receptor binding
XX moiety. These can be used as analgesics for the treatment of pain. Unlike
XX opioid receptor based peptides alone, tolerance does not result from
XX their long-term use. The present sequence is one of the peptides of the
XX invention.

XX SQ Sequence 11 AA;

Query Match 85.9%; Score 61; DB 22; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0028;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | : | | | |
Db 1 rpkpqgffwlm 11

RESULT 26

AAB91412

ID AAB91412 standard; Peptide; 11 AA.

XX AAB91412;

XX 22-JUN-2001 (first entry)

DE Tachykinins peptide SEQ ID NO:588.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX Homo sapiens.
OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

XX 10-SEP-1999; 99US-0153406.

XX 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
XX peptidase degradation, useful for increasing length of in vivo activity

XX Disclosure; Page 392; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
XX comprising a therapeutically active amino acid region (iii) and a
XX reactive group (ii) (e.g. succinimidyl and maleimido groups) attached to
XX a less therapeutically active amino acid region (iv), which covalently
XX bonds with amino/hydroxyl/thiol groups on blood components to form a
XX peptidase stabilised therapeutic peptide composed of 3-30 amino acids.
XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX factors and neurotransmitters, to protect them from peptidase activity
XX in vivo for the treatment of various disorders. Endogenous therapeutic
XX peptides are not suitable as drug candidates as they require frequent
XX administration due to rapid degradation by peptidases in the body.
XX Modifying and attaching therapeutic peptides to albumin prevents or
XX reduces the action of peptidases to increase length of activity (half
XX life) and specificity as bonding to large molecules decreases
XX intracellular uptake and interference with physiological processes.
XX AAB90829 to AAB92441 represent peptides which can be used in the
XX exemplification of the present invention.

XX SQ Sequence 11 AA;

Query Match 85.9%; Score 61; DB 22; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0028;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:||||
Db 1 rpkpqgffwlm 11

RESULT 27

AAB98880
ID AAB98880 standard; Peptide; 12 AA.
XX AC AAB98880;
XX DT 14-AUG-2001 (first entry)
XX DE
XX DE Chimeric analgesic peptide #36.
XX KW Opioid receptor binding; nociceptive receptor binding; analgesic;
XX KW pain; chimeric peptide.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 2 /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 12 /label= OTHER
FT /note= "C-terminal amide"

XX WO200130371-A2.

XX 03-MAY-2001.

XX 27-OCT-2000; 2000WO-US29789.

XX 28-OCT-1999; 99US-0428692.

XX (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

XX Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

XX WPI; 2001-397593/42.

XX New chimeric peptides used for treating pain comprise opioid receptor
binding group and nociceptive receptor binding group -

XX Claim 10; Page 15-16; 34pp; English.

XX The present invention describes a number of chimeric peptides comprising
an opioid receptor binding moiety and a nociceptive receptor binding
moiety. These can be used as analgesics for the treatment of pain. Unlike
opioid receptor based peptides alone, tolerance does not result from
their long-term use. The present sequence is one of the peptides of the
invention.

XX Query Match 85.9%; Score 61; DB 22; Length 12;

Best Local Similarity 90.9%; Pred. No. 0.003;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:||||
Db 1 rpkpqgffwlm 11

RESULT 28

AAP40481
ID AAP40481 standard; Protein; 11 AA.

XX AC AAP40481;

XX DT 27-NOV-1991 (first entry)

XX DE Substance P analogue.

XX KW Substance P; analogue; antiinflammatory agent; analgesic.

XX PN US4481139-A.

XX PD 06-NOV-1984.

XX PF 13-APR-1983; 83US-0484646.

XX PR 13-APR-1983; 83US-0484646.

XX PA (UYTE-) UNIVERSITY OF TEXAS SYSTEM.

XX PI Folkers K, Ji-cheng X;

XX DR WPI; 1984-294258/47.

XX FT Peptide analogues of substance P - useful as antagonists, e.g. as
antiinflammatory agents and analgesics.

XX PS Claim 4; page 5; 5pp; English.

XX CC The peptide is a D-Arg1, D-Pro2, D-Phe 5, D-Trp7, D-Trp9, Leu11
analogue of substance P. The peptide is a substance P antagonist
with higher activity than known substance P analogues. It may be
used as a biological research tool, ophthalmological antiinflammatory
agent and analgesic.

XX SQ Sequence 11 AA;

Query Match 84.5%; Score 60; DB 5; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.0039;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:||||
Db 1 rpkpqgffwlm 11

RESULT 29

AAP80316
ID AAP80316 standard; protein; 11 AA.

XX AC AAP80316;

XX DT 14-SEP-1990 (first entry)

XX DE Sequence of neuropeptide antagonist D which binds with polypeptide
receptor for bombesin type polypeptides.

XX KW Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;

XX KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides.

XX OS Swiss 3T3 cells.

XX FH Key Location/Qualifiers

FT Misc-difference 1 /label=OTHER

FT /note="DArg"

FT Misc-difference 5 /label=OTHER

FT /note="Dphe"

FT Misc-difference 7

FT /label=OTHER
 FT Misc-difference 9 /note="D-Trp"
 FT /label=OTHER
 FT /note="D-Trp"
 FT Misc-difference 11
 FT /label=OTHER
 FT /note="Leu-NH2"
 PN W08807551-A.
 XX
 XX
 PD 06-OCT-1988.
 XX
 XX 31-MAR-1988; 88WO-GB00255.
 XX
 XX 25-NOV-1987; 87GB-0027638.
 XX
 XX (IMCR) IMPERIAL CANCER RES.
 XX
 XX Rosengurt E, Zachary I, Woll P;
 XX
 XX WPI; 1988-292842/41.
 DR
 XX

XX New polypeptide receptor for bombesin type polypeptide(s) -
 PT is isolated from surface of Swiss 3T3 cells, and antibodies and
 PT antagonists are useful for treating uncontrolled cell proliferation
 XX
 XX Disclosure; Table 2; 42pp; English.

XX The patent claims a polypeptide isolated from the surface of Swiss 3T3
 CC cells which binds selectively with polypeptides of the bombesin type and
 CC binds with antagonist A and antagonist D. Antagonist A is a
 CC commercially available structural variant of substance P, known as
 CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
 CC [D-Pro2] spantide. Antagonist B is also commercially available structural
 CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
 CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
 CC substance P antagonists (see AAP80313-80322) were tested for their
 CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
 CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
 CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
 CC potent than either A or D. Spantide (B) had no antagonist activity even
 CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
 CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
 CC growth is associated with disorders of proteins of the bombesin family.
 XX Sequence 11 AA;

Query Match 84.5%; Score 60; DB 9; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.0039;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFNLM 11
 |||||
 Db 1 rpkpfgfwll 11

RESULT 30
 AAW50979
 ID AAW50979 standard; peptide; 11 AA.
 XX
 AC AAW50979;
 XX

31-JUL-1998 (first entry)

Substance P analogue [D-Trp2,7,9].

Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
 KW Substance P; cancer; inhibition; growth hormone releasing factor;
 KW spantide.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FH Misc-difference 2 /note= "D-form residue"
 FT
 FT Misc-difference 7 /note= "D-form residue"
 FT
 FT Misc-difference 9 /note= "D-form residue"
 FT
 FT Misc-difference 11 /note= "D-form residue"
 FT
 FT Modified-site 11 /note= "C-terminal amide"
 FT
 XX

XX EP835662-A2.
 PN
 XX
 XX 15-APR-1998.
 XX
 XX 11-DEC-1996; 96EP-0309012.
 PF
 XX 08-OCT-1996; 96US-0727679.
 PR
 XX 16-AUG-1996; 96IN-0001822.
 XX
 XX (NAIM-) NAT INST IMMUNOLOGY.
 PA
 XX

Jaggi M, Mukherjee R;

WPI; 1998-208959/19.

XX Composition containing analogues of vasoactive intestinal peptide,
 PT somatostatin - bombesin and substance P, for treatment of tumours
 PT and for inhibiting over-expression of these peptide(s)
 PT
 XX

Disclosure; Page 13; 49pp; English.

XX The invention relates to a new composition which comprises: (i) the
 CC somatostatin analogue SOM2 AGCKNFTdWKPTSDC (3-14 disulphide bridge),
 CC and (ii) at least 4 of the peptides: antagonist of vasoactive
 CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
 CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
 CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
 CC more general compositions containing peptide analogues of somatostatin,
 CC VIP, bombesin and substance P. The compositions are used in human or
 CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
 CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
 CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
 CC breast, kidney or particularly rectum and colon, and (b) to prevent,
 CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
 CC cells express receptors for VIP, somatostatin, bombesin and/or substance
 CC P. The present sequence represents a substance P analogue.

XX Sequence 11 AA;

Query Match 84.5%; Score 60; DB 19; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0039;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFNLM 11
 | | | | |
 Db 1 rwkpgqgfwlm 11

RESULT 31
 AAW50972
 ID AAW50972 standard; peptide; 11 AA.
 XX
 AC AAW50972;
 XX

31-JUL-1998 (first entry)

Substance P analogue, [D-Arg1,D-Phe5,D-Trp7,9,Leu11].

Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
 KW Substance P; cancer; inhibition; growth hormone releasing factor;
 KW spantide.

```

XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 1 /note= "D-form residue"
XX FT Misc-difference 5 /note= "D-form residue"
XX FT Misc-difference 7 /note= "D-form residue"
XX FT Misc-difference 9 /note= "D-form residue"
XX FT Misc-difference 11 /note= "D-form residue"
XX FT Modified-site 13 /note= "C-terminal amide"
XX PN EP835662-A2.
XX PD 15-APR-1998.
XX PF 11-DEC-1996; 96EP-0309012.
XX PR 08-OCT-1996; 96US-0727679.
XX PR 16-AUG-1996; 96IN-0001822.
XX PA (NAIM-) NAT INST IMMUNOLOGY.
XX PI Jaggi M, Mukherjee R;
XX DR WPI; 1998-208959/19.
XX PT Composition containing analogues of vasoactive intestinal peptide,
XX PT somatostatin - bombesin and substance P, for treatment of tumours
XX PT and for inhibiting over-expression of these peptide(s)
XX PS Disclosure; Page 13; 49pp; English.
XX CC The invention relates to a new composition which comprises: (i) the
XX CC somatostatin analogue SOM2 AGCKNFDWKPTSDC (3-14 disulphide bridge),
XX CC and (ii) at least 4 of the peptides: antagonist of vasoactive
XX CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
XX CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
XX CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
XX CC more general compositions containing peptide analogues of somatostatin,
XX CC VIP, bombesin and substance P. The compositions are used in human or
XX CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
XX CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
XX CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
XX CC breast, kidney or particularly rectum and colon, and (b) to prevent,
XX CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
XX CC cells express receptors for VIP, somatostatin, bombesin and/or substance
XX CC P. The present sequence represents a substance P analogue.
XX SQ Sequence 11 AA;

Query Match 84.5%; Score 60; DB 19; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.0039;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
Db 1 rpkipqfwll 11

RESULT 32
AAW50942
ID AAW50942 standard; peptide; 11 AA.
XX AC AAW50942;
XX DT 31-JUL-1998 (first entry)
XX DE Substance P antagonist (SP1).

```

```

XX KW Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
XX OS Substance P; cancer; inhibition.
XX FH Synthetic.
XX FT Key Location/Qualifiers
XX FT Misc-difference 1 /note= "D-form residue"
XX FT Misc-difference 5 /note= "D-form residue"
XX FT Misc-difference 7 /note= "D-form residue"
XX FT Misc-difference 9 /note= "D-form residue"
XX FT Modified-site 13 /note= "C-terminal amide"
XX PN EP835662-A2.
XX PD 15-APR-1998.
XX PF 11-DEC-1996; 96EP-0309012.
XX PR 08-OCT-1996; 96US-0727679.
XX PR 16-AUG-1996; 96IN-0001822.
XX PA (NAIM-) NAT INST IMMUNOLOGY.
XX PI Jaggi M, Mukherjee R;
XX DR WPI; 1998-208959/19.
XX PT Composition containing analogues of vasoactive intestinal peptide,
XX PT somatostatin - bombesin and substance P, for treatment of tumours
XX PT and for inhibiting over-expression of these peptide(s)
XX PS Claim 1; Page 4; 49pp; English.
XX CC The invention relates to a new composition which comprises: (i) the
XX CC somatostatin analogue SOM2 AGCKNFDWKPTSDC (3-14 disulphide bridge),
XX CC and (ii) at least 4 of the peptides: antagonist of vasoactive
XX CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
XX CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
XX CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
XX CC more general compositions containing peptide analogues of somatostatin,
XX CC VIP, bombesin and substance P. The compositions are used in human or
XX CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
XX CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
XX CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
XX CC breast, kidney or particularly rectum and colon, and (b) to prevent,
XX CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
XX CC cells express receptors for VIP, somatostatin, bombesin and/or substance
XX CC P. The present sequence represents substance P antagonist (SP1).
XX SQ Sequence 11 AA;

Query Match 84.5%; Score 60; DB 19; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.0039;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
Db 1 rpkipqfwll 11

RESULT 33
AAB08303
ID AAB08303 standard; peptide; 11 AA.
XX AC AAB08303;
XX DE

```

DT 04-DEC-2000 (first entry)
XX Amino acid sequence of Substance P analogue SP1.
DE
XX
XX Vasoactive intestinal peptide; VIP; analogue; somatostatin; SOM1; SOM2;
KW VIP1; VIP2; VIP3; BOM1; bombesin; SP1; substance P; MuJ-7; tumour growth;
KW tumour angiogenesis; metastasis; cancer; angiogenesis; adenocarcinoma;
KW leukaemia; lymphoma.
XX
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Misc-difference 5 /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
XX
XX WO200047221-A1.
XX
XX 17-AUG-2000.
XX
XX 11-FEB-2000; 2000WO-US03559.
XX
XX 11-FEB-1999; 99US-0248381.
XX
XX (NAIM-) NAT INST IMMUNOLOGY.
PA (DABU-) DABUR RES FOUND.
PA (CORD/) CORD J I.
XX
XX Mukherjee R, Jaggi M, Prasad S, Burman AC, Rajendran P, Mathur A;
PI Singh A;
XX
XX WPI; 2000-549083/50.
XX
XX Novel therapeutically active composition comprising at least 5
PT peptides, useful for treating angiogenesis especially as a result of
PT adenocarcinomas -
XX
XX Disclosure; Page 8; 42pp; English.
XX
XX The present sequence represents an analogue of Substance P. The
CC specification describes therapeutically active compositions comprising
CC at least one analogue of somatostatin (chosen from SOM1 and SOM2), and
CC at least four analogues chosen from vasoactive intestinal peptide (VIP) 1
CC (a VIP antagonist), VIP2 (a VIP receptor binding inhibitor), VIP3 (a VIP
CC receptor antagonist), BOM1 (a bombesin antagonist), and SP1 (a substance
CC P antagonist). The combination of these 7 analogues is known as MuJ-7.
CC MuJ-7 is used as an anticancer drug to restrict tumour growth and spread
CC by inhibiting tumour angiogenesis. MuJ-7, in addition, inhibits
CC metastasis through its antiangiogenic activity in all cancers. The
CC peptides are useful for the treatment and prevention of angiogenesis,
CC especially as a result of adenocarcinomas of the colon, breast, lung,
CC prostate, kidney, leukemias or lymphomas.
XX
XX Sequence 11 AA;
SQ

Query Match 84.5%; Score 60; DB 21; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.0039;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RPKPQQWFWM 11
Db 1 rpkpfgfwll 11
RESULT 34
AAB91414
ID AAB91414 standard; Peptide; 11 AA.

XX AAB91414;
AC
XX 22-JUN-2001 (first entry)
DT
XX Tachykinins peptide SEQ ID NO:590.
DE
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200069900-A2.
PN
XX 23-NOV-2000.
PD
XX 17-MAY-2000; 2000WO-US13576.
PF
XX 17-MAY-1999; 99US-0134406.
PR
XX 10-SEP-1999; 99US-0153406.
PR
XX 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX Disclosure; Page 392; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX Sequence 11 AA;
SQ

Query Match 84.5%; Score 60; DB 22; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.0039;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RPKPQQWFWM 11
Db 1 rpkpfgfwll 11
RESULT 35
AAB08313
ID AAB08313 standard; peptide; 11 AA.
XX
XX AAB08313;
AC
XX 04-DEC-2000 (first entry)
DT

Query Match 76.1%; Score 54; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQQWFWM 11
| | | | | | | |
Db 1 pqqwfwlm 8

RESULT 37

AAW50970
ID AAW50970 standard; peptide; 8 AA.

XX AC AAW50970;

XX DT 31-JUL-1998 (first entry)

XX DE Substance P analogue residues 4-11, [D-Pro4,D-Trp7,9].

XX KW Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
XX KW Substance P; cancer; inhibition; growth hormone releasing factor;
XX KW spantide.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 4 /note= "D-form residue"

FT Misc-difference 6 /note= "D-form residue"

FT Modified-site 8 /note= "D-form residue"

FT Modified-site 8 /note= "C-terminal amide"

XX EP835662-A2.

XX 15-APR-1998.

XX 11-DEC-1996; 96EP-0309012.

XX 08-OCT-1996; 96US-0727679.

XX 16-AUG-1996; 96IN-0001822.

XX (NAIM-) NAT INST IMMUNOLOGY.

XX Jaggi M, Mukherjee R;

XX WPI; 1998-208959/19.

XX Composition containing analogues of vasoactive intestinal peptide,
XX somatostatin - bombesin and substance P, for treatment of tumours
XX and for inhibiting over-expression of these peptide(s)

XX Disclosure; Page 13; 49pp; English.

XX The invention relates to a new composition which comprises: (i) the
XX somatostatin analogue SOM2 ACCKNFFQWKPTSC (3-14 disulphide bridge),
XX and (ii) at least 4 of the peptides: antagonist of vasoactive
XX intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
XX receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
XX antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
XX more general compositions containing peptide analogues of somatostatin,
XX VIP, bombesin and substance P. The compositions are used in human or
XX veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
XX or cancer cells, particularly for treatment of leukaemia, lymphoma,
XX adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
XX breast, kidney or particularly rectum and colon, and (b) to prevent,
XX inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
XX cells express receptors for VIP, somatostatin, bombesin and/or substance
XX P. The present sequence represents a substance P analogue.

XX Sequence 8 AA;

Query Match 76.1%; Score 54; DB 19; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQQWFWM 11
| | | | | | | |
Db 1 pqqwfwlm 8

RESULT 38

AAW50970

ID AAR28392 standard; peptide; 11 AA.

XX AC AAR28392;

XX DT 18-MAR-1993 (first entry)

XX DE Bradykinin receptor antagonist CT-0008.

XX KW Bradykinin receptor antagonist; heterodimer; higher oligomer;
XX KW potency; duration; CP-0088; burns; migraine; shock CNS injury; asthma;
XX KW rhinitis; premature labour; inflammatory arthritis; homodimer;
XX KW inflammatory bowel disease.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 2 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "D-form residue"

FT Modified-site 11 /label= Nle

XX WO9217201-A.

XX 15-OCT-1992.

XX 30-MAR-1992; 92WO-US02431.

XX 01-APR-1991; 91US-0677391.

XX 27-MAR-1992; 92US-0859582.

XX (CORT-) CORTECH INC.

XX Allen LG, Blodgett JK, Cheronis JC, Eubanks SR, Nguyen KT;
XX Whalley ET;

XX WPI; 1992-365995/44.

XX Bradykinin antagonists comprising linked bradykinin antagonist
XX chains - are for treatment of post-operative pain, asthma and
XX aseptic shock

XX Disclosure; Page 76; 109pp; English.

XX The sequence given is a bradykinin receptor antagonist which can form
XX homo- or heterodimers or higher oligomers. It demonstrates greater
XX potency and/or duration of action than the parent peptide itself.
XX Bradykinin receptors antagonists such as this can be used in the
XX treatment of burns, peroperative pain, migraine and other forms of
XX pain, shock CNS injury, asthma, rhinitis, premature labour,
XX inflammatory arthritis, inflammatory bowel disease etc.

XX Sequence 11 AA;

Query Match 71.8%; Score 51; DB 13; Length 11;
Best Local Similarity 80.0%; Pred. No. 0.089;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RPKPQOWFWL 10
| | | | : | | |
Db 1 rpkpqffwl 10

RESULT 39

AAP30141
ID AAP30141 standard; peptide; 11 AA.

XX AC AAP30141;

XX DT 14-JUN-1992 (first entry)

XX DE Sequence of peptide with substance P inhibiting activity.

XX KW Substance P antagonist; pain therapy; hypertension.

XX FH Key Location/Qualifiers

FT Modified-site 2

FT Modified-site 7 /label= D-P, D-p-Cl-F

FT Modified-site 7 /label= D-W

FT Misc-difference 8

FT Modified-site 9 /label= F,I

FT Modified-site 9 /label= D-W

FT Modified-site 11 /label= M,I

FT /note= "bonded to NH2"

XX WO801251-A.

XX PN 14-APR-1983.

XX PD 09-OCT-1981; 81WO-DE00171.

XX PF 09-OCT-1981; 81WO-DE00171.

XX PR 09-OCT-1981; 81EP-0902802.

XX XX (FERR) FERRING ARZNEIMITTE.

XX PA (HORI/) HORIG J.

XX PI Horig J;

XX DR WPI; 1983-39155K/16 (39155K).

XX PT Undecapeptide derivs. with substance P inhibiting activity -

XX PT useful for treating pain and hypertension

XX PS Claim 1; Page 18; 25pp; German.

XX XX The peptides of the invention are powerful antagonists of Substance

XX CC P and so are useful in human and veterinary medicine, for treating

XX CC pain and hypertension (esp.) chronic conditions. A 10 microm concn.

XX CC of AAP30142 produced about 50% inhibition at a Substance P concn. of

XX CC 7.5-20 nanom.

XX XX Sequence 11 AA;

Query Match

Best Local Similarity 70.4%; Score 50; DB 4; Length 11;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 RPKPQOWFWL 10

| | | | | |

Db 1 rxkpgqwxwl 10

RESULT 40

AAR21934

ID AAR21934 standard; Protein; 11 AA.

XX AC AAR21934;

XX DT 25-JUN-1992 (first entry)

XX DE Substance P [Tyr7] and fragment (7-11) [Tyr 7].

XX KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;

XX KW syndrome; hereditary cerebral haemorrhage.

XX OS Synthetic.

XX PN WO9202248-A.

XX PD 20-FEB-1992.

XX PF 29-JUL-1991; 91WO-US05323.

XX PR 27-JUL-1990; 90US-0559173.

XX PA (CHIL-) CHILDRENS MED CENT.

XX PI Yankner BA;

XX DR WPI; 1992-079804/10.

XX PT Treatment of neuronal accumulation of beta-amyloid - using

XX PT tachykinin agonists e.g. substance P, physalaemin and neurokinin

XX PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX PS Claim 10; Page 21; 35pp; English.

XX CC The peptide is the tachykinin agonist substance P with a Tyr

XX CC residue substituted at position 7. The peptide was synthesised

XX CC by standard solid phase synthesis. A N-terminal deleted peptide

XX CC (7-11) with the Tyr substitution was also synthesised. Neuronal

XX CC accumulation of beta-amyloid may be treated by administration

XX CC of tachykinin agonists. The peptides can reduce the neurotoxic

XX CC effects of a beta-amyloid related polypeptide on cultured neurons.

XX CC The peptide and its analogues are useful for controlling diseases

XX CC characterised by beta amyloid accumulation in the brain such as

XX CC Alzheimer's disease and Down's syndrome.

XX CC See also AAR21932-75.

XX SQ Sequence 11 AA;

Query Match

Best Local Similarity 69.0%; Score 49; DB 13; Length 11;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RPKPQOWFWL 11

| | | | | : | |

Db 1 rpkpqyfglm 11

RESULT 41

AAR28443

ID AAR28443 standard; peptide; 11 AA.

XX AC AAR28443;

XX DT 22-MAR-1993 (first entry)

XX DE Neurokinine 1 ligand #1.

XX KW NK1 receptor; tumour; malignant glioma; pheochromocytoma;

XX KW paraganglia; small cell lung cancer; nerve regeneration; lymphoma;

XX KW granuloma; Crohn's disease.

OS Synthetic.
XX Key Location/Qualifiers
FH Modified-site 9
FT /label= MeGly
FT Modified-site 11
FT /label= OTHER
FT /note= "Met(O)2-NH2"
XX WO9218536-A.
XX 29-OCT-1992.
XX 22-APR-1992; 92WO-US03307.
XX 22-APR-1991; 91EP-0200955.
XX (MILCW) MALLINCKRODT MEDICAL INC.
PA Bakker WH, Hagen PM, Krenning EP, Lamberts SWJ, Visser TJ;
XX WPI; 1992-382047/46.
XX Detection and localisation of tissues with neurokinine-1 receptors
PT - for detecting and treating tumours having neurokinine-1
PT receptors e.g. malignant glioma, small cell lung cancer etc.
XX Disclosure; Page 4; 22pp; English.
XX This peptide or its Tyr0 deriv. is a preferred peptide having a
CC selective affinity to neurokinine-1 receptors which (when
CC labelled with a radioactive isotope) can be used in imaging methods.
CC A generic formula for preferred peptides is AAR28441. Such peptides
CC are thus useful in diagnosis and treatment of conditions that are
CC related to NK1 receptors and in visualising NK1 receptors on certain
CC tissues. See AAR28442-R28446.
XX Sequence 11 AA;
SQ
Query Match 69.0%; Score 49; DB 13; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.18;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RPKPQQWFWM 11
Db 1 rpkpqffmlm 11
RESULT 42
AAW92666
ID AAW92666 standard; peptide; 11 AA.
XX
AC AAW92666;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #12.
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodysplasia.
XX Homo sapiens.
OS
XX US5876948-A.
PN
XX
XX 02-MAR-1999.
PD
XX 27-JUL-1991; 91US-0737371.
PF
XX 29-JUL-1991; 91US-0737371.
XX
PR 27-JUL-1990; 90US-03559173.
PR

XX (CHIL-) CHILDRENS MEDICAL CENT.
PA Yankner BA;
XX WPI; 1999-189630/16.
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
PT
XX Disclosure; Column 15-16; 28pp; English.
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodysplasia with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX Sequence 11 AA;
SQ
Query Match 69.0%; Score 49; DB 20; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.18;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RPKPQQWFWM 11
Db 1 rpkpqyfglm 11
RESULT 43
AAP80318
ID AAP80318 standard; protein; 8 AA.
XX
XX AAP80318;
XX
DT 14-SEP-1990 (first entry)
XX
DE Sequence of neuropeptide antagonist F which binds with polypeptide
DE receptor for bombesin type polypeptides.
XX Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist F.
XX Swiss 3T3 cells.
OS
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /label=OTHER
FT /note="DPro"
FT Misc-difference 4 /label=OTHER
FT /note="DTrp"
FT Misc-difference 6 /label=OTHER
FT /note="DTrp"
FT Misc-difference 7 /label=OTHER
FT /note="DTrp"
FT Misc-difference 8 /label=OTHER
FT /note="Met-NH2"
FT
XX WO8807551-A.
XX
XX 06-OCT-1988.
PD
XX 31-MAR-1988; 88WO-GH00255.
XX

XX 25-NOV-1987; 87GB-0027638.
XX (IMCR) IMPERIAL CANCER RES.
XX Rosengurt E, Zachary I, Woll P;
XX WPI; 1988-292842/41.
XX
XX New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation
XX
XX Disclosure; Table 2; 42pp; English.
XX
XX The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.
XX
XX Sequence 8 AA;
SQ

Query Match 67.6%; Score 48; DB 9; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 PQQWFWM 11
Db 1 pqqwfwmm 8

RESULT 44
AAR15359
ID AAR15359 standard; Protein; 8 AA.
XX
XX AAR15359;
XX
XX 02-MAR-1992 (first entry)
XX
XX Substance P antagonist (1).
XX
XX Analgesic; antiinflammatory; oxidation; resistance; sterilisation;
KW central nervous system.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 1 /label= D-Pro
FT Modified-site 4 /label= D-Trp
FT Modified-site 6 /label= D-Trp
FT Modified-site 7 /label= D-Trp
FT Modified-site 7 /label= D-2-ethyl-Trp
XX
XX WO9118016-A.
XX
XX 28-NOV-1991.
XX

PF 17-APR-1991; 91WO-EP00727.
XX
XX 11-MAY-1990; 90IT-0020273.
XX (DEGH/) DEGHENGI R.
XX Deghenghi R;
XX WPI; 1991-369186/50.
XX
XX New bioactive peptide(s) - having D-tryptophan replaced by
PT D-2-alkyl-tryptophan to increase resistance to oxidative
PT degradation
XX
XX Claim 9; Page 21; 26pp; English.
XX
XX The peptides represented in AAR15359 and AAR15360 are antagonists of
CC substance P. Substance P is a neurotransmitter used by sensory
CC neurons that convey responses of pain or other noxious stimuli to
CC the central nervous system. These peptides have analgesic and
CC antiinflammatory activity.
CC The D-2-alkyl-Trp provides increased oxidation resistance to the
CC peptide while maintaining the same pharmacological effect as
CC analogous bioactive peptides in which the tryptophan residue
CC is not replaced. Oxidative degradation may take place e.g in the
CC presence of reactive radicals or during high energy sterilisation.
CC See also AAR15357-63.
XX
XX Sequence 8 AA;
SQ

Query Match 67.6%; Score 48; DB 12; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 PQQWFWM 11
Db 1 pqqwfwmm 8

RESULT 45
AAW50974
ID AAW50974 standard; peptide; 8 AA.
XX
XX AAW50974;
XX
XX 31-JUL-1998 (first entry)
XX
XX Substance P analogue residues 4-11, [D-Pro4,D-Trp7,9,10].
XX
XX Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
KW Substance P; cancer; inhibition; growth hormone releasing factor;
KW spantide.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Misc-difference 4 /note= "D-form residue"
FT Misc-difference 6 /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 8 /note= "D-form residue"
FT Modified-site 8 /note= "C-terminal amide"
XX
XX EP835662-A2.
XX
XX 15-APR-1998.
XX
XX 11-DEC-1996; 96EP-0309012.
XX

XX 08-OCT-1996; 96US-0727679.
PR 16-AUG-1996; 96IN-0001822.
XX (NATM-) NAT INST IMMUNOLOGY.
XX Jaggi M, Mukherjee R;
PI WPI; 1998-208959/19.
DR Composition containing analogues of vasoactive intestinal peptide,
PT somatostatin - bombesin and substance P, for treatment of tumours
PT and for inhibiting over-expression of these peptide(s)
XX Disclosure; Page 13; 49pp; English.
XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 AGCKNFRDWRPTSDC (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SPI). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.
XX Sequence 8 AA;
SQ

Query Match 67.6%; Score 48; DB 19; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 PQQWFWM 11
DB 1 pqqwfwm 8

RESULT 46
AAP61480
ID AAP61480 standard; peptide; 11 AA.
AC AAP61480;
XX
XX 22-AUG-1991 (first entry)
DT Sequence of undeca peptide substance P1.
XX Hypertension therapy; sleep disorder; anti-stress agent.
KW
FH Key Location/Qualifiers
FT Misc-difference 11 /label= Met-NH2
FT
XX DD229593-A.
XX
XX 13-NOV-1985.
PD
XX 28-NOV-1984; 84DD-0269954.
XX
XX 28-NOV-1984; 84DD-0269954.
XX
XX (DEAK) AKAD WISSENSCHAFT DDR.
XX
XX Oehme P, Hecht K, Wachtel E, Roske I, Kolometseva IA;
PI Alarapetjan M, Blenert M, Vogt WE, Hilse H, Gores E, Poppei M;
PI Nieber K, Bergmann J;

XX WPI; 1986-069587/11.
DR Cpd. having N-terminal sequences of undeca;peptide substance P -
PT are medicinal agents with anti-stress activity
XX
XX Claim 1; Page 1; 15pp; German.
XX The inventors claim an antistress compound which contains the N-
CC terminal SQ of AAP61480, pref. Arg-Pro-Lys-Pro-X (X= COOH or NH2).
CC Compared with the full undecapeptide they have much reduced
CC side effects (acute hypotension, spastic effects on the ileum and
CC histamine release from peritoneal mast cells).
XX Sequence 11 AA;
SQ

Query Match 67.6%; Score 48; DB 7; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPQOWFWLM 11
DB 1 rpkpqffglm 11

RESULT 47
AAP80312
ID AAP80312 standard; protein; 11 AA.
XX
XX AAP80312;
DT 14-SEP-1990 (first entry)
XX
XX Sequence of neuropeptide substance P which binds with polypeptide
DE receptor for bombesin type polypeptides.
XX
XX Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW substance P.
XX Swiss 3T3 cells.
XX
XX Key Location/Qualifiers
FT Misc-difference 11 /label=OTHER
FT /note="Met-NH2"
XX
XX WO8807551-A.
XX
XX 06-OCT-1988.
XX
XX 31-MAR-1988; 88WO-GB00255.
XX
XX 25-NOV-1987; 87GB-0027638.
XX
XX (IMCR) IMPERIAL CANCER RES.
XX
XX Rosengurt E, Zachary I, Woll P;
PI
XX WPI; 1988-292842/41.
XX
XX New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation
XX
XX Disclosure; Table 2; 42pp; English.
XX
XX The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as

CC [D-Pro2] spantide. Antagonist B is also commercially available structural
 CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
 CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
 CC substance P antagonists (see AAP80313-80322) were tested for their
 CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
 CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
 CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
 CC potent than either A or D. Spantide (B) had no antagonist activity even
 CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
 CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
 CC growth is associated with disorders of proteins of the bombesin family.
 XX Sequence 11 AA;

Query Match 67.6%; Score 48; DB 9; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.25;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RPKPQOWFWLM 11
 |||||: ||
 Db 1 rpkpqgffglm 11

RESULT 48
 AAP80320
 ID AAP80320 standard; protein; 11 AA.
 XX AAP80320;
 AC
 DT 14-SEP-1990 (first entry)
 XX
 DE Sequence of neuropeptide antagonist H which binds with polypeptide
 DE receptor for bombesin type polypeptides.
 XX
 KW Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
 KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
 KW antagonist H.
 XX
 OS Swiss 3T3 cells.

FH Key Location/Qualifiers
 FT Misc-difference 1 /label=OTHER
 FT /note="DArg"
 FT Misc-difference 2 /label=OTHER
 FT /note="DPro"
 FT Misc-difference 7 /label=OTHER
 FT /note="DPhe"
 FT Misc-difference 9 /label=OTHER
 FT /note="DHis"
 FT Misc-difference 11 /label=OTHER
 FT /note="Met-NH2"

XX W08807551-A.
 PN
 XX
 PD 06-OCT-1988.
 XX
 PF 31-MAR-1988; 8BWO-GB00255.
 XX
 PR 25-NOV-1987; 87GB-0027638.
 XX
 PA (IMCR) IMPERIAL CANCER RES.
 XX
 PI Rosengurt E, Zachary I, Woll P;
 XX
 DR WPI; 1988-292842/41.
 XX
 PT New polypeptide receptor for bombesin type polypeptide(s) -

PT is isolated from surface of Swiss 3T3 cells, and antibodies and
 PT antagonists are useful for treating uncontrolled cell proliferation
 XX
 PS Disclosure; Table 2; 42pp; English.
 XX
 CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
 CC cells which binds selectively with polypeptides of the bombesin type and
 CC binds with antagonist A and antagonist D. Antagonist A is a
 CC commercially available structural variant of substance P, known as
 CC [D-Arg1, D-Pro2, D-Trp7, 9, Leu11] substance P. It is also known as
 CC [D-Pro2] spantide. Antagonist B is also commercially available structural
 CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
 CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
 CC substance P antagonists (see AAP80313-80322) were tested for their
 CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
 CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
 CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
 CC potent than either A or D. Spantide (B) had no antagonist activity even
 CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
 CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
 CC growth is associated with disorders of proteins of the bombesin family.
 XX Sequence 11 AA;

Query Match 67.6%; Score 48; DB 9; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.25;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQOWFWLM 11
 |||||: ||
 Db 1 rpkpqgffglm 11

RESULT 49
 AAR13162
 ID AAR13162 standard; Protein; 11 AA.
 XX AAR13162;
 AC
 DT 10-OCT-1991 (first entry)
 XX
 DE Sialic acid-bonded polypeptide (2).
 XX
 KW Sialic acid; cataract; immune disorder.
 XX
 OS Synthetic.

FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminally glycosylated by 5-acetamido-
 FT 2,4,7,8,9-penta-O-acetyl-3,5-deoxy-beta-
 FT D-glycero-D-galactononulopyranosyl"
 XX JP03151398-A.
 PN
 XX
 PD 27-JUN-1991.
 XX
 PF 06-NOV-1989; 89JP-0288560.
 XX
 PR 06-NOV-1989; 89JP-0288560.
 XX
 PA (MECT-) MECT KK.
 XX
 DR WPI; 1991-233839/32.

XX New sialic acid derivs. bonded to physiologically active
 PT polypeptide - for treatment of cataracts, immune disorders etc.
 PT with prolonged half-life
 XX
 PS Example 4; Page 6; 7pp; Japanese.
 XX
 CC The prod. has prolonged half-life and is used as a pharmaceutical

CC for treatment of various diseases, such as cataract and immune
CC disorders. It comprises a peptide, N-terminally glycosylated by
CC (opt. acetylated) sialic acid.
CC See also AAR12332, AAR13162 and AAR13201.

XX
SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 12; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:11
Db 1 rpkpqffglm 11

RESULT 50
AAR11854
ID AAR11854 standard; peptide; 11 AA.

XX
AC AAR11854;

XX
DT 09-JUL-1991 (first entry)

XX
DE Undecapeptide substance P.

XX
KW Undecapeptide; pharmaceutical; stress; sleep.

XX
OS Synthetic.

XX
PN DD285097-A.

XX
PD 05-DEC-1990.

XX
PF 21-JUN-1989; 89DD-0329831.

XX
PR 21-JUN-1989; 89DD-0329831.

XX
PA (DEAK) INST WIRKSTOFF AKAD.

XX
PA (FARF) VEB CHEM BITTERFELD.

XX
PI Beyermann M, Bienert M, Egler H, Haupke K, Krause E;

XX
PI Schwarzw J, Walz H;

XX
DR WPI; 1991-133498/19.

XX
PT Undeca-peptide substance pharmaceutical intermediate prepn. - by

PT forming dipeptide between nitro-arginine and proline and

PT reacting with polymer-bound non-peptide

XX
PS Calim 1; Page 1; 8pp; German.

XX
CC The peptide is prepared by solid phase synthesis.

CC It can be used in the preparation of pharmaceuticals which can be

CC used to treat certain stress-induced disturbances of the sleep

XX
SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 12; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:11
Db 1 rpkpqffglm 11

RESULT 51
AAR21938
ID AAR21938 standard; Protein; 11 AA.

XX
AC AAR21938;
DT 25-JUN-1992 (first entry)
XX
DE Substance P [Me-Leu 10].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Modified-site 10
FT /label= OTHER
FT /note= "OTHER = Me-Leu"

XX
PN W09202248-A.

XX
PD 20-FEB-1992.

XX
PF 29-JUL-1991; 91WO-US05323.

XX
PR 27-JUL-1990; 90US-0559173.

XX
PA (CHIL-) CHILDRENS MED CENT.

XX
PI Yankner BA;

XX
DR WPI; 1992-079804/10.

XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX
PS Claim 10; Page 21; 35pp; English.

XX
CC The peptide is the tachykinin agonist substance P with Me-Leu
CC substituted at position 10. The peptide was synthesised
CC by standard solid phase synthesis. Neuronal accumulation of
CC beta-amyloid may be treated by administration of tachykinin
CC agonists. The peptides can reduce the neurotoxic effects of a
CC beta-amyloid related polypeptide on cultured neurons. The peptide
CC and its analogues are useful for controlling diseases characterised
CC by beta amyloid accumulation in the brain such as Alzheimer's
CC disease and Down's syndrome.
CC See also AAR21932-75.

XX
SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 13; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:11
Db 1 rpkpqffglm 11

RESULT 52
AAR21942
ID AAR21942 standard; Protein; 11 AA.

XX
AC AAR21942;

XX
DT 25-JUN-1992 (first entry)

XX
DE Substance P [MeMet 11].

XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.

XX

```
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 11
FT /label= OTHER
FT /note= "OTHER = Methyl Methionine"
XX
XX WO9202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991; 91WO-US05323.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 10; Page 21; 35pp; English.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 10; Page 21; 35pp; English.
XX
XX The peptide is the tachykinin agonist substance P with a methyl
XX methionine residue substituted at position 11. The peptide was
XX synthesised by standard solid phase synthesis. Neuronal
XX accumulation of beta-amyloid may be treated by administration of
XX tachykinin agonists. The peptide can reduce the neurotoxic effects
XX of a beta-amyloid related polypeptide on cultured neurons. The
XX peptide and its analogues are useful for controlling diseases
XX characterised by beta amyloid accumulation in the brain such as
XX Alzheimer's disease and Down's syndrome.
XX See also AAR21932-75.
XX
XX Sequence 11 AA;
XX SQ

Query Match 67.6%; Score 48; DB 13; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQWFWM 11
Db |||||:| |
1 rpkpqgffglm 11

RESULT 53
AAR21946
ID AAR21946 standard; Protein; 11 AA.
XX
XX AAR21946;
XX
XX 25-JUN-1992 (first entry)
XX
XX Substance P [Me-Phe 8].
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 8
FT /label= OTHER
FT /note= "OTHER = Methyl phenylalanine"
XX
XX WO9202248-A.
XX
XX 20-FEB-1992.
XX

Query Match 67.6%; Score 48; DB 13; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQWFWM 11
Db |||||:| |
1 rpkpqgffglm 11

RESULT 54
AAR21954
ID AAR21954 standard; Protein; 11 AA.
XX
XX AAR21954;
XX
XX 25-JUN-1992 (first entry)
XX
XX Substance P [Me-Gly 9].
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 9
FT /label= OTHER
FT /note= "OTHER = Methyl glycine"
XX
XX WO9202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991; 91WO-US05323.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
```

XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
PS Claim 10; Page 22; 35pp; English.
XX
CC The peptide is the tachykinin agonist substance P with a methyl
CC glycine residue substituted at position 9. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
XX Sequence 11 AA;
SQ

Query Match 67.6%; Score 48; DB 13; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:| |
Db 1 rpkpqgffglm 11

RESULT 55
AAR21962
ID AAR21962 standard; Peptide; 11 AA.
XX
AC AAR21962;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P [Me Gly 6, Met (O2) 11].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 6 /label= OTHER
FT /note= "OTHER - Methyl glycine"
FT
FT Misc-difference 11
FT /label= OTHER
FT /note= "OTHER - Met (O2)"
XX
PN WO9202248-A.
XX
PD 20-FEB-1992.
XX
PF 29-JUL-1991; 91WO-US05323.
XX
PR 27-JUL-1990; 90US-0559173.
XX (CHIL-) CHILDRENS MED CENT.
XX Yankner BA;
XX
DR WPI; 1992-079804/10.
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 10; Page 22; 35pp; English.

CC The peptide is the tachykinin agonist, substance P with methyl
CC glycine substituted at position 9 and Met (O2) at position 11.
CC The peptide was synthesised by standard solid phase synthesis.
CC Neuronal accumulation of beta-amyloid may be treated by administ-
CC ration of tachykinin agonists. The peptide can reduce the neuro-
CC toxic effects of a beta-amyloid related polypeptide on cultured
CC neurons. The peptide and its analogues are useful for controlling
CC diseases characterised by beta amyloid accumulation in the brain
CC such as Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
XX Sequence 11 AA;
SQ

Query Match 67.6%; Score 48; DB 13; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:| |
Db 1 rpkpqgffglm 11

RESULT 56
AAR21963
ID AAR21963 standard; Peptide; 11 AA.
XX
AC AAR21963;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P [p-Chloro-Phe 7,8].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 7 /label= OTHER
FT /note= "OTHER - p-Chloro-phenylalanine"
FT
FT Modified-site 8 /label= OTHER
FT /note= "OTHER - p-Chloro-phenylalanine"
XX
PN WO9202248-A.
XX
PD 20-FEB-1992.
XX
PF 29-JUL-1991; 91WO-US05323.
XX
PR 27-JUL-1990; 90US-0559173.
XX (CHIL-) CHILDRENS MED CENT.
XX Yankner BA;
XX
DR WPI; 1992-079804/10.
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 10; Page 22; 35pp; English.
XX
CC The peptide is the tachykinin agonist, substance P fragment
CC with p-Chloro-phenylalanine residues substituted at positions 7 and
CC 8. The peptide was synthesised by standard solid phase synthesis.
CC Neuronal accumulation of beta-amyloid may be treated by administ-
CC ration of tachykinin agonists. The peptide can reduce the neuro-
CC toxic effects of a beta-amyloid related polypeptide on cultured
CC neurons. The peptide and its analogues are useful for controlling

CC diseases characterised by beta amyloid accumulation in the brain
 CC such as Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.

XX SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 13; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.25;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
 |||||:| |

Db 1 rpkpqffglm 11

RESULT 57

AAR28442
 ID AAR28442 standard; peptide; 11 AA.

XX AC AAR28442;

XX DT 22-MAR-1993 (first entry)

XX DE Substance P.

XX KW NK1 receptor; tumour; malignant glioma; pheochromocytoma;
 KW paraganglia; small cell lung cancer; nerve regeneration; lymphoma;
 KW granuloma; Crohn's disease.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Modified-site 11 /note= "amidated"

XX PN W09218536-A.

XX PD 29-OCT-1992.

XX PF 22-APR-1992; 92WO-US03307.

XX PR 22-APR-1991; 91EP-0200955.

XX PA (MLCW) MALLINCKRODT MEDICAL INC.

XX PI Bakker WH, Hagen PM, Krenning EP, Lamberts SWJ, Visser TJ;

XX DR WPI; 1992-382047/46.

XX PT Detection and localisation of tissues with neurokinine-1 receptors
 PT - for detecting and treating tumours having neurokinine-1
 PT receptors e.g. malignant glioma, small cell lung cancer etc.

XX PS Disclosure; Page 4; 22pp; English.

XX CC Substance P or its Tyr0 deriv. is a preferred peptide having a
 CC selective affinity to neurokinine-1 receptors which (when
 CC labelled with a radioactive isotope) can be used in imaging methods.
 CC A generic formula for preferred peptides is AAR28441. Such peptides
 CC are thus useful in diagnosis and treatment of conditions that are
 CC related to NK1 receptors and in visualising NK1 receptors on certain
 CC tissues. See also AAR28443-R28446.

XX SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 13; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.25;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
 |||||:| |

Db 1 rpkpqffglm 11

RESULT 58

AAR42646
 ID AAR42646 standard; peptide; 11 AA.

XX AC AAR42646;

XX DT 19-APR-1994 (first entry)

XX DE Neurokinin 1 receptor affinity-contg. peptide (Substance P).

XX KW Neurokinin 1; somatostatin; receptor; cytokine; growth factor;
 KW hormone; intra-operativ; tumour; low energy gamma photon;
 KW radionuclide.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Modified-site 11 /note= "the C-terminal is amidated"

XX PN W09318797-A.

XX PD 30-SEP-1993.

XX PF 24-MAR-1993; 93WO-US02772.

XX PR 25-MAR-1992; 92EP-0200848.

XX PA (MLCW) MALLINCKRODT MEDICAL INC.

XX PI Doedens BJ, Ensing GJ, Panek KJ;

XX DR WPI; 1993-320461/40.

XX PT Intra-operatively detecting and locating tumour tissues - using
 PT specific peptide(s) labelled with low energy gamma photon
 PT emitting radionuclide

XX PS Disclosure; Page 4; 3lpp; English.

XX CC The method of intraoperatively detecting and locating tumoral
 CC tissues makes use of peptides having selective neurokinin 1
 CC receptor affinity (AAR42644: generic formula; AAR42645-R42650:
 CC specific examples), peptides having selective somatostatin
 CC receptor affinity (AAR42645: generic formula; AAR42651-R42660:
 CC specific examples), and peptides selected from cytokines,
 CC growth factors and hormones.

XX SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 14; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.25;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
 |||||:| |

Db 1 rpkpqffglm 11

RESULT 59

AAR42647
 ID AAR42647 standard; peptide; 11 AA.

XX AC AAR42647;

XX DT 19-APR-1994 (first entry)

XX DE Neurokinin 1 receptor affinity-contg. peptide.

KW Neurokinin 1; somatostatin; receptor; cytokine; growth factor;
 KW hormone; intra-operativ; tumour; low energy gamma photon;
 OS radionuclide.

XX Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 9

FT FT /label= MeGly

FT Modified-site 11

FT FT /note= "Met is Met(O2); the C-terminal is amidated"

XX KW W09318797-A.

XX PN

XX PD

XX XX 30-SEP-1993.

XX XX 24-MAR-1993; 93WO-US02772.

XX XX 25-MAR-1992; 92EP-0200848.

XX XX (MLCW) MALLINCKRODT MEDICAL INC.

XX XX Doedens BJ, Ensing GJ, Panek KJ;

XX XX WPI; 1993-320461/40.

XX XX Intra-operatively detecting and locating tumour tissues - using

XX XX specific peptide(s) labelled with low energy gamma photon

XX XX emitting radionuclide

XX XX Disclosure; Page 5; 31pp; English.

XX XX The method of intraoperatively detecting and locating tumoral

XX XX tissues makes use of peptides having selective neurokinin 1

XX XX receptor affinity (AA42644; generic formula; AA42646-R42650;

XX XX specific examples), peptides having selective somatostatin

XX XX receptor affinity (AA42645; generic formula; AA42651-R42660;

XX XX specific examples), and peptides selected from cytokines,

XX XX growth factors and hormones.

XX XX Sequence 11 AA;

XX XX Query Match 67.6%; Score 48; DB 14; Length 11;

XX XX Best Local Similarity 81.8%; Pred. No. 0.25;

XX XX Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

XX XX QY 1 RPKPQOWFWLM 11

XX XX |||||:| |

XX XX Db 1 rpkpqgffxlm 11

XX XX RESULT 60

XX XX AAR85243

XX XX ID AAR85243 standard; peptide; 11 AA.

XX XX AC AAR85243;

XX XX DT 18-AUG-1997 (first entry)

XX XX DE Substance P peptide.

XX XX KW Ligand; antibody; receptor; SELEX; random library; amplification; PCR;

XX XX KW Systematic Evolution of Ligands by EXponential enrichment; primer;

XX KW polymerase chain reaction; structure; mimicry; substance P; tachykinin;

XX KW neuropeptide; rheumatoid arthritis; atherosclerosis; cancer;

XX KW diabetic retinopathy.

XX XX Synthetic.

XX XX OS

XX XX FH Key

XX XX Modified-site 11

XX XX /note= "contains C-terminal NH2 group"

XX XX FT

XX W09530775-A1.

XX PN

XX PD

XX XX 16-NOV-1995.

XX XX 03-MAY-1995; 95WO-US05600.

XX XX 21-DEC-1994; 94US-0361795.

XX XX 06-MAY-1994; 94US-0238863.

XX XX 24-MAY-1994; 94US-0248632.

XX XX 09-SEP-1994; 94US-0303362.

XX XX 11-JUN-1990; 90US-0536428.

XX XX 10-JUN-1991; 91US-0714131.

XX XX 21-OCT-1992; 92US-0964624.

XX XX (UYRE-) UNIV RES CORP.

XX XX Allen P, Doudna JA, Feigon J, Gold L, Nieuwlandt D;

XX XX Schneider DJ, Sullenger BA, Wecker M;

XX XX WPI; 1995-404132/51.

XX XX Systematic evolution of ligands by exponential enrichment - for

XX XX identifying nucleic acid ligands used in the treatment of, e.g. type

XX XX B insulin resistance and HIV

XX XX Example 10; Fig 8; 209pp; English.

XX XX The invention relates to a novel method of isolating ligands that bind

XX XX to target proteins e.g. antibodies or receptors, which bind other

XX XX proteins or ligands. The method, designated Systematic Evolution of

XX XX Ligands by EXponential enrichment (SELEX), comprises generating a library

XX XX of random oligonucleotide sequences, about 40-60 nucleotides in length,

XX XX and binding these sequences to the target proteins. After removal of

XX XX unbound material, the remaining bound nucleotides sequences are amplified

XX XX e.g. by PCR, and the newly amplified material is bound again with the

XX XX target protein. This cycle continues until a sufficiently pure

XX XX oligonucleotide sequence is isolated. The method allows the isolation of

XX XX oligonucleotide sequences which structurally mimic the target protein's

XX XX ligand. Ligands AAT06098-130 are examples of nucleic acid ligands which

XX XX bind the tachykinin-family neuropeptide Substance P (this sequence). The

XX XX new ligands were split into 2 groups based on their affinities for

XX XX Substance P. Class 1 ligands had binding affinities up to 2 micromolar

XX XX whereas class 2 ligands bound at above 2 micromolar. This sequence

XX XX represents the consensus of the class 1 ligands. The ligands can be

XX XX used to block the activity of Substance P and is useful in the treatment

XX XX of e.g. rheumatoid arthritis, atherosclerosis, diabetic retinopathy or

XX XX cancer.

XX XX Sequence 11 AA;

XX XX Query Match 67.6%; Score 48; DB 16; Length 11;

XX XX Best Local Similarity 81.8%; Pred. No. 0.25;

XX XX Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

XX XX QY 1 RPKPQOWFWLM 11

XX XX |||||:| |

XX XX Db 1 rpkpqgffxlm 11

XX XX RESULT 61

XX XX AAR77310

XX XX ID AAR77310 standard; peptide; 11 AA.

XX XX AC AAR77310;

XX XX DT 08-MAR-1996 (first entry)

XX XX DE Substance P.

XX XX KW Substance P; neurokinin; neurokinin receptor antagonist;

XX KW sensory perception; tachykinin receptor; therapy;

KW neurodegenerative disorder; Alzheimer's disease; demyelinating disease;
KW multiple sclerosis; respiratory disease; opthalmic disease;
KW addiction disorder; adverse immune reaction; gastrointestinal disorder;
KW bladder function disorder; fibrosing disease; collagen disease;
KW diagnosis.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 11
FT Modified-site 11 /note= "amided"
XX PN US5434158-A.
XX PD 18-JUL-1995.
XX PF 26-APR-1994; 94US-0233487.
XX PR 26-APR-1994; 94US-0233487.
XX PA (MERI) MERCK & CO INC.
XX PI Shah SK;
XX DR WPI; 1995-268290/35.
XX PT New 1'-substd. spiro-indoline-3,4'-piperidine derivs. - useful as
PT selective neurokinin-3 antagonists, e.g. for treating CNS disorders,
PT migraine or esp. asthma.
XX PS Disclosure; Column 1; 16pp; English.
XX CC This sequence represents Substance P. This sequence, and those shown in
CC AAR77311 and AAR77312 are tachykinins. These three sequences are
CC pharmacologically active neuropeptides, and are neurokinin receptor
CC agonists. Neurokinin receptors are widely distributed throughout the
CC mammalian nervous system, circulatory system and peripheral tissues.
CC Neurokinin receptors are involved in sensory perception. These
CC sequences were used in the design and testing of neurokinin antagonists.
CC These antagonists could be used in the treatment of conditions
CC characterised by overstimulation of tachykinin receptors. The
CC antagonists can also be used, for the treatment of neurodegenerative
CC disorders (e.g. Alzheimer's disease), demyelinating diseases (e.g.
CC multiple sclerosis), respiratory diseases, opthalmic diseases, addiction
CC disorders, adverse immune reactions, gastrointestinal disorders, bladder
CC function disorders, fibrosing and collagen diseases. The antagonists can
CC also be used as diagnostic agents.
XX SQ Sequence 11 AA;
Query Match 67.6%; Score 48; DB 16; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPQOQFWLM 11
Db 1 rpkpqffglm 11
RESULT 62
AAW33180
ID AAW33180 standard; peptide; 11 AA.
XX AC AAW33180;
XX DT 29-JAN-1998 (first entry)
XX DE Mono-DTPA-Arg1 Substance P.
XX KW Substance P; radiolabel; diagnostic imaging; therapy;
XX KW mono-DTPA-Arg1.

OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 11 /note= "DTPA-Arg"
FT Modified-site 11 /note= "amided"
XX PN WO9640292-A1.
XX PD 19-DEC-1996.
XX PF 07-JUN-1996; 96WO-US09706.
XX PR 07-JUN-1995; 95US-0480372.
XX PA (MLCW) MALLINCKRODT MEDICAL INC.
XX PI Srinivasan A;
XX DR WPI; 1997-087027/08.
XX PT Prepn. of pure radio-labelled peptide, e.g. for diagnostic imaging -
PT by combining protected poly:amino:carboxylate ligand with peptide
PT and forming complex with radionuclide
XX PS Example 3; Page 12; 20pp; English.
XX CC Preparing a radiolabelled peptide composition, comprises combining
CC a triamine or diamine chelating agent with a peptide, e.g. the
CC present peptide, in a solid phase peptide synthesiser, and
CC complexing a radionuclide with the chelate-peptide conjugate.
CC Radiolabelled peptides or peptidomimetics can be used as diagnostic
CC imaging agents, or in therapeutic applications, e.g. iodine(111)
CC labelled pentetreotide can be used for somatostatin receptor
CC imaging of neuroendocrine tumours. The radiolabelled products are
CC obtained efficiently and inexpensively in high purity. The
CC protected polyaminocarboxylate ligands can be added to the peptide
CC by standard solution or solid phase peptide synthesis and
CC deprotected with conventional reagents to give only the
CC mono-addition product, free of di-addition product impurities. The
CC deprotected product can be labelled with medically useful
CC radionuclides, e.g. lanthanides or actinides, at any desired
CC location. Pre-derivatisation of individual amino acids is not
CC required.
XX SQ Sequence 11 AA;
Query Match 67.6%; Score 48; DB 18; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPQOQFWLM 11
Db 1 rpkpqffglm 11
RESULT 63
AAW04616
ID AAW04616 standard; peptide; 11 AA.
XX AC AAW04616;
XX DT 13-AUG-1997 (first entry)
XX DE Substance P peptide for mass spectrometry analysis.
XX KW Mass spectrometry; polymer analysis; biopolymer analysis.
XX OS Synthetic.
XX PN WO9636986-A1.

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XX PD 21-NOV-1996.
XX PF 17-MAY-1996; 96WO-US07146.
XX PR 19-MAY-1995; 95US-0447175.
XX PR 19-MAY-1995; 95US-0446055.
XX PA (PERS-) PERCEPTIVE BIOSYSTEMS INC.
XX PI Patterson DH, Tarr GE;
XX DR WPI; 1997-012308/01.
XX PT Sequencing polymers, e.g. DNA, RNA, peptide nucleic acids, proteins,
XX PT etc. - by obtaining mass to charge ratios of polymer fragments,
XX PT pref. using mass spectrometer, and performing statistical analysis
XX PS Example 2; Page 32; 86pp; English.
XX CC A method of obtaining sequence information about a polymer (e.g. DNA,
XX CC RNA, peptide nucleic acids, proteins, peptides and carbohydrates)
XX CC comprising monomers of known mass has been claimed. The present
XX CC sequence represents a substance P peptide, and was used as
XX CC an example as a digestion before analysis by mass spectrometry,
XX CC using this novel on-plate strategy. Total sequence information
XX CC from a nine well digestion can be represented in a single digestion or
XX CC it is often derived from two or more wells. The methods, apparatus and
XX CC kit (claimed) can be used for the analysis of polymers, particularly
XX CC biopolymers, e.g. DNA, RNA, peptide nucleic acids, proteins, peptides
XX CC and carbohydrates. It provides a rapid, automated and cost effective
XX CC sequencing of polymers, with a statistical certainty.
XX SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 18; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
   |||||:|
Db 1 rpkpqgffglm 11

RESULT 64
AAW50978
ID AAW50978 standard; peptide; 11 AA.
XX AC AAW50978;
XX DT 31-JUL-1998 (first entry)
XX DE Substance P analogue [D-Arg1,D-Pro2,D-Phe7,D-His9].
XX KW Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
XX KW Substance P; cancer; inhibition; growth hormone releasing factor;
XX KW spantide.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT FT Misc-difference 1 /note= "D-form residue"
FT FT Misc-difference 2 /note= "D-form residue"
FT FT Misc-difference 7 /note= "D-form residue"
FT FT Misc-difference 9 /note= "D-form residue"
FT FT Modified-site 11 /note= "C-terminal amide"
XX FT
XX FT

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PN EP835662-A2.
XX 15-APR-1998.
XX PF 11-DEC-1996; 96EP-0309012.
XX PR 08-OCT-1996; 96US-072679.
XX PR 16-AUG-1996; 96IN-0001822.
XX PA (NAIM-) NAT INST IMMUNOLOGY.
XX PI Jaggi M, Mukherjee R;
XX DR WPI; 1998-208959/19.
XX PT Composition containing analogues of vasoactive intestinal peptide,
XX PT somatostatin - bombesin and substance P, for treatment of tumours
XX PT and for inhibiting over-expression of these peptide(s)
XX PS Disclosure; Page 13; 49pp; English.
XX CC The invention relates to a new composition which comprises: (i) the
XX CC somatostatin analogue SOM2 AGCKNFFDKWPTSGC (3-14 disulphide bridge),
XX CC and (ii) at least 4 of the peptides: antagonist of vasoactive
XX CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
XX CC antagonist (VIP3); somatostatin analogue (SOM1); bombesin
XX CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
XX CC more general compositions containing peptide analogues of somatostatin,
XX CC VIP, bombesin and substance P. The compositions are used in human or
XX CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
XX CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
XX CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
XX CC breast, kidney or particularly rectum and colon, and (b) to prevent,
XX CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
XX CC cells express receptors for VIP, somatostatin, bombesin and/or substance
XX CC P. The present sequence represents a substance P analogue.
XX SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 19; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
   |||||:|
Db 1 rpkpqgffglm 11

RESULT 65
AAW42973
ID AAW42973 standard; Protein; 11 AA.
XX AC AAW42973;
XX DT 01-MAY-1998 (first entry)
XX DE Substrate P reporter epitope.
XX KW Beta-amyloid peptide; BAP; extracellular BAP plaque;
XX KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;
XX KW amyloid precursor protein; APP; secretase; BAP aggregation;
XX KW abnormal proteolytic cleavage; substrate P reporter epitope.
XX OS Synthetic.
XX PN US5703209-A.
XX PD 30-DEC-1997.
XX PR 05-JUN-1995; 95US-0464248.
XX PF 20-SEP-1993; 93US-0123659.
XX PR

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XX This sequence represents substance P used in the method of the
 CC invention. The method is for enhancing opioid analgesia within a human
 CC subject for a duration of 15 minutes comprises concurrent administration
 CC of substance P, or one of its precursors. The method is used to elicit
 CC opioid analgesia and anaesthesia, either prior to or after the occurrence
 CC of a nociceptive event. The components have a synergistic effect. The
 CC method allows use of low doses of opioid that produce little or no
 CC physiological effect reducing conventional risks of toxicity and its
 CC addiction, and allows the use of low doses of substance P and its related
 CC analogs that limit their in vivo physiological consequences. The
 CC analgesia is naloxone reversible allowing diminishment or complete
 CC elimination of opioid analgesia if desired and on demand. The treatment
 CC provides a durable analgesic effect, but only minimally disturbs and
 CC interrupts the normal metabolic processes of the body.

XX Sequence 11 AA;

Query Match 67.6%; Score 48; DB 20; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.25;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
 |||||:| |
 Db 1 rpkpqffglm 11

RESULT 68

AAW92715
 ID AAW92715 standard; peptide; 11 AA.

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AC AAW92715;

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DT 30-APR-1999 (first entry)

XX

DE Human tachykinin agonist beta-amyloid peptide fragment #61.

XX

KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

XX

KW Alzheimer's disease; Down's syndrome; amyloidosis; human;

XX

KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.

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OS Homo sapiens.

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FH Key Location/Qualifiers

FT Modified-site 10

FT /label= MeLeu

FT /note= "N-methyl-leucine"

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XX US5876948-A.

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CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.

XX Sequence 11 AA;

Query Match 67.6%; Score 48; DB 20; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.25;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
 |||||:| |
 Db 1 rpkpqffglm 11

RESULT 69

AAW92719

ID AAW92719 standard; peptide; 11 AA.

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AC AAW92719;

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Query Match

67.6%; Score 48; DB 20; Length 11;

CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage,
 CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.

XX Sequence 11 AA;

Query Match 67.6%; Score 48; DB 20; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.25;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage,
 CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.

XX Sequence 11 AA;

Query Match

67.6%; Score 48; DB 20; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
|||||:|
Db 1 rpkpqffglm 11

RESULT 70

AAW92720
ID AAW92720 standard; peptide; 11 AA.

XX AC AAW92720;

XX AC 30-APR-1999 (first entry)

XX DE Human tachykinin agonist beta-amyloid peptide fragment #66.

XX DE Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Modified-site 10

FT FT /label= Meleu
FT FT /note= "N-methyl-leucine"

XX PN US5876948-A.

XX XX 02-MAR-1999.

XX XX 27-JUL-1991; 91US-0737371.

XX XX 29-JUL-1991; 91US-0737371.

XX PR 27-JUL-1990; 90US-0559173.

XX XX (CHIL-) CHILDRENS MEDICAL CENT.

XX PI Yankner BA;

XX DR WPI; 1999-189630/16.

XX XX Screening for neurotoxin inhibitors - by testing compounds for their
FT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX PS Disclosure; Column 39-40; 28pp; English.

XX CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

XX SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 20; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
|||||:|
Db 1 rpkpqffglm 11

RESULT 71

AAW92708

ID AAW92708 standard; peptide; 11 AA.

XX AC AAW92708;

XX DT 30-APR-1999 (first entry)

XX DE Human tachykinin agonist beta-amyloid peptide fragment #54.

XX DE Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Modified-site 7

FT FT /note= "Modification results in p-chloro-Phe"
FT FT Modified-site 8

FT FT /note= "Modification results in p-chloro-Phe"

XX PN US5876948-A.

XX XX 02-MAR-1999.

XX XX 27-JUL-1991; 91US-0737371.

XX PR 29-JUL-1991; 91US-0737371.

XX PR 27-JUL-1990; 90US-0559173.

XX XX (CHIL-) CHILDRENS MEDICAL CENT.

XX XX Yankner BA;

XX XX WPI; 1999-189630/16.

XX XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX PS Disclosure; Column 33-34; 28pp; English.

XX CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

XX SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 20; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
|||||:|
Db 1 rpkpqffglm 11

RESULT 72

AAW92680

ID AAW92680 standard; peptide; 11 AA.

XX AC AAW92680;

XX DT 30-APR-1999 (first entry)

XX DE Human tachykinin agonist beta-amyloid peptide fragment #26.

XX DE Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Modified-site 8
 FT /note= "Residue is N-methyl-phenylalanine"
 XX
 XX US5876948-A.
 PN
 XX
 PD 02-MAR-1999.
 XX
 XX 27-JUL-1991; 91US-0737371.
 PF
 XX 29-JUL-1991; 91US-0737371.
 PR
 PR 27-JUL-1990; 90US-0559173.
 XX
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA
 XX Yankner BA;
 PI
 XX WPI; 1999-189630/16.
 DR
 XX Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 PT
 XX Disclosure; Column 21-22; 28pp; English.
 XX
 XX This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 67.6%; Score 48; DB 20; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.25;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RPKPQQWFWM 11
 Db 1 rpkpqgffglm 11
 DE
 DE 30-APR-1999 (first entry)
 XX
 XX Human tachykinin agonist beta-amyloid peptide fragment #27.
 DE
 DE Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Modified-site 8
 FT /note= "Residue is N-methyl-glycine"
 XX
 XX US5876948-A.
 PN
 XX
 PD 02-MAR-1999.
 XX
 XX 27-JUL-1991; 91US-0737371.
 PF
 XX 29-JUL-1991; 91US-0737371.
 PR
 PR 27-JUL-1990; 90US-0559173.
 XX
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA
 XX Yankner BA;
 PI
 XX WPI; 1999-189630/16.
 DR
 XX Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 PT
 XX Disclosure; Column 21-22; 28pp; English.
 XX
 XX This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 67.6%; Score 48; DB 20; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.25;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RPKPQQWFWM 11
 Db 1 rpkpqgffglm 11
 DE
 DE 30-APR-1999 (first entry)
 XX
 XX Human tachykinin agonist beta-amyloid peptide fragment #27.
 DE
 DE Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Modified-site 8
 FT /note= "Residue is N-methyl-glycine"
 XX
 XX US5876948-A.
 PN
 XX
 PD 02-MAR-1999.
 XX
 XX 27-JUL-1991; 91US-0737371.
 PF
 XX 29-JUL-1991; 91US-0737371.
 PR
 PR 27-JUL-1990; 90US-0559173.
 XX
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA
 XX Yankner BA;
 PI

PD 02-MAR-1999.
 XX
 XX 27-JUL-1991; 91US-0737371.
 XX
 XX 29-JUL-1991; 91US-0737371.
 PR
 PR 27-JUL-1990; 90US-0559173.
 XX
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA
 XX Yankner BA;
 PI
 XX WPI; 1999-189630/16.
 DR
 XX Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 PT
 XX Disclosure; Column 21-22; 28pp; English.
 XX
 XX This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 67.6%; Score 48; DB 20; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.25;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RPKPQQWFWM 11
 Db 1 rpkpqgffglm 11
 DE
 DE 30-APR-1999 (first entry)
 XX
 XX Human tachykinin agonist beta-amyloid peptide fragment #22.
 DE
 DE Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Modified-site 9
 FT /label= MeGly
 FT /note= "N-methyl-glycine (Sarcosine)"
 XX
 XX US5876948-A.
 PN
 XX
 PD 02-MAR-1999.
 XX
 XX 27-JUL-1991; 91US-0737371.
 PF
 XX 29-JUL-1991; 91US-0737371.
 PR
 PR 27-JUL-1990; 90US-0559173.
 XX
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA
 XX Yankner BA;
 PI

XX WPI; 1999-189630/16.
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX
XX Disclosure; Column 19-20; 28pp; English.
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodysplasia with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 20; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RPKPOQWFWM 11
| | | | | | | |
Db 1 rpkpqgffglm 11

RESULT 75
AAW92731
ID AAW92731 standard; peptide; 11 AA.
XX
AC AAW92731;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #77.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodysplasia.
XX
OS Homo sapiens.
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Disclosure; Column 43-44; 28pp; English.
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodysplasia with cerebral

CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 20; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RPKPOQWFWM 11
| | | | | | | |
Db 1 rpkpqgffglm 11

RESULT 76
AAW9662
ID AAW9662 standard; peptide; 11 AA.
XX
AC AAW9662;
XX
DT 02-MAR-1999 (first entry)
XX
DE Substance P derivative having complex glycosylation.
XX
KW Substance P; mannose; glycosylation; solubility.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..4 /note= "optionally the first four residues may be
FT Modified-site 5 /note= "the side chain amide group is N-substituted
FT with N-acetyl-D-glucosamine (GlcNAc) which in turn
FT is extended in the 4-position with a complex type
FT sugar chain, a high mannose type sugar chain or a
FT mixed type sugar chain"
FT Modified-site 11 /note= "Met-NH2, i.e. C-terminal amide"
XX
PN JP10306099-A.
XX
PD 17-NOV-1998.
XX
PF 28-NOV-1997; 97JP-0343979.
XX
PR 04-MAR-1997; 97JP-0065372.
XX
PA (NOGK) 2H NOGUCHI KENKYUSHO.
XX
DR WPI; 1999-054306/05.
XX
PT New substance P derivatives with side chain containing sugar - has
PT improved solubility
XX
PS Claim 1; Page 2; 8pp; Japanese.
XX
CC The sequence represents the peptide portion of a new Substance P
CC derivative having complex glycosylation on the Gln(5) position. The
CC derivative has improved solubility compared with Substance P.
XX
SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 20; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RPKPOQWFWM 11
| | | | | | | |
Db 1 rpkpqgffglm 11

```

RESULT 77
AAW79663
ID AAW79663 standard; peptide; 11 AA.
XX AC AAW79663;
XX DT 02-MAR-1999 (first entry)
XX DE Substance P derivative having complex glycosylation.
XX KW Substance P; mannose; glycosylation; solubility.
XX OS Synthetic.
XX FT
XX FT Key Location/Qualifiers
XX FT Modified-site 6
XX FT /note= "the side chain amide group is N-substituted
XX FT with N-acetyl-D-glucosamine (GlcNAc) which in turn
XX FT is extended in the 4-position with a complex type
XX FT sugar chain, a high mannose type sugar chain or a
XX FT mixed type sugar chain"
XX FT Modified-site 11
XX FT /note= "Met-NH2, i.e. C-terminal amide"
XX FT
XX FT JF10306099-A.
XX PN
XX PD 17-NOV-1998.
XX XX
XX PF 28-NOV-1997; 97JP-0343979.
XX PR 04-MAR-1997; 97JP-0065372.
XX PA (NOGK ) ZH NOGUCHI KENKYUSHO.
XX XX
XX DR WPI; 1999-054306/05.
XX PT New substance P derivatives with side chain containing sugar - has
XX PT improved solubility
XX PS Claim 1; Page 2; 8pp; Japanese.
XX CC The sequence represents the peptide portion of a new Substance P
XX CC derivative having complex glycosylation on the Gln(6) position. The
XX CC derivative has improved solubility compared with Substance P.
XX SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 20; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
DB 1 rpkpqffglm 11
|||||:|

RESULT 78
AAB18483
ID AAB18483 standard; peptide; 11 AA.
XX AC AAB18483;
XX DT 15-JAN-2001 (first entry)
XX DE Peptide substrate used to test prolyl-tripeptidyl peptidase activity.
XX KW Prolyl tripeptidyl-peptidase; amidolytic activity; periodontal disease;
XX KW gingivitis; periodontitis.
XX OS Synthetic.

Query Match 67.6%; Score 48; DB 21; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
DB 1 rpkpqffglm 11
|||||:|

RESULT 79
AAB23027
ID AAB23027 standard; peptide; 11 AA.
XX AC AAB23027;
XX DT 16-JAN-2001 (first entry)
XX DE Human/rat tachykinin Substance P.
XX KW Substance P; tachykinin; human; rat; magnesium binding defect;
XX KW sodium sensitive essential hypertension; insulin resistance;
XX KW type 2 diabetes; antibody; immunoassay; quantification.
XX OS Homo sapiens.
XX OS Rattus sp.
XX FT
XX FT Key Location/Qualifiers
XX FT Modified-site 11
XX FT /note= "C-terminal amide"

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XX FT Key Location/Qualifiers
XX FT Modified-site 1
XX FT /note= "hydrogen attached"
XX FT Modified-site 11
XX FT /note= "amidated residue"
XX PN W0200052147-A2.
XX PD 08-SEP-2000.
XX PF 03-MAR-2000; 2000WO-US05551.
XX PR 05-MAR-1999; 99US-0123148.
XX PA (UYGF-) UNIV GEORGIA RES FOUND INC.
XX PA (TRAV/) TRAVIS J.
XX PA (POTE/) POTEMPA J.
XX PA (BANB/) BANBULA A.
XX PI Travis J, Potempa J, Banbula A;
XX DR WPI; 2000-594181/56.
XX XX
XX PT Prolyl tripeptidyl-peptidase, active analog, fragment or variant useful
XX PT for identifying its inhibitor which is useful for protecting an animal
XX PT from a periodontal disease such as gingivitis and periodontitis.
XX PS Example 4; Page 37; 58pp; English.
XX CC The present sequence represents a substrate which was used to test
XX CC the activity of prolyl tripeptidyl-peptidases PTP-A and PTP IV. The
XX CC prolyl tripeptidyl-peptidase has an amidolytic activity, and cleaves
XX CC a peptide bond in a target polypeptide having at least 4 amino acids.
XX CC This bond is between a proline and an amino acid attached to the
XX CC alpha-carboxyl group end of the proline. The polypeptide is useful for
XX CC identifying inhibitors. These inhibitors are then useful for reducing
XX CC the growth of bacterium or for protecting an animal from a periodontal
XX CC disease such as gingivitis and periodontitis caused by Porphyromonas
XX CC gingivalis.
XX SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 21; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
DB 1 rpkpqffglm 11
|||||:|

RESULT 79
AAB23027
ID AAB23027 standard; peptide; 11 AA.
XX AC AAB23027;
XX DT 16-JAN-2001 (first entry)
XX DE Human/rat tachykinin Substance P.
XX KW Substance P; tachykinin; human; rat; magnesium binding defect;
XX KW sodium sensitive essential hypertension; insulin resistance;
XX KW type 2 diabetes; antibody; immunoassay; quantification.
XX OS Homo sapiens.
XX OS Rattus sp.
XX FT
XX FT Key Location/Qualifiers
XX FT Modified-site 11
XX FT /note= "C-terminal amide"

```


XX PN WO200054053-A1.
 XX PD 14-SEP-2000.
 XX PF 09-MAR-2000; 2000WO-US03707.
 XX PR 10-MAR-1999; 99US-0265690.
 XX PA (WELLS) WELLS I C.
 XX PI Wells IC;
 XX DR WPI; 2000-587457/55.
 XX PT Detecting magnesium binding defects associated with abnormal
 PT physiological states such as sodium-sensitive essential hypertension
 PT and type 2 insulin-resistant diabetes mellitus, comprises measuring a
 PT specific pentapeptide in blood -
 XX Disclosure; Page 5; 21pp; English.
 XX The invention relates to a method for detecting magnesium binding
 CC defects. The method comprises quantitating a tachykinin C-terminal
 CC pentapeptide (e.g., AAB23025) and its degradation products (e.g.,
 CC AAB23026) in blood using an antibody specific for the generalised
 CC mammalian tachykinin C-terminal pentapeptide
 CC Phe-(Phe/Val)-Gly-Leu-Met-NH₂ (AAB23028). The method is useful for
 CC detecting cellular magnesium binding defects which are associated with
 CC abnormal physiological states such as sodium-sensitive essential
 CC hypertension and type 2 diabetes mellitus. The present sequence
 CC represents the tachykinin Substance P from human and rat. C-terminal
 CC fragments (AAB23025, AAB23026) of the present sequence may be assayed
 CC according to the method of the invention.
 XX SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 21; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.25;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RPKPQQWFWM 11
 Db 1 rpkpqgffglm 11
 RESULT 80
 AAY32382
 ID AAY32382 standard; Peptide; 11 AA.
 XX AC AAY32382;
 XX DT 28-FEB-2000 (first entry)
 XX DE Cell differentiation, proliferation and maintenance factor peptide.
 XX KW Cell differentiation; cell proliferation; cell maintenance;
 KW ectoderm-like cell; embryonic stem cell; pluripotent cell;
 KW gene therapy; cell therapy; tissue transplant; organ transplant;
 KW xerodermpigment; allotransplant; concomitant transplantation;
 KW transgenic animal; substance P.
 XX OS Synthetic.
 XX PN WO9953021-A1.
 XX PD 21-OCT-1999.
 XX PF 09-APR-1999; 99WO-AU00265.
 XX PR 09-APR-1998; 98AU-0002912.
 PR 23-SEP-1998; 98AU-0006097.

XX PA (BRES-) BRESAGEN LTD.
 XX PI Bettess MD, Rathjen PD, Rathjen J;
 XX DR WPI; 2000-061970/05.
 XX PT New isolated biologically active factor capable of influencing
 PT differentiation, proliferation or maintenance of pluripotent cells
 XX Claim 3; Page 123; 189pp; English.
 XX This sequence represents a peptide (substance P free acid) that can
 CC form the low mol.wt. component of a novel biologically active factor
 CC that is capable of influencing the differentiation, proliferation
 CC and/or maintenance of pluripotent cells. The factor consists of a
 CC low mol.wt. component selected from Pro, Pro-Ala, Ala-Pro-Gly,
 CC Pro-OH-Pro, Gly-Pro-Ala, Gly-Pro-OH-Pro, a peptide given in
 CC AAY32378-82, or a protease digested (including collagenase digested)
 CC collagen fragment, and a high mol.wt. component such as fibronectin.
 CC The biologically active factor is obtained from conditioned media of
 CC hepatic or hepatoma cells or cell lines or extraembryonic endodermal
 CC cells or cell lines. The factor is capable of causing the
 CC transition of pluripotent cells (e.g. embryonic stem cells in
 CC adherent culture and in suspension culture) to pluripotent cells
 CC having different properties, more specifically primitive
 CC ectoderm-like (EPL) cells. The factor is also capable of
 CC maintaining and supporting proliferation of these cells in vitro.
 CC It also allows the isolation and maintenance of EPL cells derived
 CC from in vitro and in vivo primitive ectoderm. These cells can be
 CC used in allo-, concomitant- or xeno-transplantation, cell therapy,
 CC tissue and organ augmentation or replacement, and gene therapy.
 CC They can also be used for producing chimeric or transgenic animals.
 XX SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 21; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.25;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RPKPQQWFWM 11
 Db 1 rpkpqgffglm 11
 RESULT 81
 AAG62768
 ID AAG62768 standard; peptide; 11 AA.
 XX AC AAG62768;
 XX DT 17-SEP-2001 (first entry)
 XX DE Amino acid sequence of substance P.
 XX KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 FT Modified-site 11
 FT /note= "amidated residue"
 XX PN WO200153336-A1.
 XX PD 26-JUL-2001.
 XX PF 17-JAN-2001; 2001WO-US01529.
 XX PR 19-JAN-2000; 2000US-0489667.
 XX PA (ALLR) ALLERGAN SALES INC.

XX
PI Donovan S;
XX
DR WPI; 2001-451900/48.
XX
XX
PT Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -
XX
XX
PS Disclosure; Page 61; 77pp; English.
XX
XX The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin
CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
CC The targeting moiety comprises a light chain and an amine end segment of
CC a heavy chain and comprises Substance P as the targeting moiety. The pain
CC alleviating effects persist for 2-6 months. The present sequence
CC represents substance P, and is used in the course of the invention.
XX
SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 22; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11
DB 1 rpkkpqffgilm 11

RESULT 82
AAG99354
ID AAG99354 standard; Peptide; 11 AA.
XX
AC AAG99354;
XX
DT 25-SEP-2001 (first entry)
XX
DE Substance P peptide.
XX
XX Atypical tachykinin; ATT; human; hypertension.
XX
XX Unidentified.
XX
XX WO200146415-A1.
XX
XX 28-JUN-2001.
XX
XX 21-DEC-2000; 2000WO-JP09083.
XX
XX 21-DEC-1999; 99JP-0362638.
XX
XX 10-MAR-2000; 2000JP-0066714.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Kitada C, Inatomi N;
XX
XX WPI; 2001-441676/47.
XX
XX Atypical tachykinin peptides of human origin and DNA encoding them for
XX screening potential agents for treatment of hypertension -
XX
XX Disclosure; Page 9; 153pp; Japanese.
XX
XX The present invention relates to atypical tachykinin proteins of human
XX origin and their esters, amides, salts and partial peptides. These can be
XX used in the treatment, prevention and diagnosis of hypertension. The
XX present sequence is a protein fragment described in the exemplification
XX of the invention.

SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 22; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11
DB 1 rpkkpqffgilm 11

RESULT 83
AAB84527
ID AAB84527 standard; peptide; 11 AA.
XX
AC AAB84527;
XX
XX 05-SEP-2001 (first entry)
XX
XX Amino acid sequence of human substance P.
XX
XX Substance P; cell toxin; Pseudomonas exotoxin; cell ablation;
XX NK-1 receptor; chronic pain; tumour; neurological dysfunction;
XX basal ganglia; cholinergic interneuron; Parkinson's disease.
XX
XX Homo sapiens.
XX
XX WO200131020-A1.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-US29064.
XX
XX 22-OCT-1999; 99US-0161159.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Fitzgerald DJ, Iadarola MJ;
XX
XX WPI; 2001-417560/44.
XX
XX Making cell toxin to treat chronic pain, by forming substance
XX P-Pseudomonas exotoxin disulfide-linked conjugate, by reacting modified
XX exotoxin and substance P having additional cysteine residue at its
XX N-terminus -
XX
XX Disclosure; Page 10; 54pp; English.
XX
XX The present sequence represents a human substance P. The peptide is
XX used to produce a cell toxin. The cell toxin comprises a substance
XX P-Pseudomonas exotoxin disulfide-linked conjugate. The cell toxin is
XX useful for ablating NK-1 receptor expressing cells, such as dorsal horn
XX cell, a stratum cell or a brain parenchyma cell, for treating chronic
XX pain in epineurium cells, perineurium cells, nerve ganglia, nerve
XX sheaths, nerve linings, meninges, pia mater cells, arachnoid membrane
XX cells, duramembrane cells, cells lining a joint or brain or spinal cord
XX parenchymal cells, without significantly affecting basal nociceptive
XX responses. The cell toxin is thus useful for treating chronic pain or
XX tumours that binds substance P. It is also useful for neurological
XX dysfunctions of the basal ganglia by targeting cholinergic interneurons
XX that express substance P e.g. Parkinson's disease.
XX
SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 22; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11
DB 1 rpkkpqffgilm 11

```
RESULT 84
AAB98866
ID AAB98866 standard; Peptide; 11 AA.
XX
AC AAB98866;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #22.
XX
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 11
FT /label= OTHER
FT /note= "C-terminal amide"
XX
PN WO200130371-A2.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
PA (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX
DR WPI; 2001-397593/42.
XX
XX New chimeric peptides used for treating pain comprise opioid receptor
binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 15; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
an opioid receptor binding moiety and a nociceptive receptor binding
moieties. These can be used as analgesics for the treatment of pain. Unlike
opioid receptor based peptides alone, tolerance does not result from
their long-term use. The present sequence is one of the peptides of the
invention.
XX
SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 22; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQWFWM 11
Db 1 rpkpqffglm 11

RESULT 85
AAB82070
ID AAB82070 standard; peptide; 11 AA.
XX
AC AAB82070;
XX
DT 22-JUN-2001 (first entry)
XX
DE Substance P.
XX
KW Antigen; immunostimulant; vaccine; pharmaceutical composition; antiviral;
KW viral infection; substance P.
XX
```

```
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 11
FT /note= "C-terminal amide"
XX
PN WO200124822-A2.
XX
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-EP09657.
XX
PR 01-OCT-1999; 99AT-0001680.
XX
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PI Fleitmann J, Mattner F, Buschle M, Meiling J;
XX
DR WPI; 2001-290577/30.
XX
XX New pharmaceutical composition comprising an antigen, an
immunostimulating substance and a polycationic polymer, useful in
manufacturing vaccines
XX
XX Example 3; Page 14; 20pp; English.
XX
CC The present invention relates to a pharmaceutical composition comprising
(a) an antigen; (b) an immunostimulating substance consisting of
neuroactive compounds, hormones, compounds having growth hormone activity
or their mixtures; and (c) a polycationic polymer. The composition is
useful in manufacturing vaccines. To illustrate the present invention, a
murine tyrosinase related protein-2 peptide (TRP-2 peptide; see
AAB82064), was used. Mice were injected subcutaneously with either the
TRP-2 peptide, TRP-2 peptide + poly-L-arginine 60 (pr60) or TRP-2 peptide
+ pr60 + substance P (the present peptide). Animals were sacrificed 10
days post injection, and spleen tissue was harvested. Lymphocytes were
prepared from the spleen tissue and were re-stimulated with TRP-2 peptide
or with an ovalbumin-derived peptide (AAB82065), with the same major
histocompatibility complex (MHC) restriction serving as negative control.
Spots representing single T cells specific for the peptide used for
re-stimulation were counted. No spots were detected when the ovalbumin
derived peptide was used, while TRP-2 peptide + pr60 + substance P showed
the highest number of spots or single T cells.
XX
SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 22; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQWFWM 11
Db 1 rpkpqffglm 11

RESULT 86
AAB91411
ID AAB91411 standard; Peptide; 11 AA.
XX
AC AAB91411;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:587.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy1; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
```

PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
XF 17-MAY-2000; 2000WO-US13576.
XX
PF 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure; Page 392; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 22; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | : | |
Db 1 rpkpqqffhlm 11

RESULT 87
AAB91436
ID AAB91436 standard; Peptide; 11 AA.
XX
AC AAB91436;
XX
DT 22-JUN-2001 (first entry)
DE
DE Tachykinins peptide SEQ ID NO:612.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX

PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure; Page 399; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 22; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | : | |
Db 1 rpkpqqffhlm 11

RESULT 88
AAB91449
ID AAB91449 standard; Peptide; 11 AA.
XX
AC AAB91449;
XX
DT 22-JUN-2001 (first entry)
DE
DE Tachykinins peptide SEQ ID NO:625.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.
XX (CONJ-) CONJUCHEM INC.
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
XX peptidase degradation, useful for increasing length of in vivo activity
XX
XX Disclosure; Page 403; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
XX comprising a therapeutically active amino acid region (III) and a
XX reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
XX bonds with amino/hydroxyl/thiol groups on blood components to form a
XX peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX factors and neurotransmitters, to protect them from peptidase activity
XX in vivo for the treatment of various disorders. Endogenous therapeutic
XX peptides are not suitable as drug candidates as they require frequent
XX administration due to rapid degradation by peptidases in the body.
XX Modifying and attaching therapeutic peptides to albumin prevents or
XX reduces the action of peptidases to increase length of activity (half
XX life) and specificity as bonding to large molecules decreases
XX intracellular uptake and interference with physiological processes.
XX AAB90829 to AAB92441 represent peptides which can be used in the
XX exemplification of the present invention.
XX
SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 22; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
DB 1 rpkpqgfglm 11

RESULT 89
AAB91450
ID AAB91450 standard; Peptide; 11 AA.
XX
XX AAB91450;
XX
XX 22-JUN-2001 (first entry)
XX
XX Tachykinins peptide SEQ ID NO:626.
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX blood component; modification; succinimidyl; maleimido group; amino;
XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200069900-A2.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US13576.
XX
XX 17-MAY-1999; 99US-0134406.
XX
XX 10-SEP-1999; 99US-0153406.
XX
XX 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
XX

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
XX peptidase degradation, useful for increasing length of in vivo activity
XX
XX Disclosure; Page 403; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
XX comprising a therapeutically active amino acid region (III) and a
XX reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
XX bonds with amino/hydroxyl/thiol groups on blood components to form a
XX peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX factors and neurotransmitters, to protect them from peptidase activity
XX in vivo for the treatment of various disorders. Endogenous therapeutic
XX peptides are not suitable as drug candidates as they require frequent
XX administration due to rapid degradation by peptidases in the body.
XX Modifying and attaching therapeutic peptides to albumin prevents or
XX reduces the action of peptidases to increase length of activity (half
XX life) and specificity as bonding to large molecules decreases
XX intracellular uptake and interference with physiological processes.
XX AAB90829 to AAB92441 represent peptides which can be used in the
XX exemplification of the present invention.
XX
SQ Sequence 11 AA;

Query Match 67.6%; Score 48; DB 22; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
DB 1 rpkpqgfglm 11

RESULT 90
AAB50544
ID AAB50544 standard; peptide; 11 AA.
XX
XX AAB50544;
XX
XX 16-MAR-2001 (first entry)
XX
XX Prolyl endopeptidase inhibitor substance P peptide.
XX
XX Prolyl endopeptidase inhibitor; PEP inhibitor; central nervous system;
XX CNS; nootropic; brain function disorder; Alzheimer's disease; amnesia.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX Modified-site 11 /note= "amidated"
XX
XX WO200071144-A1.
XX
XX 30-NOV-2000.
XX
XX 16-MAY-2000; 2000WO-JP03135.
XX
XX 19-MAY-1999; 99JP-0138791.
XX
XX (DOME-) DOME INC.
XX
XX Kayahara H, Tsukahara K, Inagaki T;
XX WPI; 2001-070833/08.
XX

PT Prolyl endopeptidase inhibitor comprises cereal extract including new
XX ketone compound.

PS Disclosure; Fig 1; 27pp; Japanese.

XX The present invention describes prolyl endopeptidase (PEP) inhibitors
CC comprising a cereal extract. Also described are:
CC (i) a 7-octadecenyl-7,10-henecosadienyl ketone;
CC (ii) germinating brown rice having prolyl brain function disorders; and
CC activity for preventing and/or relieving brain function disorders; and
CC (iii) foods for preventing or relieving brain function disorders;
CC comprising the above PEP inhibitor or the above germinated brown rice.
CC The PEP inhibitors can have central nervous system (CNS) and nootropic
CC activity. The PEP inhibitors can be used for preventing and relieving
CC brain function disorders including Alzheimer's disease and amnesia.
CC The present sequence represents a PEP inhibitor peptide given in the
XX exemplification of the present invention.

XX Sequence 11 AA;

Query Match 67.6%; Score 48; DB 22; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
DB 1 rpkpqffglm 11

RESULT 91

AAB50306
ID AAB50306 standard; peptide; 11 AA.

AC AAB50306;

DT 08-MAR-2001 (first entry)

DE Substance P.

XX Antibacterial; Botulinum toxin inhibitor; BttXB;
KW prelin; tetanus neurotoxin; buforinin; substance P.

XX Unidentified.

XX WO2000069891-A2.

XX 23-NOV-2000.

XX 15-MAY-2000; 2000WO-US13215.

XX 17-MAY-1999; 99US-0134446.

XX (USSA) US DEPT OF THE ARMY.

XX Gordon RK, Moorad DR, Doctor BP, Garcia GE;

XX WPI; 2001-025001/03.

XX Novel Previn compounds useful for inhibiting the protease activity of
PT Botulinum B and tetanus toxins -

XX Claim 7; Page 29; 47pp; English.

XX The present sequence was investigated in the search for Botulinum
CC toxin inhibitors (BttXB). Previn compounds which inhibit the enzymatic
CC activity of BttXB and tetanus neurotoxins were isolated. Previn
CC may be used to construct compounds such as buforinins.

XX Sequence 11 AA;

Query Match 67.6%; Score 48; DB 22; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
DB 1 rpkpqffglm 11

RESULT 92

AAR32798
ID AAR32798 standard; peptide; 12 AA.

AC AAR32798;

DT 17-JUN-1993 (first entry)

DE Tyr-1 substance P used for binding assay.

XX human substance P receptor protein; SP; neurotransmitter;
KW neuromodulator; central nervous system; peripheral nervous system;
KW gastrointestinal disorders; inflammation; immune disease.

XX Homo sapiens.

XX WO9303137-A.

XX 18-FEB-1993.

XX 05-AUG-1992; 92WO-US06532.

XX 07-AUG-1991; 91US-0741200.

XX (UNIW) UNIV WASHINGTON.

XX Krause JE;

XX WPI; 1993-076495/09.

XX New human substance P receptor protein and DNA encoding it - used
PT e.g. for screening substance P antagonists

XX Example; Page 8; 40pp; English.

XX This sequence represents Tyr-1 substance P and was used in its
CC 125-Iodinated form in a ligand binding assay of COS-7 cells
CC transfected with substance P receptor coding plasmids (see AAQ37210).

XX Sequence 12 AA;

Query Match 67.6%; Score 48; DB 14; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.28;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
DB 2 rpkpqffglm 12

RESULT 93

AAR85244
ID AAR85244 standard; peptide; 12 AA.

AC AAR85244;

DT 18-AUG-1997 (first entry)

DE Substance P analogue peptide Cys-SP.

XX Ligand; antibody; receptor; SELEX; random library; amplification; PCR;
KW Systematic Evolution of Ligands by EXponential enrichment; primer;
KW polymerase chain reaction; structure; mimicry; substance P; tachykinin;
KW neuropeptide; rheumatoid arthritis; atherosclerosis; cancer;

KW diabetetic retinopathy.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Ac-Arg"
XX
XX WO9530775-A1.
XX
XX 16-NOV-1995.
XX
XX 03-MAY-1995; 95WO-US05600.
XX
XX 21-DEC-1994; 94US-0361795.
PR 06-MAY-1994; 94US-0238863.
PR 24-MAY-1994; 94US-0248632.
PR 09-SEP-1994; 94US-0303362.
PR 11-JUN-1990; 90US-0536428.
PR 10-JUN-1991; 91US-0714131.
PR 21-OCT-1992; 92US-0964624.
XX
XX (UYRE-) UNIV RES CORP.
XX
XX Allen P, Doudna JA, Feigon J, Gold L, Nieuwlandt D;
PI Schneider DJ, Sullenger BA, Wecker M;
XX
XX WPI: 1995-404132/51.
XX
XX Systematic evolution of ligands by exponential enrichment - for
PT identifying nucleic acid ligands used in the treatment of, e.g. type
PT B insulin resistance and HIV
XX
XX Example 11; Fig 8; 209pp; English.
XX
XX The invention relates to a novel method of isolating ligands that bind
CC to target proteins e.g. antibodies or receptors, which bind other
CC proteins or ligands. The method, designated Systematic Evolution of
CC Ligands by Exponential enrichment (SELEX), comprises generating a library
CC of random oligonucleotide sequences, about 40-60 nucleotides in length,
CC and binding these sequences to the target proteins. After removal of
CC unbound material, the remaining bound nucleotide sequences are amplified
CC e.g. by PCR, and the newly amplified material is bound again with the
CC target protein. This cycle continues until a sufficiently pure
CC oligonucleotide sequence is isolated. The method allows the isolation of
CC oligonucleotide sequences which structurally mimic the target protein's
CC ligand. This peptide represents an analogue of Substance P (AAR85243) in
CC which the N-terminal amine has been acylated in order to determine
CC whether this functional group interacts with nucleic acid ligands binding
CC substance P (see AAT06098-130). The ligands can be used to block the
CC activity of Substance P and is useful in the treatment of e.g. rheumatoid
CC arthritis, atherosclerosis, diabetetic retinopathy or cancer.
XX
XX Sequence 12 AA;
SQ

Query Match 67.6%; Score 48; DB 16; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.28;
Matches 9; Conservative 1; Mismatches 0; Gaps 0;
Oy 1 RPKPQQWFWM 11
| | | | | | | |
Db 1 rpkpqffglm 11

RESULT 94
AAY03157
ID AAY03157 standard; peptide; 12 AA.
XX
AC AAY03157;
XX
DT 10-JUN-1999 (first entry)
XX

Query Match 67.6%; Score 48; DB 20; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.28;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 1 RPKPQQWFWM 11
| | | | | | | |
Db 1 rpkpqffglm 11

RESULT 95
AAW94412
ID AAW94412 standard; peptide; 12 AA.
XX
AC AAW94412;
XX
DT 15-APR-1999 (first entry)
XX
DE Cancer protease-sensitive amino acid linker PAP-215 and PAP-216.
XX
KW Ricin-like toxin; cancer; viral infection; parasitic infection;
KW linker; B chain; A chain; protease; fungal infection; malaria;
KW leucocyte proliferation; cytomegalovirus; herpes; hepatitis;
KW rhinovirus; laryngotracheitis; poliomyelitis; varicella zoster;
KW cystic fibrosis; multiple sclerosis.
XX
OS Unidentified.
OS Synthetic.
XX

DE Substance P-Glycine.
XX
KW Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
KW substance P.
XX
OS Synthetic.
XX
PN US5891842-A.
XX
PD 06-APR-1999.
XX
XX 12-APR-1996; 96US-0631434.
XX
PR 09-APR-1993; 93US-0044954.
PR 12-APR-1996; 96US-0631434.
XX
PA (TUFT) TUFTS COLLEGE.
XX
PI Kream RM;
XX
XX WPI: 1999-253906/21.
XX
XX Synergistic method for enhancing opioid analgesia and anaesthesia
PT within a human
XX
XX Disclosure; Column 14; 20pp; English.
XX
XX This sequence represents substance P used in the method of the
CC invention. The method is for enhancing opioid analgesia within a human
CC subject for a duration of 15 minutes comprises concurrent administration
CC of substance P, or one of its precursors. The method is used to elicit
CC opioid analgesia and anaesthesia, either prior to or after the occurrence
CC of a nociceptive event. The components have a synergistic effect. The
CC method allows use of low doses of opioid that produce little or no
CC physiological effect reducing conventional risks of toxicity and
CC addiction, and allows the use of low doses of substance P and its related
CC analogs that limit their in vivo physiological consequences. The
CC analgesia is naloxone reversible allowing diminishment or complete
CC elimination of opioid analgesia if desired and on demand. The treatment
CC provides a durable analgesic effect, but only minimally disturbs and
CC interrupts the normal metabolic processes of the body.
XX
XX Sequence 12 AA;
SQ

PN WO9849311-A2.
XX
PD
XX
PF 05-NOV-1998.
XX
PR 30-APR-1998; 98WO-CA00394.
XX
PR 29-OCT-1997; 97US-0063715.
XX
PR 30-APR-1997; 97US-0045148.
XX
PA (DNOV-) DE NOVO ENZYME CORP.
XX
XX Borgford T;
PI
XX
XX WPI; 1999-009431/01.
XX
XX New nucleic acid encoding ricin-like toxin with an interchain linker
PT cleaved by protease - is specific for diseased cells, useful for,
PT e.g. killing selectively cancer or infected cells
XX
XX Claim 24; Fig 21; 352pp; English.
XX
XX The present invention describes new purified and isolated nucleic acids
CC (I) encoding: (1) the A and B chains of a ricin-like toxin (II); and
CC (II) a heterologous linker, joining the two chains and including a
CC cleavage recognition site for a disease-specific protease (III). Also
CC described are: (1) plasmids or baculovirus transfer vectors that contain
CC (I); and (2) recombinant protein (IV) consisting of the A and B chains
CC of (II) joined by the specified linker. (IV), produced by expression of
CC (I) in host cells, are used to inhibit or kill diseased cells that
CC produce (III), particularly for treating cancers (e.g. leucocyte
CC proliferation; cancer of ovary, pancreas, breast or prostate; glioma) or
CC infections caused by fungi, parasites (e.g. malaria) or viruses (e.g.
CC cytomegalovirus (CMV), herpes, hepatitis, rhinovirus, laryngeotracheitis,
CC polymyelitis or varicella zoster), also cystic fibrosis and multiple
CC sclerosis. Alternatively, (I) is used to express (IV) in vivo. (IV) is
CC toxic specifically for (III)-expressing cells and does not depend for
CC specificity on a cell-binding component. When used to treat virus-
CC infected cells, transcytosis and cytotoxicity of (IV) are increased by
CC retrograde translocation from endoplasmic reticulum to cytoplasm (which
CC some viruses exploit to avoid immune detection), so selectivity and
CC safety are further improved. (IV) are not toxic until chain A is
CC released and this occurs only in target cells. The present sequence
CC represents a specifically claimed cancer protease-sensitive amino acid
CC linker from the present invention.
XX
XX Sequence 12 AA;
SQ

Query Match 67.6%; Score 48; DB 20; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.28;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | : | | |
Db 1 rpkpqgffglm 11

RESULT 96
AAG62769
ID AAG62769 standard; peptide; 12 AA.
XX
AC AAG62769;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of substance P precursor.
XX
KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX
OS Unidentified.
XX
XX WO200153336-A1.
PN
XX

PD 26-JUL-2001.
XX
PF 17-JAN-2001; 2001WO-US01529.
XX
PR 19-JAN-2000; 2000US-0489667.
XX
PA (ALLR) ALLERGAN SALES INC.
XX
XX Donovan S;
XX
XX WPI; 2001-451900/48.
DR
XX
XX Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -
PT
XX
XX Disclosure; Page 62; 77pp; English.
PS
XX
XX The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin
CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
CC The targeting moiety comprises a light chain and an amino end segment of
CC a heavy chain and comprises Substance P as the targeting moiety. The pain
CC alleviating effects persist for 2-6 months. The present sequence
CC represents substance P precursor, and is used in the course of the
CC invention.
XX
XX Sequence 12 AA;
SQ

Query Match 67.6%; Score 48; DB 22; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.28;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | : | | |
Db 1 rpkpqgffglm 11

RESULT 97
AAG62772
ID AAG62772 standard; peptide; 12 AA.
XX
AC AAG62772;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of carboxy-ester substance P precursor.
XX
KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 12
FT /note= "methylated residue"
XX
XX WO200153336-A1.
PN
XX
XX 26-JUL-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US01529.
XX
XX 19-JAN-2000; 2000US-0489667.
XX
XX (ALLR) ALLERGAN SALES INC.
XX
XX Donovan S;
XX
XX WPI; 2001-451900/48.
DR
XX

PT Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -
XX Disclosure; Page 64; 77pp; English.
XX The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin
CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
CC The targeting moiety comprises a light chain and an amine end segment of
CC a heavy chain and comprises Substance P as the targeting moiety. The pain
CC alleviating effects persist for 2-6 months. The present sequence
CC represents a substance P precursor, and is used in the course of the
CC invention.
XX
XX
SQ Sequence 12 AA;
Query Match 67.6%; Score 48; DB 22; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.28;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RPKPQQWFWM 11
| | | | | | | |
Db 1 rpkpqffglm 11
RESULT 98
AAG62775
ID AAG62775 standard; peptide; 12 AA.
XX
AC AAG62775;
XX
XX 17-SEP-2001 (first entry)
XX
XX Amino acid sequence of carboxy-ester substance P precursor.
XX Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 12 /note= "ethylated residue"
XX
XX WO200153336-A1.
XX
XX 26-JUL-2001.
XX
XX 17-JAN-2001; 2001WO-US01529.
XX
XX 19-JAN-2000; 2000US-0489667.
XX
XX (ALLR) ALLERGAN SALES INC.
XX
XX Donovan S;
XX
XX WPI; 2001-451900/48.
XX
XX Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -
XX Disclosure; Page 67; 77pp; English.
XX
XX The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin
CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
CC The targeting moiety comprises a light chain and an amine end segment of

CC a heavy chain and comprises Substance P as the targeting moiety. The pain
CC alleviating effects persist for 2-6 months. The present sequence
CC represents a substance P precursor, and is used in the course of the
CC invention.
XX
XX
SQ Sequence 12 AA;
Query Match 67.6%; Score 48; DB 22; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.28;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RPKPQQWFWM 11
| | | | | | | |
Db 1 rpkpqffglm 11
RESULT 99
AAB84528
ID AAB84528 standard; peptide; 12 AA.
XX
AC AAB84528;
XX
XX 05-SEP-2001 (first entry)
XX
XX Amino acid sequence of a modified substance P.
XX
XX Substance P; cell toxin; Pseudomonas exotoxin; cell ablation;
KW NK-1 receptor; chronic pain; tumour; neurological dysfunction;
KW basal ganglia; cholinergic interneuron; Parkinson's disease.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200131020-A1.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-US29064.
XX
XX 22-OCT-1999; 99US-0161159.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Fitzgerald DJ, Iadarola MJ;
XX
XX WPI; 2001-417560/44.
XX
XX Making cell toxin to treat chronic pain, by forming substance
PT P-Pseudomonas exotoxin disulfide-linked conjugate, by reacting modified
PT exotoxin and substance P having additional cysteine residue at its
PT N-terminus -
XX
XX Example 1; Page 10; 54pp; English.
XX
XX The present sequence represents a modified substance P. The peptide is
CC used to produce a cell toxin. The cell toxin comprises a substance
CC P-Pseudomonas exotoxin disulfide-linked conjugate. The cell toxin is
CC useful for ablating NK-1 receptor expressing cells, such as dorsal horn
CC cell, a stratum cell or a brain parenchyma cell, for treating chronic
CC pain in epineurium cells, perineurium cells, nerve ganglia, nerve
CC sheaths, nerve linings, meninges, pia mater cells, arachnoid membrane
CC cells, duramembrane cells, cells lining a joint or brain or spinal cord
CC parenchymal cells, without significantly affecting basal nociceptive
CC responses. The cell toxin is thus useful for treating chronic pain or
CC tumours that binds substance P. It is also useful for neurological
CC dysfunctions of the basal ganglia by targeting cholinergic interneurons
CC that express substance P e.g. Parkinson's disease.
XX
XX
SQ Sequence 12 AA;
Query Match 67.6%; Score 48; DB 22; Length 12;

PD 03-MAY-2001.
 XX
 PF 27-OCT-2000; 2000WO-US29789.
 XX
 PR 28-OCT-1999; 99US-0428692.
 XX
 PA (NEWF-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
 XX
 PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
 XX
 DR WPI; 2001-397593/42.
 XX
 XX New chimeric peptides used for treating pain comprise opioid receptor
 PT binding group and nociceptive receptor binding group
 XX
 PS Claim 10; Page 15; 34pp; English.
 XX
 CC The present invention describes a number of chimeric peptides comprising
 CC an opioid receptor binding moiety and a nociceptive receptor binding
 CC moiety. These can be used as analgesics for the treatment of pain. Unlike
 CC opioid receptor based peptides alone, tolerance does not result from
 CC their long-term use. The present sequence is one of the peptides of the
 CC invention.
 XX
 SQ Sequence 12 AA;
 Query Match 67.6%; Score 48; DB 22; Length 12;
 Best Local Similarity 81.8%; Pred. No. 0.28;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RPKPQOWFWLM 11
 DB |||||:| ||
 1 rpkpqffglm 11
 RESULT 103
 AAY03158
 ID AAY03158 standard; peptide; 13 AA.
 XX
 AC AAY03158;
 XX
 DT 10-JUN-1999 (first entry)
 XX
 DE Substance P-Glycine-Lysine.
 XX
 KW Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
 XX substance P.
 XX
 OS Synthetic.
 XX
 PN US5891842-A.
 XX
 PD 06-APR-1999.
 XX
 PF 12-APR-1996; 96US-0631434.
 XX
 PR 09-APR-1993; 93US-0044954.
 XX
 PR 12-APR-1996; 96US-0631434.
 XX
 PA (TUFT) TUFTS COLLEGE.
 XX
 PI Kream RM;
 XX
 DR WPI; 1999-253906/21.
 XX
 XX Synergistic method for enhancing opioid analgesia and anaesthesia
 PT within a human
 XX
 PS Disclosure; Column 14; 20pp; English.
 XX
 CC This sequence represents substance P used in the method of the
 CC invention. The method is for enhancing opioid analgesia within a human

CC subject for a duration of 15 minutes comprises concurrent administration
 CC of substance P, or one of its precursors. The method is used to elicit
 CC opioid analgesia and anaesthesia, either prior to or after the occurrence
 CC of a nociceptive event. The components have a synergistic effect. The
 CC method allows use of low doses of opioid that produce little or no
 CC physiological effect reducing conventional risks of toxicity and
 CC addiction, and allows the use of low doses of substance P and its related
 CC analogs that limit their in vivo physiological consequences. The
 CC analgesia is naloxone reversible allowing diminishment or complete
 CC elimination of opioid analgesia if desired and on demand. The treatment
 CC provides a durable analgesic effect, but only minimally disturbs and
 CC interrupts the normal metabolic processes of the body.
 XX
 SQ Sequence 13 AA;
 Query Match 67.6%; Score 48; DB 20; Length 13;
 Best Local Similarity 81.8%; Pred. No. 0.3;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RPKPQOWFWLM 11
 DB |||||:| ||
 1 rpkpqffglm 11
 RESULT 104
 AAG62770
 ID AAG62770 standard; peptide; 13 AA.
 XX
 AC AAG62770;
 XX
 DT 17-SEP-2001 (first entry)
 XX
 DE Amino acid sequence of substance P precursor.
 XX
 KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
 XX
 OS Unidentified.
 XX
 PN WO200153336-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01529.
 XX
 PR 19-JAN-2000; 2000US-0489667.
 XX
 PA (ALLR) ALLERGAN SALES INC.
 XX
 PI Donovan S;
 XX
 DR WPI; 2001-451900/48.
 XX
 PT Agent useful for treating pain comprises a clostridial neurotoxin (or
 PT component) attached to a targeting moiety
 XX
 PS Disclosure; Page 62; 77pp; English.
 XX
 CC The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected
 CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin
 CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents substance P precursor, and is used in the course of the
 CC invention.
 XX
 SQ Sequence 13 AA;

Query Match 67.6%; Score 48; DB 22; Length 13;
Best Local Similarity 81.8%; Pred. No. 0.3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:| |
Db 1 rpkpgqffglm 11

RESULT 105

AAG62773
ID AAG62773 standard; peptide; 13 AA.

XX AC AAG62773;

XX DT 17-SEP-2001 (first entry)

XX DE Amino acid sequence of carboxy-ester substance P precursor.

XX KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.

XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT Modified-site 13
XX FT /note= "methylated residue"

XX PN WO200153336-A1.

XX PD 26-JUL-2001.

XX PF 17-JAN-2001; 2001WO-US01529.

XX PR 19-JAN-2000; 2000US-0489667.

XX PA (ALLR) ALLERGAN SALES INC.

XX PI Donovan S;

XX DR WPI; 2001-451900/48.

XX PT Agent useful for treating pain comprises a clostridial neurotoxin (or
XX PT component) attached to a targeting moiety -

XX PS Disclosure; Page 65; 77pp; English.

XX CC The specification describes an agent, comprising a clostridial neurotoxin
XX CC attached to a targeting moiety, where the targeting moiety is selected
XX CC from transmission compounds, and compounds substantially similar to the
XX CC transmission compounds. The agent may be used for treating pain, where
XX CC the clostridial neurotoxin component is derived from botulinum toxin
XX CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
XX CC The targeting moiety comprises a light chain and an amine end segment of
XX CC a heavy chain and comprises Substance P as the targeting moiety. The pain
XX CC alleviating effects persist for 2-6 months. The present sequence
XX CC represents a substance P precursor, and is used in the course of the
XX CC invention.

XX SQ Sequence 13 AA;

Query Match 67.6%; Score 48; DB 22; Length 13;
Best Local Similarity 81.8%; Pred. No. 0.3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:| |
Db 1 rpkpgqffglm 11

RESULT 106

AAG62776
ID AAG62776 standard; peptide; 13 AA.

XX AC AAG62776;
XX DT 17-SEP-2001 (first entry)
XX DE Amino acid sequence of carboxy-ester substance P precursor.
XX KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT Modified-site 13
XX FT /note= "ethylated residue"

XX PN WO200153336-A1.

XX PD 26-JUL-2001.

XX PF 17-JAN-2001; 2001WO-US01529.

XX PR 19-JAN-2000; 2000US-0489667.

XX PA (ALLR) ALLERGAN SALES INC.

XX PI Donovan S;

XX DR WPI; 2001-451900/48.

XX PT Agent useful for treating pain comprises a clostridial neurotoxin (or
XX PT component) attached to a targeting moiety -

XX PS Disclosure; Page 68; 77pp; English.

XX CC The specification describes an agent, comprising a clostridial neurotoxin
XX CC attached to a targeting moiety, where the targeting moiety is selected
XX CC from transmission compounds, and compounds substantially similar to the
XX CC transmission compounds. The agent may be used for treating pain, where
XX CC the clostridial neurotoxin component is derived from botulinum toxin
XX CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
XX CC The targeting moiety comprises a light chain and an amine end segment of
XX CC a heavy chain and comprises Substance P as the targeting moiety. The pain
XX CC alleviating effects persist for 2-6 months. The present sequence
XX CC represents a substance P precursor, and is used in the course of the
XX CC invention.

XX SQ Sequence 13 AA;

Query Match 67.6%; Score 48; DB 22; Length 13;
Best Local Similarity 81.8%; Pred. No. 0.3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:| |
Db 1 rpkpgqffglm 11

RESULT 107

AAB98868
ID AAB98868 standard; Peptide; 13 AA.

XX AC AAB98868;

XX DT 14-AUG-2001 (first entry)

XX DE Chimeric analgesic peptide #24.

XX KW Opioid receptor binding; nociceptive receptor binding; analgesic;
XX KW pain; chimeric peptide.

XX OS Synthetic.

XX XX

PH Key Location/Qualifiers
FT Modified-site 13
FT /label= OTHER
FT /note= "C-terminal amide"
XX
PN WO200130371-A2.
XX
XX 03-MAY-2001.
XX
XX 27-OCT-2000; 2000WO-US29789.
XX
XX 28-OCT-1999; 99US-0428692.
XX
XX (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX
XX WPI; 2001-397593/42.
XX
XX New chimeric peptides used for treating pain comprise opioid receptor binding group and nociceptive receptor binding group
XX
XX Claim 10; Page 15; 34pp; English.
XX
XX The present invention describes a number of chimeric peptides comprising an opioid receptor binding moiety and a nociceptive receptor binding moiety. These can be used as analgesics for the treatment of pain. Unlike opioid receptor based peptides alone, tolerance does not result from their long-term use. The present sequence is one of the peptides of the invention.
XX
SQ Sequence 13 AA;

Query Match 67.6%; Score 48; DB 22; Length 13;
Best Local Similarity 81.8%; Pred. No. 0.3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQWFWM 11
Db 1 rpqpqffglm 11

RESULT 108
AAB98871
ID AAB98871 standard; Peptide; 13 AA.
XX
AC AAB98871;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #27.
XX
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Modified-site 13
FT /label= OTHER
FT /note= "modified by Ome"
XX
PN WO200130371-A2.
XX
XX 03-MAY-2001.
XX
XX 27-OCT-2000; 2000WO-US29789.
XX
XX 28-OCT-1999; 99US-0428692.
XX
XX (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX
XX WPI; 2001-397593/42.
XX
XX New chimeric peptides used for treating pain comprise opioid receptor binding group and nociceptive receptor binding group
XX
XX Claim 10; Page 15; 34pp; English.
XX
XX The present invention describes a number of chimeric peptides comprising an opioid receptor binding moiety and a nociceptive receptor binding moiety. These can be used as analgesics for the treatment of pain. Unlike opioid receptor based peptides alone, tolerance does not result from their long-term use. The present sequence is one of the peptides of the invention.
XX
SQ Sequence 13 AA;

Query Match 67.6%; Score 48; DB 22; Length 13;
Best Local Similarity 81.8%; Pred. No. 0.3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQWFWM 11
Db 1 rpqpqffglm 11

RESULT 108
AAB98871
ID AAB98871 standard; Peptide; 13 AA.
XX
AC AAB98871;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #27.
XX
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Modified-site 13
FT /label= OTHER
FT /note= "modified by Ome"
XX
PN WO200130371-A2.
XX
XX 03-MAY-2001.
XX
XX 27-OCT-2000; 2000WO-US29789.
XX
XX 28-OCT-1999; 99US-0428692.
XX
XX (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX

PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX
XX WPI; 2001-397593/42.
XX
XX New chimeric peptides used for treating pain comprise opioid receptor binding group and nociceptive receptor binding group
XX
XX Claim 10; Page 15; 34pp; English.
XX
XX The present invention describes a number of chimeric peptides comprising an opioid receptor binding moiety and a nociceptive receptor binding moiety. These can be used as analgesics for the treatment of pain. Unlike opioid receptor based peptides alone, tolerance does not result from their long-term use. The present sequence is one of the peptides of the invention.
XX
SQ Sequence 13 AA;

Query Match 67.6%; Score 48; DB 22; Length 13;
Best Local Similarity 81.8%; Pred. No. 0.3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQWFWM 11
Db 1 rpqpqffglm 11

RESULT 109
AAB98874
ID AAB98874 standard; Peptide; 13 AA.
XX
AC AAB98874;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #30.
XX
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Modified-site 13
FT /label= OTHER
FT /note= "modified by Oeth"
XX
PN WO200130371-A2.
XX
XX 03-MAY-2001.
XX
XX 27-OCT-2000; 2000WO-US29789.
XX
XX 28-OCT-1999; 99US-0428692.
XX
XX (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX
XX WPI; 2001-397593/42.
XX
XX New chimeric peptides used for treating pain comprise opioid receptor binding group and nociceptive receptor binding group
XX
XX Claim 10; Page 15; 34pp; English.
XX
XX The present invention describes a number of chimeric peptides comprising an opioid receptor binding moiety and a nociceptive receptor binding moiety. These can be used as analgesics for the treatment of pain. Unlike opioid receptor based peptides alone, tolerance does not result from their long-term use. The present sequence is one of the peptides of the invention.
XX

XX
SQ Sequence 13 AA;

Query Match 67.6%; Score 48; DB 22; Length 13;
Best Local Similarity 81.8%; Pred. No. 0.32;
Matches 9; Conservative 1; Mismatches 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:| |
Db 1 rpkpqgffglm 11

RESULT 110

AAV03159
ID AAV03159 standard; peptide; 14 AA.

XX
AC AAY03159;

XX 10-JUN-1999 (first entry)

XX Substance P-Glycine-Lysine-Arginine.

XX Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
KW substance P.

XX Synthetic.

XX US5891842-A.

XX 06-APR-1999.

XX 12-APR-1996; 96US-0631434.

XX 09-APR-1993; 93US-0044954.

XX 12-APR-1996; 96US-0631434.

XX (TUFT) TUFTS COLLEGE.

XX Kream RM;

XX WPI; 1999-253906/21.

XX Synergistic method for enhancing opioid analgesia and anaesthesia
PT within a human

XX Disclosure; Column 14; 20pp; English.

CC This sequence represents substance P used in the method of the
CC invention. The method is for enhancing opioid analgesia within a human
CC subject for a duration of 15 minutes comprises concurrent administration
CC of substance P, or one of its precursors. The method is used to elicit
CC opioid analgesia and anaesthesia, either prior to or after the occurrence
CC of a nociceptive event. The components have a synergistic effect. The
CC method allows use of low doses of opioid that produce little or no
CC physiological effect reducing conventional risks of toxicity and
CC addiction, and allows the use of low doses of substance P and its related
CC analogs that limit their in vivo physiological consequences. The
CC analgesia is naloxone reversible allowing diminishment or complete
CC elimination of opioid analgesia if desired and on demand. The treatment
CC provides a durable analgesic effect, but only minimally disturbs and
CC interrupts the normal metabolic processes of the body.

XX Sequence 14 AA;

Query Match 67.6%; Score 48; DB 20; Length 14;
Best Local Similarity 81.8%; Pred. No. 0.32;
Matches 9; Conservative 1; Mismatches 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:| |
Db 1 rpkpqgffglm 11

RESULT 111

AAG62771

ID AAG62771 standard; peptide; 14 AA.

XX
AC AAG62771;

XX 17-SEP-2001 (first entry)

XX Amino acid sequence of substance P precursor.

XX Clostridial neurotoxin; pain; botulinum toxin; Substance P.

XX Unidentified.

XX WO200153336-A1.

XX 26-JUL-2001.

XX 17-JAN-2001; 2001WO-US01529.

XX 19-JAN-2000; 2000US-0489667.

XX (ALLR) ALLERGAN SALES INC.

XX Donovan S;

XX WPI; 2001-451900/48.

XX Agent useful for treating pain comprises a clostridial neurotoxin (or
XX component) attached to a targeting moiety -
XX Disclosure; Page 63; 77pp; English.

XX The specification describes an agent, comprising a clostridial neurotoxin
XX attached to a targeting moiety, where the targeting moiety is selected
XX from transmission compounds, and compounds substantially similar to the
XX transmission compounds. The agent may be used for treating pain, where
XX the clostridial neurotoxin component is derived from botulinum toxin
XX selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
XX The targeting moiety comprises a light chain and an amine end segment of
XX a heavy chain and comprises substance P as the targeting moiety. The pain
XX alleviating effects persist for 2-6 months. The present sequence
XX represents substance P precursor, and is used in the course of the
XX invention.

XX Sequence 14 AA;

Query Match 67.6%; Score 48; DB 22; Length 14;
Best Local Similarity 81.8%; Pred. No. 0.32;
Matches 9; Conservative 1; Mismatches 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:| |
Db 1 rpkpqgffglm 11

RESULT 112

AAG62774

ID AAG62774 standard; peptide; 14 AA.

XX
AC AAG62774;

XX 17-SEP-2001 (first entry)

XX Amino acid sequence of carboxy-ester substance P precursor.
XX Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX Synthetic.

XX

PH Key Location/Qualifiers
FT Modified-site 14
FT /note= "methylated residue"

PN WO200153336-A1.

XX 26-JUL-2001.

XX 17-JAN-2001; 2001WO-US01529.

XX 19-JAN-2000; 2000US-0489667.

XX (ALLR) ALLERGAN SALES INC.

XX Donovan S;

XX WPI; 2001-451900/48.

XX Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -

XX Disclosure; Page 66; 77pp; English.

XX The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin
CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
CC The targeting moiety comprises a light chain and an amine end segment of
CC a heavy chain and comprises Substance P as the targeting moiety. The pain
CC alleviating effects persist for 2-6 months. The present sequence
CC represents a substance P precursor, and is used in the course of the
CC invention.

XX SQ Sequence 14 AA;

Query Match 67.6%; Score 48; DB 22; Length 14;
Best Local Similarity 81.8%; Pred. No. 0.32;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RPKPQQWFWM 11
|||||:|
Db 1 rpqpqffglm 11

RESULT 113

AAG62777
ID AAG62777 standard; peptide; 14 AA.

XX AC AAG62777;

XX DT 17-SEP-2001 (first entry)

XX Amino acid sequence of carboxy-ester substance P precursor.

XX Clostridial neurotoxin; pain; botulinum toxin; Substance P.

XX OS Synthetic.

XX Key Location/Qualifiers
FT Modified-site 14
FT /note= "ethylated residue"

XX WO200153336-A1.

XX 26-JUL-2001.

XX 17-JAN-2001; 2001WO-US01529.

XX 19-JAN-2000; 2000US-0489667.

XX

PA (ALLR) ALLERGAN SALES INC.

XX Donovan S;

XX WPI; 2001-451900/48.

XX Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -

XX Disclosure; Page 69; 77pp; English.

XX The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin
CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
CC The targeting moiety comprises a light chain and an amine end segment of
CC a heavy chain and comprises Substance P as the targeting moiety. The pain
CC alleviating effects persist for 2-6 months. The present sequence
CC represents a substance P precursor, and is used in the course of the
CC invention.

XX SQ Sequence 14 AA;

Query Match 67.6%; Score 48; DB 22; Length 14;
Best Local Similarity 81.8%; Pred. No. 0.32;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RPKPQQWFWM 11
|||||:|
Db 1 rpqpqffglm 11

RESULT 114

AAB98869
ID AAB98869 standard; Peptide; 14 AA.

XX AC AAB98869;

XX DT 14-AUG-2001 (first entry)

XX Chimeric analgesic peptide #25.

XX Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.

XX OS Synthetic.

XX Key Location/Qualifiers
FT Modified-site 14
FT /label= OTHER
FT /note= "C-terminal amide"

XX WO200130371-A2.

XX PD 03-MAY-2001.

XX 27-OCT-2000; 2000WO-US29789.

XX 28-OCT-1999; 99US-0428692.

XX (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

XX Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

XX WPI; 2001-397593/42.

XX New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group -

XX Claim 10; Page 15; 34pp; English.

XX The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 14 AA;

Query Match 67.6%; Score 48; DB 22; Length 14;
Best Local Similarity 81.8%; Pred. No. 0.32;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:| |
Db 1 rpkpqgffgim 11

RESULT 115
AAB98872
ID AAB98872 standard; Peptide; 14 AA.
XX AC
XX XX
DT 14-AUG-2001 (first entry)
XX DE
XX Chimeric analgesic peptide #28.
XX KW
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX OS
XX Synthetic.
XX FH
FH Key Location/Qualifiers
FT Modified-site 14
FT /label= OTHER
FT /note= "modified by OMe"
XX PN
PN WO200130371-A2.
XX PD
PD 03-MAY-2001.
XX PF
PF 27-OCT-2000; 2000WO-US29789.
XX PR
PR 28-OCT-1999; 99US-0428692.
XX XX
XX (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX PA
XX Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX PI
XX WPI; 2001-397593/42.
XX DR
XX New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group
XX PS
PS Claim 10; Page 15; 34pp; English.
XX XX
XX The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 14 AA;

Query Match 67.6%; Score 48; DB 22; Length 14;
Best Local Similarity 81.8%; Pred. No. 0.32;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:| |
Db 1 rpkpqgffgim 11

RESULT 116
AAB98875
ID AAB98875 standard; Peptide; 14 AA.
XX AC
XX AAB98875;
XX XX
DT 14-AUG-2001 (first entry)
XX DE
XX Chimeric analgesic peptide #31.
XX KW
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX OS
XX Synthetic.
XX FH
FH Key Location/Qualifiers
FT Modified-site 14
FT /label= OTHER
FT /note= "modified by Oeth"
XX PN
PN WO200130371-A2.
XX PD
PD 03-MAY-2001.
XX PF
PF 27-OCT-2000; 2000WO-US29789.
XX PR
PR 28-OCT-1999; 99US-0428692.
XX XX
XX (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX PA
XX Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX PI
XX WPI; 2001-397593/42.
XX DR
XX New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group
XX PS
PS Claim 10; Page 15; 34pp; English.
XX XX
XX The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 14 AA;

Query Match 67.6%; Score 48; DB 22; Length 14;
Best Local Similarity 81.8%; Pred. No. 0.32;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:| |
Db 1 rpkpqgffgim 11

RESULT 117
AAB91440
ID AAB91440 standard; Peptide; 14 AA.
XX AC
XX AAB91440;
XX XX
DT 22-JUN-2001 (first entry)
XX DE
XX Tachykinins peptide SEQ ID NO:616.
XX XX

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX Homo sapiens.
OS Synthetic.
XX WO200069900-A2.
XX 23-NOV-2000.
XX 17-MAY-2000; 2000WO-US13576.
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX (CONJ-) CONJUCHEM INC.
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
PI WPI; 2001-112059/12.
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX Disclosure; Page 400; 733pp; English.
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
XX exemplification of the present invention.

XX Sequence 14 AA;
Query Match 67.6%; Score 48; DB 22; Length 14;
Best Local Similarity 81.8%; Pred. No. 0.32;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|
Db 1 rpkpqqffglm 11

RESULT 118
AAB06258
ID AAB06258 standard; peptide; 20 AA.
XX AAB06258;
XX 16-OCT-2000 (first entry)
XX Substance P analogue #2.

XX Substance P; SP; neurokinin-1 receptor; NK-1R; nociception; NTE-SAP;
KW saparin; SAP; analgesic; anti-inflammatory; neuroprotective;
KW anti-asthmatic; anti-allergic; dermatological; anti-ulcer;
KW tranquiliser; immunosuppressive; anti-migraine; cytostatic;

KW substance P antagonist; cytotoxic; ribosome inactivator;
KW prostaglandin antagonist; cancer; respiratory disease; asthma;
KW allergic rhinitis; ophthalmic disease; conjunctivitis;
KW allergic dermatitis; psoriasis; ulcerative colitis; Crohn's disease;
KW gastrointestinal disorder; anxiety; psychosis; rheumatoid arthritis;
KW carcinoma; lupus erythematosus conjunctivitis.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 20 /note= "C-terminal amide"
FT
XX US6063758-A.
XX 16-MAY-2000.
XX 09-JUL-1997; 97US-0890157.
XX 09-JUL-1997; 97US-0890157.
XX (ADTA-) ADVANCED TARGETING SYSTEMS INC.
XX Lappi DA, Wiley RG;
XX WPI; 2000-430049/37.
XX New conjugates comprising substance P or its analog, and a
PT ribosome-inactivating protein (for example saparin), for alleviating
PT pain and treating disorders associated with neurokinin-1 receptor -
XX Claim 1; Column 2; 21pp; English.

XX The present sequence is an analogue of substance P (SP). SP, which binds
CC to the neurokinin-1 receptor (NK-1R), is best known for its role in
CC nociception. It is secreted by small unmyelinated C-fibres of the
CC peripheral nervous system that are thought to be primary nociceptive
CC neurons. The present sequence may be conjugated to Saparin (SAP), a
CC ribosome-inactivating protein, to produce NTE-SAP. The conjugate may be
CC used to control chronic pain by specifically targeting cells having NK1
CC receptors, and inhibiting proliferation of or causing death of these
CC cells. It may also be used to treat NK-1R-associated disorders
CC including respiratory conditions (e.g. asthma, allergic rhinitis),
CC ophthalmic conditions (e.g. conjunctivitis), cutaneous conditions (e.g.
CC allergic dermatitis, psoriasis), intestinal conditions (e.g. ulcerative
CC colitis, Crohn's disease), gastrointestinal disorders, central nervous
CC system disorders (e.g. anxiety, psychosis), inflammatory diseases (e.g.
CC rheumatoid arthritis), proliferative conditions (e.g. carcinoma),
CC disorders related to immune enhancement or suppression (e.g. lupus
CC erythematosus conjunctivitis), and especially migraine.

XX Sequence 20 AA;

Query Match 67.6%; Score 48; DB 21; Length 20;
Best Local Similarity 81.8%; Pred. No. 0.45;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|
Db 10 rpkpqqffglm 20

RESULT 119
AAP70431
ID AAP70431 standard; protein; 129 AA.
XX AAP70431;
XX 17-JAN-1991 (first entry)
DT Human beta-preprotachykinin.
DE
XX

KW Preprotachykinin; substance P; neurokinin A; tachykinin;

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Region 20..56

XX FT /label=claimed polypeptide

XX FT Region 1..126

XX FT /label=claimed polypeptide

XX FT Region 111..126

XX FT /label=claimed polypeptide

XX PN WO8707643-A.

XX PD 17-DEC-1987.

XX PF 03-JUN-1987; 87WO-GB00382.

XX PR 03-JUN-1986; 86GB-0013431.

XX PA (RESE) RESEARCH CORPORATION LTD.

XX PI Harnar AJ, Pascall J, McKeown A;

XX DR WPI; 1987-362730/51.

XX DR N-PSDB; AAN70688.

XX PT New DNA sequence coding for the new polypeptide preprotachykinin -

XX PT a precursor for substance P, etc., useful as neurotransmitters,

XX PT diagnostic reagents, etc.

XX PS Claim 1; page 15; 25pp; English.

XX CC Beta-preprotachykinin includes sequences identical to tachykinins, eg

XX CC substance P, neurokinin A, or other biologically active peptides, eg

XX CC neuropeptide K. These peptides are, eg neurotransmitters, hormones,

XX CC analgesics and anti-inflammatories. The polypeptides can be used

XX CC as reagents in RIA, eg to monitor or diagnose carcinoid syndrome.

XX SQ Sequence 129 AA;

XX SQ Sequence 129 AA;

Query Match

Best Local Similarity 67.6%; Score 48; DB 8; Length 129;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11

DB 58 rpqpgffglm 68

RESULT 120

AAG99353

ID AAG99353 standard; Protein; 129 AA.

XX AC AAG99353;

XX DT 25-SEP-2001 (first entry)

XX DE Human atypical tachykinin protein fragment SEQ ID NO: 63.

XX KW Atypical tachykinin; ATT; human; hypertension.

XX OS Homo sapiens.

XX PN WO200146415-A1.

XX PD 28-JUN-2001.

XX PF 21-DEC-2000; 2000WO-JP09083.

XX PR 21-DEC-1999; 99JP-0362638.

XX PR 10-MAR-2000; 2000JP-0066714.

XX (TAKE) TAKEDA CHEM IND LTD.

XX PI Itoh Y, Nishi K, Kitada C, Inatomi N;

XX DR WPI; 2001-441676/47.

XX PT Atypical tachykinin peptides of human origin and DNA encoding them for

XX PT screening potential agents for treatment of hypertension -

XX PS Example 14; Page 143; 153pp; Japanese.

XX CC The present invention relates to atypical tachykinin proteins of human

XX CC origin and their esters, amides, salts and partial peptides. These can be

XX CC used in the treatment, prevention and diagnosis of hypertension. The

XX CC present sequence is a protein fragment described in the exemplification

XX CC of the invention.

XX SQ Sequence 129 AA;

Query Match

Best Local Similarity 67.6%; Score 48; DB 22; Length 129;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11

DB 58 rpqpgffglm 68

RESULT 121

AAW16339

ID AAW16339 standard; Protein; 401 AA.

XX AC AAW16339;

XX DT 05-SEP-1997 (first entry)

XX DE DAB389-SP-Gly fusion toxin.

XX KW DAB389-SP-Gly; amidated polypeptide binding ligand; drug delivery;

XX KW diphtheria toxin; substance P; cancer; therapy.

XX OS Synthetic.

XX PN WO9713410-A1.

XX PD 17-APR-1997.

XX PF 11-OCT-1996; 96WO-US16237.

XX PR 13-OCT-1995; 95US-0005431.

XX PA (BOST-) BOSTON MEDICAL CENT CORP.

XX PI Fisher CE, Leeman SE, Murphy JR, Vanderspek JC;

XX DR WPI; 1997-235583/21.

XX DR N-PSDB; AAT63359.

XX PT Hybrid molecule for targeting compound, especially a toxin, into

XX PT cells - includes polypeptide able to transport the compound across

XX PT cytoplasmic membranes and amidated ligand, useful for treatment of

XX PT cancer

XX PS Example 1; Page 22-23; 51pp; English.

XX CC DAB389-SP-Gly (AAW16339) is a hybrid toxin comprising DAB389 (i.e.

XX CC amino acids 1-386 plus His-484 and Ala-485 of mature diphtheria

XX CC toxin) fused to C-terminal glycine-extended substance P. It was

XX CC expressed in E. coli HMS174(DE3) transformants using a vector

XX CC that carried DAB389-SP-Gly DNA (see also AAT63359). The fusion

XX CC protein was then amidated using peptidylglycino-alpha-amidating

CC monoxigenase. The amidated fusion protein used to target DAB389
CC toxin to specific cells contg. substance P receptors, esp. cancer
CC cells. For human IM9 (chronic myelogenous leukaemia) cells contg.
CC approx. 4000 substance P receptors per cell, the IC50 for amidated
CC DAB389-SP-Gly was 18 pM.

XX Sequence 401 AA;

Query Match 67.6%; Score 48; DB 18; Length 401;
Best Local Similarity 81.8%; Pred. No. 8.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11
|||||:||||
Db 390 rpkpqffgilm 400

RESULT 122

AAW26510
ID AAW26510 standard; Protein; 487 AA.

XX AAW26510;

XX 06-JAN-1998 (first entry)

XX Amyloid precursor protein substrate APP-REP 751.

XX Anyloid precursor protein; APP; beta-amyloid protein; BAP;
KW substrate; mutein; secretase; Alzheimer's disease; human;
KW APP-REP 751; pCLL621.

XX Chimeric Homo sapiens.
OS Chimeric synthetic.

XX Key Location/Qualifiers

FT Peptide 362..372
FT /label= SP
FT /note= "substance P reporter epitope"

FT Domain 389..430

FT /label= BAP

FT /note= "beta-amyloid protein"

FT Cleavage-site 404..405

FT /note= "secretase cleavage site"

FT Domain 417..440

FT /label= Transmembrane

XX US5656477-A.

PN 12-AUG-1997.

PD 01-MAY-1992; 92US-0877675.

PF 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobsen JS, Vitek MP;

PI WPI; 1997-414594/38.

XX P-PSDB; AAT87083.

XX Nucleic acid encoding amyloid precursor mutein(s) - comprising
PT reporter gene and coding sequence, for identifying compounds which
PT modify the activity of proteolytic enzymes which cleave APP

XX Disclosure; Fig 8; 84pp; English.

XX This polypeptide, designated APP-REP 761, comprises an amyloid
CC precursor protein (APP) that has a 276-amino acid deletion of the
CC native APP and which carries a Substance P epitope markers placed
CC N-terminal to the beta-amyloid protein (BAP) domain. APP-REP 751

CC can be used in a claimed method for screening for a compound which
CC reduces the formation of beta-amyloid protein, determined by
CC measuring the amount of marker in a medium containing transfected
CC cells. The method is used to detect compounds which inhibit the
CC activity of proteolytic enzymes which cleave APP to generate BAP
CC fragments. Such compounds can be used in the treatment of e.g.
CC Alzheimer's disease. The deletion of a 276 amino acid portion of
CC APP distinguishes the construct from endogenously expressed APP,
CC and beneficially increases the resolution of APP-REP fragments
CC resulting from the proteolytic cleavage by secretase or other
CC amyloidogenic, BAP-generating cleavage events.

XX Sequence 487 AA;

Query Match 67.6%; Score 48; DB 18; Length 487;
Best Local Similarity 81.8%; Pred. No. 9.7;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11
|||||:||||
Db 362 rpkpqffgilm 372

RESULT 123

AAW26394
ID AAW26394 standard; Protein; 487 AA.

XX AAW26394;

XX 15-DEC-1997 (first entry)

XX Amyloid precursor protein substrate APP-REP 751.

XX Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KW substrate; mutein; secretase; Alzheimer's disease; human;
KW APP-REP 751; pCLL621.

XX Chimeric Homo sapiens;
OS Chimeric synthetic.

XX Key Location/Qualifiers

FT Peptide 362..372
FT /label= SP
FT /note= "substance P reporter epitope"

FT Domain 389..430

FT /label= BAP

FT /note= "beta-amyloid protein"

FT Cleavage-site 404..405

FT /note= "secretase cleavage site"

FT Domain 417..440

FT /label= Transmembrane

XX US5652092-A.

PN 29-JUL-1997.

PD 01-MAY-1992; 92US-0877675.

PF 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

XX 05-JUN-1995; 95US-0462859.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobsen JS, Vitek MP;

PI WPI; 1997-392937/36.

XX N-PSDB; AAT84562.

XX Screening for compounds which reduce beta-amyloid protein formation
PT - using cells which express a construct encoding a marker and an
PT amyloid precursor mutin derived from APP isoforms

XX Disclosure; Fig 8; 84pp; English.

XX This polypeptide, designated APP-REP 761, comprises an amyloid

CC precursor protein (APP) that has a 276-amino acid deletion of the

CC native APP and which carries a Substance P epitope markers placed

CC N-terminal to the beta-amyloid protein (BAP) domain. APP-REP 751

CC can be used in a claimed method for screening for a compound which

CC reduces the formation of beta-amyloid protein, determined by

CC measuring the amount of marker in a medium containing transfected

CC cells. The method is used to detect compounds which inhibit the

CC activity of proteolytic enzymes which cleave APP to generate BAP

CC fragments. Such compounds can be used in the treatment of e.g.

CC Alzheimer's disease. The deletion of a 276 amino acid portion of

CC APP distinguishes the construct from endogenously expressed APP,

CC and beneficially increases the resolution of APP-REP fragments

CC resulting from the proteolytic cleavage by secretase or other

CC amyloidogenic, BAP-generating cleavage events.

XX Sequence 487 AA;

Query Match 67.6%; Score 48; DB 18; Length 487;

Best Local Similarity 81.8%; Pred. No. 9.7;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11

Db 362 rpkpqffglm 372

|||||:| |

RESULT 124

AAW44745

ID AAW44745 standard; Protein; 487 AA.

XX

AC AAW44745;

XX

DT 01-JUN-1998 (first entry)

XX

DE APP-REP 751 protein from pCLL621.

XX

KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;

KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;

KW Alzheimer's disease; cleavage.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN US5693478-A.

XX

PD 02-DEC-1997.

XX

PF 05-JUN-1995; 95US-0464247.

XX

PR 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

PR 05-JUN-1995; 95US-0464247.

XX

PA (AMCY) AMERICAN CYANAMID CO.

XX

PI Jacobsen JS, Vitek MP;

XX

DR WPI: 1998-031744/03.

DR N-PSDB; AAV05850.

XX

XX Amyloid precursor muten reporter molecule assay containing antibody

PT recognised marker - used to study pathways associated with

PT Alzheimer's disease

XX

PS Disclosure; Fig 8; 84pp; English.

XX

CC This is the amino acid sequence of a novel amyloid precursor protein

CC (APP) designated APP-REP 751, contained in construct pCLL621. The

CC sequence comprises a mutant version of the APP 751 isoform of human APP

CC which contains a deletion of 276 amino acids from the central region.

CC The deleted region is replaced by a substrate P reporter epitope

CC sequence (RPKPQOWFWLM). In contrast to the APP-REP 751 encoded by the

CC construct pCLL602 (AAW44744), this sequence does not contain a

CC Met-enkephalin reporter epitope (YGGFM) fused at the C-terminus of the

CC coding sequence. The shorter protein is generated for ease of detection

CC based on size difference with the wild type APP protein and also by

CC detection of the reporter epitopes. The mutant protein can be used in a

CC method to study secretase and beta-amyloid protein (BAP)-generating

CC pathways associated with Alzheimer's disease by studying proteolytic

CC cleavage of the reporter polypeptides.

XX Sequence 487 AA;

Query Match 67.6%; Score 48; DB 19; Length 487;

Best Local Similarity 81.8%; Pred. No. 9.7;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11

Db 362 rpkpqffglm 372

|||||:| |

RESULT 125

AAW42979

ID AAW42979 standard; Protein; 487 AA.

XX

XX AAW42979;

AC

XX

DT 01-MAY-1998 (first entry)

XX

DE Amyloid precursor protein mutant APP-ARP 751.

XX

KW Beta-amyloid peptide; BAP; extracellular BAP plaque;

KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;

KW amyloid precursor protein; APP; secretase; BAP aggregation;

KW abnormal proteolytic cleavage.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN US5703209-A.

XX

PD 30-DEC-1997.

XX

PF 05-JUN-1995; 95US-0464248.

XX

PR 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

XX

PA (AMCY) AMERICAN CYANAMID CO.

XX

PI Jacobsen JS, Vitek MP;

XX

DR WPI: 1998-076482/07.

DR N-PSDB; AAV04866.

XX

PT Amyloid precursor protein fusion polypeptides - comprising APP

PT fragment and marker, useful for research and drug screening

XX

PS Disclosure; Fig 8A-Q; 84pp; English.

XX

CC The present sequence represents an amyloid precursor protein (APP),

CC which has a deletion of 276 amino acids to within 15 amino acids of the

CC beta-amyloid peptide (BAP) domain. The protein also contains the Abnormal

CC accumulation of extracellular BAP in plaques and cerebrovascular deposits

CC is characteristic in brains of individuals suffering from Alzheimers

CC disease and Downs syndrome. BAP is a poorly soluble, self-aggregating

CC protein which is derived from a larger amyloid precursor protein (APP).

CC APP is expressed as an integral membrane protein, and is cleaved by

CC secretase, between BAP 16Lys and 17Leu. Cleavage at this site precludes

CC amyloidogenesis and results in the release of the amino-terminal APP
 CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and
 CC APP-770. These isoforms are derived by alternative splicing. APP-RP 751
 CC is constructed by ligating restriction fragments representing N- and
 CC C-terminal APP-751 cDNA and substrate P reporter epitope sequences.
 CC APP can be used as a substrate for studying abnormal proteolytic cleavage
 CC which results in the release of BAP, and also to screen for drugs that
 CC will inhibit such cleavage.

XX SQ Sequence 487 AA;

Query Match 67.6%; Score 48; DB 19; Length 487;

Best Local Similarity 81.8%; Pred. No. 9.7;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQWFWM 11
 |||||:| |
 Db 362 rpqpqffglm 372

RESULT 126

AAW26509
 ID AAW26509 standard; Protein; 492 AA.

XX AC AAW26509;

XX DT 20-JUN-1994 (first entry)

XX DE APP-REP 751 amyloid precursor protein/reporter protein.

XX KW Amyloid precursor protein; APP; beta amyloid protein; BAP;

XX KW detection; Alzheimer's disease; Down's syndrome.

XX OS Homo sapiens.

XX PN AU9338358-A.

XX PD 04-NOV-1993.

XX PF 03-MAY-1993; 93AU-0038358.

XX PR 01-MAY-1992; 92US-0877675.

XX PA (AMCY) AMERICAN CYANAMID CO.

XX PI Jacobsen JS, Vitek MP;

XX DR WPI; 1993-406194/51.

XX DR N-PSDB; AAQ54257.

XX PT New mutant forms of amyloid precursor protein - for detecting

XX PT cpds. that modify activity of enzymes involved in precursor

XX PT cleavage, also new nucleic acid encoding them

XX PS Claim 5; Figure 7; 66pp; English.

XX CC This mutant form of amyloid precursor protein comprises from the 5'

XX CC to the 3' end a sequence encoding a marker and either (1) a

XX CC sequence encoding the N-terminus of an amyloid precursor protein

XX CC (APP) up to, but not including, the nucleotides encoding the beta

XX CC amyloid protein (BAP) domain or (2) the BAP domain. Recombinant

XX CC polypeptides generated from this proteins coding sequence can be

XX CC used to detect drugs or compounds that inhibit/augment the

XX CC activity of proteolytic enzymes which cleave APP to generate BAP

XX CC fragments (deposition of which occurs in patients with Alzheimers

XX CC disease and Down's syndrome).

XX SQ Sequence 492 AA;

Query Match

Best Local Similarity 81.8%; Score 48; DB 14; Length 492;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RPKPOQWFWM 11
 |||||:| |
 Db 362 rpqpqffglm 372

RESULT 127

AAW26509

ID AAW26509 standard; Protein; 492 AA.

XX AC AAW26509;

XX DT 06-JAN-1998 (first entry)

XX DE Amyloid precursor protein substrate APP-REP 751.

XX KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;

XX KW substrate; mutin; secretase; Alzheimer's disease; human;

XX KW APP-REP 751; pCLL602.

XX OS Chimeric Homo sapiens.

XX OS Chimeric synthetic.

XX PH Key Location/Qualifiers

XX FT Peptide 362..372

XX FT /label= SP

XX FT /note= "substance P reporter epitope"

XX FT Domain 389..430

XX FT /label= BAP

XX FT /note= "beta-amyloid protein"

XX FT Cleavage-site 404..405

XX FT /note= "secretase cleavage site"

XX FT Domain 417..440

XX FT /label= Transmembrane

XX FT Peptide 488..492

XX FT /label= ME

XX FT /note= "Met-enkephalin reporter epitope"

XX PN US5656477-A.

XX PD 12-AUG-1997.

XX PF 01-MAY-1992; 92US-0877675.

XX PR 20-SEP-1993; 93US-0123659.

XX PR 01-MAY-1992; 92US-0877675.

XX PA (AMCY) AMERICAN CYANAMID CO.

XX PI Jacobsen JS, Vitek MP;

XX DR WPI; 1997-414594/38.

XX DR P-PSDB; AAT87083.

XX PT Nucleic acid encoding amyloid precursor mutin(s) - comprising

XX PT reporter gene and coding sequence, for identifying compounds which

XX PT modify the activity of proteolytic enzymes which cleave APP

XX PS Disclosure: Fig 7; 84pp; English.

XX CC This polypeptide, designated APP-REP 761, comprises an amyloid

XX CC precursor protein (APP) that has a 276-amino acid deletion of the

XX CC native APP and which carries Substance P and Met-enkephalin epitope

XX CC markers placed, respectively, on the N-terminal and C-terminal

XX CC sites of the beta-amyloid protein (BAP) domain. APP-REP 751 can

XX CC be used in a claimed method for screening for a compound which

XX CC reduces the formation of beta-amyloid protein, determined by

XX CC measuring the amount of marker in a medium containing transfected

XX CC cells. The method is used to detect compounds which inhibit the

XX CC activity of proteolytic enzymes which cleave APP to generate BAP

XX CC fragments. Such compounds can be used in the treatment of e.g.

XX CC Alzheimer's disease. The deletion of a 276 amino acid portion of

CC APP distinguishes the construct from endogenously expressed APP,
CC and beneficially increases the resolution of APP-REP fragments
CC resulting from the proteolytic cleavage by secretase or other
CC amyloidogenic, BAP-generating cleavage events.

XX Sequence 492 AA;

Query Match 67.6%; Score 48; DB 18; Length 492;
Best Local Similarity 81.8%; Pred. No. 9.8;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Caps 0;

QY 1 RPKPQQWFWM 11
|||||:| |
Db 362 rpkpqgffglm 372

RESULT 128

AAW26393
ID AAW26393 standard; Protein; 492 AA.

XX AC AAW26393;

XX 15-DEC-1997 (first entry)

DE Amyloid precursor protein substrate APP-REP 751.

KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KW substrate; muten; secretase; Alzheimer's disease; human;
KW APP-REP 751; pCLL602.

XX Chimeric Homo sapiens;
OS Chimeric synthetic.

PH Key Location/Qualifiers
FT Peptide 362..372

FT /label= SP
FT /note= "substance P reporter epitope"

FT Domain 389..430

FT /label= BAP
FT /note= "beta-amyloid protein"

FT Cleavage-site 404..405

FT /note= "secretase cleavage site"

FT Domain 417..440

FT /label= Transmembrane

FT Peptide 488..492

FT /label= ME
FT /note= "Met-enkephalin reporter epitope"

FT XX US5652092-A.

XX XX 29-JUL-1997.

PD 01-MAY-1992; 92US-0877675.

XX 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

PR 05-JUN-1995; 95US-0462859.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobsen JS, Vitek MP;

PI WPI; 1997-392937/36.

DR N-PSDB; AAT84561.

XX Screening for compounds which reduce beta-amyloid protein formation

PT - using cells which express a construct encoding a marker and an
PT amyloid precursor muten derived from APP isoforms
XX Disclosure; Fig 7; 84pp; English.

XX This polypeptide, designated APP-REP 761, comprises an amyloid

CC precursor protein (APP) that has a 276-amino acid deletion of the
CC native APP and which carries Substance P and Met-enkephalin epitope
CC markers placed, respectively, on the N-terminal and C-terminal
CC sites of the beta-amyloid protein (BAP) domain. APP-REP 751 can
CC be used in a claimed method for screening for a compound which
CC reduces the formation of beta-amyloid protein, determined by
CC measuring the amount of marker in a medium containing transfected
CC cells. The method is used to detect compounds which inhibit the
CC activity of proteolytic enzymes which cleave APP to generate BAP
CC fragments. Such compounds can be used in the treatment of e.g.
CC Alzheimer's disease. The deletion of a 276 amino acid portion of
CC APP distinguishes the construct from endogenously expressed APP,
CC and beneficially increases the resolution of APP-REP fragments
CC resulting from the proteolytic cleavage by secretase or other
CC amyloidogenic, BAP-generating cleavage events.

XX Sequence 492 AA;

Query Match 67.6%; Score 48; DB 18; Length 492;
Best Local Similarity 81.8%; Pred. No. 9.8;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Caps 0;

QY 1 RPKPQQWFWM 11
|||||:| |

Db 362 rpkpqgffglm 372

RESULT 129

AAW44744
ID AAW44744 standard; Protein; 492 AA.

XX AC AAW44744;

XX 01-JUN-1998 (first entry)

DE APP-REP 751 protein from pCLL602.

XX Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
KW Alzheimer's disease; cleavage.

XX Homo sapiens.

OS Synthetic.

XX US5693478-A.

PN 02-DEC-1997.

PD 05-JUN-1995; 95US-0464247.

XX 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

PR 05-JUN-1995; 95US-0464247.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobsen JS, Vitek MP;

PI WPI; 1998-031744/03.

DR N-PSDB; AAV05849.

XX Amyloid precursor muten reporter molecule assay containing antibody

PT recognised marker - used to study pathways associated with

PT Alzheimer's disease

XX Disclosure; Fig 7; 84pp; English.

XX This is the amino acid sequence of a novel amyloid precursor protein
CC (APP) designated APP-REP 751, contained in construct pCLL602. The
CC sequence comprises a mutant version of the APP 751 isoform of human APP
CC which contains a deletion of 276 amino acids from the central region.
CC The deleted region is replaced by a substrate P reporter; epitope sequence

CC (RPKPOQFFGLM) and a Met-enkephalin reporter epitope (YGGFM) is fused at
CC the C-terminus. The shorter protein is generated for ease of detection
CC based on size difference with the wild type APP protein and also by
CC detection of the reporter epitopes. The mutant protein can be used in
CC a method to study secretase and beta-amyloid protein (BAP)-generating
CC pathways associated with Alzheimer's disease by studying proteolytic
CC cleavage of the reporter polypeptides.
XX
SQ Sequence 492 AA;

Query Match 67.6%; Score 48; DB 19; Length 492;
Best Local Similarity 81.8%; Pred. No. 9.8;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGLM 11
Db 362 rpkpqffglm 372
|||||:|

RESULT 130
AAW42978
ID AAW42978 standard; Protein; 492 AA.
XX
AC AAW42978;
XX
DT 01-MAY-1998 (first entry)
XX
DE Amyloid precursor protein mutant APP-APP 751.
XX
DE Beta-amyloid peptide; BAP; extracellular BAP plaque;
KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;
KW amyloid precursor protein; APP; secretase; BAP aggregation;
KW abnormal proteolytic cleavage.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Protein 1..487
FT /note= "APP-APP 751"
FT Peptide 488..492
FT /note= "Met-enkephalin reporter epitope"
XX
XX
PN US5703209-A.
XX
PD 30-DEC-1997.
XX
XX
PF 05-JUN-1995; 95US-0464248.
XX
PR 20-SEP-1993; 93US-0123659.
PR 01-MAY-1992; 92US-0877675.
XX
XX (AMCY) AMERICAN CYANAMID CO.
XX
XX Jacobsen JS, Vitek MP;
XX
XX WPI; 1998-076482/07.
DR N-PSDB; AAV04865.
XX
XX Amyloid precursor protein fusion polypeptides - comprising APP
PT fragment and marker, useful for research and drug screening
XX
XX Disclosure; Fig 7A-Q; 84pp; English.
PS
XX The present sequence represents an amyloid precursor protein (APP),
XX which has a deletion of 276 amino acids to within 15 amino acids of the
XX beta-amyloid peptide (BAP) domain. The protein also contains the
XX Met-enkephalin reporter epitope at the carboxy terminus. Abnormal
XX accumulation of extracellular BAP in plaques and cerebrovascular deposits
XX is characteristic in brains of individuals suffering from Alzheimers
XX disease and Downs syndrome. BAP is a poorly soluble, self-aggregating
XX protein which is derived from a larger amyloid precursor protein (APP).

CC APP is expressed as an integral membrane protein, and is cleaved by
CC secretase, between BAP 16lys and 17Leu. Cleavage at this site precludes
CC amyloidogenesis and results in the release of the amino-terminal APP
CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and
CC APP-770. These isoforms are derived by alternative splicing. APP-RP 751
CC is constructed by ligating restriction fragments representing N- and
CC C-terminal APP-751 cDNA and substrate P reporter epitope sequences.
CC APP can be used as a substrate for studying abnormal proteolytic cleavage
CC which results in the release of BAP, and also to screen for drugs that
XX will inhibit such cleavage.
XX
SQ Sequence 492 AA;

Query Match 67.6%; Score 48; DB 19; Length 492;
Best Local Similarity 81.8%; Pred. No. 9.8;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGLM 11
Db 362 rpkpqffglm 372
|||||:|

RESULT 131
AAR21958
ID AAR21958 standard; Peptide; 11 AA.
XX
AC AAR21958;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P [Ala 9] or [D-Ala 9].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 9
FT /note= "either L or D form"
XX
XX WO9202248-A.
XX
PD 20-FEB-1992.
XX
XX 29-JUL-1991; 91WO-US05323.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 10; Page 21; 35pp; English.
PS
XX The peptide is the tachykinin agonist substance P with an Ala (D/L)
XX residue substituted at position 9. The peptide was synthesised
XX by standard solid phase synthesis. Neuronal accumulation of
XX beta-amyloid may be treated by administration of tachykinin
XX agonists. The peptide can reduce the neurotoxic effects of a beta-
XX amyloid related polypeptide on cultured neurons. The peptide and
XX its analogues are useful for controlling diseases characterised by
XX beta amyloid accumulation in the brain such as Alzheimer's disease
XX and Down's syndrome.
XX See also AAR21932-75.
XX

```
SQ Sequence 11 AA;

Query Match
Best Local Similarity 66.2%; Score 47; DB 13; Length 11;
Matches 9; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY 1 RPKPQQWFWM 11
   |||||:| |
Db 1 rpkpqgffalm 11

RESULT 132
AAW92674
ID AAW92674 standard; peptide; 11 AA.
XX
AC AAW92674;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #20.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 9 /note= "D-form residue"
FT
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 19-20; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

Query Match
Best Local Similarity 66.2%; Score 47; DB 20; Length 11;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
   |||||:| |
Db 1 rpkpqgffalm 11

RESULT 133
AAW92675
ID AAW92675 standard; peptide; 11 AA.
XX
AC AAW92675;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P [Pro 9] or [D-Pro 9].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
```

```
XX AAW92675;
AC
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #21.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 9 /note= "D-form residue"
FT
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 19-20; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

Query Match
Best Local Similarity 66.2%; Score 47; DB 20; Length 11;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
   |||||:| |
Db 1 rpkpqgffalm 11

RESULT 134
AAW921935
ID AAR21935 standard; Protein; 11 AA.
XX
AC AAR21935;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P [Pro 9] or [D-Pro 9].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
```



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XX FH Key Location/Qualifiers
FT Modified-site 9 /note= "either L or D form"
FT
XX PN W09202248-A.
XX XX
XX PD 20-FEB-1992.
XX
XX PF 29-JUL-1991; 91WO-US05323.
XX XX
XX PR 27-JUL-1990; 90US-0559173.
XX XX
XX PA (CHIL-) CHILDRENS MED CENT.
XX PI Yankner BA;
XX XX
XX DR WPI; 1992-079804/10.
XX XX
XX PT Treatment of neuronal accumulation of beta-amyloid - using
XX PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX PS Claim 10; Page 21; 35pp; English.
XX
XX CC The peptide is the tachykinin agonist substance P with a
XX CC methionine residue substituted at position 9. The peptide was
XX CC synthesised by standard solid phase synthesis. Neuronal
XX CC accumulation of beta-amyloid may be treated by administration of
XX CC tachykinin agonists. The peptide can reduce the neurotoxic effects
XX CC of a beta-amyloid related polypeptide on cultured neurons. The
XX CC peptide and its analogues are useful for controlling diseases
XX CC characterised by beta amyloid accumulation in the brain such as
XX CC Alzheimer's disease and Down's syndrome.
XX CC See also AAR21932-75.
XX SQ Sequence 11 AA;
XX
XX Query Match 64.8%; Score 46; DB 13; Length 11;
XX Best Local Similarity 81.8%; Pred. No. 0.51;
XX Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 RPKPQQWFWM 11
XX DB 1 rpkpqgffplm 11
XX
XX RESULT 135
XX AAR21943
XX ID AAR21943 standard; Protein; 11 AA.
XX AC AAR21943;
XX XX
XX DT 25-JUN-1992 (first entry)
XX XX
XX DE Substance P [Met 7].
XX XX
XX KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX KW syndrome; hereditary cerebral haemorrhage.
XX XX
XX OS Synthetic.
XX XX
XX PN W09202248-A.
XX XX
XX PD 20-FEB-1992.
XX XX
XX PF 29-JUL-1991; 91WO-US05323.
XX XX
XX PR 27-JUL-1990; 90US-0559173.
XX XX
XX PA (CHIL-) CHILDRENS MED CENT.
XX XX
```

```
PI Yankner BA;
XX
XX DR WPI; 1992-079804/10.
XX XX
XX PT Treatment of neuronal accumulation of beta-amyloid - using
XX PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX XX
XX PS Claim 10; Page 21; 35pp; English.
XX XX
XX CC The peptide is the tachykinin agonist substance P with a
XX CC methionine residue substituted at position 7. The peptide was
XX CC synthesised by standard solid phase synthesis. Neuronal
XX CC accumulation of beta-amyloid may be treated by administration of
XX CC tachykinin agonists. The peptide can reduce the neurotoxic effects
XX CC of a beta-amyloid related polypeptide on cultured neurons. The
XX CC peptide and its analogues are useful for controlling diseases
XX CC characterised by beta amyloid accumulation in the brain such as
XX CC Alzheimer's disease and Down's syndrome.
XX CC See also AAR21932-75.
XX SQ Sequence 11 AA;
XX
XX Query Match 64.8%; Score 46; DB 13; Length 11;
XX Best Local Similarity 81.8%; Pred. No. 0.51;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 RPKPQQWFWM 11
XX DB 1 rpkpqgffplm 11
XX
XX RESULT 136
XX AAW13611
XX ID AAW13611 standard; peptide; 11 AA.
XX AC AAW13611;
XX XX
XX DT 06-JUL-1999 (first entry)
XX XX
XX DE Spantide II, a substance P antagonist.
XX XX
XX KW Substance P; antagonist; non-photosynthetic filamentous bacterium; pain;
XX KW sendide; CNS; central nervous system; respiration; allergy; inflammation;
XX KW gastrointestinal disorder; skin; fibrosis; collagen maturation; mucosa;
XX KW cardiovascular; vasospasm; immunological disorder; urinary tract;
XX KW irritation.
XX XX
XX OS Synthetic.
XX OS Vitreoscilla filiformis.
XX XX
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "Lys-Nic; D-form residue"
XX FT Modified-site 3 /note= "3-pyridyl-alanine"
XX FT Modified-site 5 /note= "dichlorophenylalanine; D-form residue"
XX FT Misc-difference 3 /note= "D-form residue"
XX FT Misc-difference 9 /note= "D-form residue"
XX FT Modified-site 11 /label= Nle
XX FT /note= "Nor-leucine; amidated C-terminus"
XX XX
XX PN EP761204-Al.
XX XX
XX PD 12-MAR-1997.
XX XX
XX PF 13-AUG-1996; 96EP-0401781.
XX XX
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PR 27-MAR-1996; 96FR-0003818.
 PR 07-SEP-1995; 95FR-0010485.
 PR 27-MAR-1996; 96FR-0003816.
 PA (OREA) L'OREAL SA.
 XX Aubert L, Breton L, De Lacharriere O, Leclaire J;
 PI Martin R;
 XX WPI; 1997-156643/15.
 DR
 XX Use of extracts of non-photosynthetic filamentous bacteria as
 PT substance P antagonists - in cosmetic and pharmaceutical compans.
 XX
 PS Claim 31; Page 7; 32pp; French.
 XX
 CC This peptide, designated spantide II, is a substance P antagonist
 CC isolated from extracts of non-photosynthetic filamentous bacteria,
 CC especially Vitreoscilla filiformis. The antagonists can be used in
 CC compositions for treating disorders associated with overproduction or
 CC excessive secretion of substance P, such as CNS disorders, respiratory
 CC disorders, allergies, inflammation, pain, gastrointestinal disorders,
 CC skin disorders, fibrosis, collagen maturation disorders, cardiovascular
 CC disorders, vasospasm, immunological disorders and/or disorders of the
 CC urinary tract; for treating sensitive skin; for preventing and/or
 CC combating skin and/or mucosal irritation.
 XX
 SQ Sequence 11 AA;

Query Match 64.8%; Score 46; DB 18; Length 11;
 Best Local Similarity 60.0%; Pred. No. 0.51;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQHFWL 10
 : | | | | |
 Db 1 kpxpxnwfwl 10

RESULT 137
 AAW92677
 ID AAW92677 standard; peptide; 11 AA.
 XX
 AC AAW92677;

30-APR-1999 (first entry)

Human tachykinin agonist beta-amyloid peptide fragment #23.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congoophilic angiopathy.
 XX

OS Homo sapiens.

XX US5876948-A.

XX 02-MAR-1999.

XX 27-JUL-1991; 91US-0737371.

XX 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Yankner BA;

XX WPI; 1999-189630/16.

XX Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX

PS Disclosure; Column 19-20; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congoophilic angiopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 SQ Sequence 11 AA;

Query Match 64.8%; Score 46; DB 20; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.51;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQHFWLM 11
 : | | | | | | | | | |
 Db 1 rpkpqffplm 11

RESULT 138
 AAW92678
 ID AAW92678 standard; peptide; 11 AA.
 XX
 AC AAW92678;

30-APR-1999 (first entry)

Human tachykinin agonist beta-amyloid peptide fragment #24.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congoophilic angiopathy.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 9 /note= "D-form residue"
 FT

XX US5876948-A.

XX 02-MAR-1999.

XX 27-JUL-1991; 91US-0737371.

XX 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Yankner BA;

XX WPI; 1999-189630/16.

XX Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX

PS Disclosure; Column 19-20; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congoophilic angiopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.

XX
SQ Sequence 11 AA;

Query Match 64.8%; Score 46; DB 20; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.51;
Matches 9; Conservative 1; Mismatches 0; Gaps 0;

QY 1 RPKPOQWFWM 11
|||||:| |
Db 1 rpqpqgfplm 11

RESULT 139

AAW92671
ID AAW92671 standard; peptide; 11 AA.

XX
AC AAW92671;

XX
DT 30-APR-1999 (first entry)

XX
DE Human tachykinin agonist beta-amyloid peptide fragment #17.

XX
DE Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.

XX
OS Homo sapiens.

XX
PN US5876948-A.

XX
PD 02-MAR-1999.

XX
PF 27-JUL-1991; 91US-0737371.

XX
PR 29-JUL-1991; 91US-0737371.

XX
PR 27-JUL-1990; 90US-0559173.

XX
PA (CHIL-) CHILDRENS MEDICAL CENT.

XX
PI Yankner BA;

XX
DR WPI; 1999-189630/16.

XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX
PS Disclosure; Column 17-18; 28pp; English.

XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodystrophy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

XX
SQ Sequence 11 AA;

Query Match 64.8%; Score 46; DB 20; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQWFWM 11
|||||:| |
Db 1 rpqpqgmfglm 11

RESULT 140

AAW91415

ID AAB91415 standard; Peptide; 11 AA.

XX
AC AAB91415;

XX
DT 22-JUN-2001 (first entry)

XX
DE Tachykinins peptide SEQ ID NO:591.

XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX
OS Homo sapiens.

XX
OS Synthetic.

XX
PN WO200069900-A2.

XX
PD 23-NOV-2000.

XX
PF 17-MAY-2000; 2000WO-US13576.

XX
PR 17-MAY-1999; 99US-0134406.

XX
PR 10-SEP-1999; 99US-0153406.

XX
PR 15-OCT-1999; 99US-0159783.

XX
PA (CONJ-) CONJUCHEM INC.

XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX
DR WPI; 2001-112059/12.

XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

XX
PS Disclosure; Page 393; 733pp; English.

XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX
SQ Sequence 11 AA;

Query Match 64.8%; Score 46; DB 22; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.51;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQWFWM 11
|||||:| |
Db 1 rpqpqgfplm 11

RESULT 141

AAW91429

ID AAB91429 standard; Peptide; 11 AA.

XX
AC AAB91429;

XX

DT 22-JUN-2001 (first entry)
XX Tachykinins peptide SEQ ID NO:605.
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200069900-A2.
PN
XX 23-NOV-2000.
PD
XX 17-MAY-2000; 2000WO-US13576.
PF
XX 17-MAY-1999; 99US-0134406.
PR
XX 10-SEP-1999; 99US-0153406.
PR
XX 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
PI
XX WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX Disclosure; Page 397; 733pp; English.
PS
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX Sequence 11 AA;
SQ
Query Match 64.8%; Score 46; DB 22; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.51;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPQOWFWLM 11
Db 1 rpkpqgffplm 11
RESULT 142
AAW50973
ID AAW50973 standard; peptide; 8 AA.
XX
XX AAW50973;
AC
XX 31-JUL-1998 (first entry)
DT
XX Substance P analogue residues 4-11, [D-Pro4,D-Trp7,9,10,Phe11].
DE
XX

KW Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
KW Substance P; cancer; inhibition; growth hormone releasing factor;
KW spantide.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 1 /note= "D-form residue"
FT
FT Misc-difference 4 /note= "D-form residue"
FT
FT Misc-difference 6 /note= "D-form residue"
FT
FT Misc-difference 7 /note= "D-form residue"
FT
FT Misc-difference 8 /note= "D-form residue"
FT
FT Modified-site /note= "C-terminal amide"
FT
XX EP835662-A2.
XX
XX 15-APR-1998.
PN
XX
XX 11-DEC-1996; 96EP-0309012.
PF
XX
XX 08-OCT-1996; 96US-0727679.
PR
XX 16-AUG-1996; 96IN-0001822.
PR
XX (NAIW-) NAT INST IMMUNOLOGY.
PA
XX Jaggi M, Mukherjee R;
XX
XX WPI; 1998-208959/19.
DR
XX
XX Composition containing analogues of vasoactive intestinal peptide,
PT somatostatin, bombesin and substance P, for treatment of tumours
PT and for inhibiting over-expression of these peptide(s)
XX
XX Disclosure; Page 13; 49pp; English.
XX
XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 AGCKNFDWKPTSGC (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.
XX
XX Sequence 8 AA;
SQ
Query Match 63.4%; Score 45; DB 19; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PQQWFW 9
Db 1 pqqwfw 6
RESULT 143
AAW50975
ID AAW50975 standard; peptide; 8 AA.
XX
XX AAW50975;
AC
XX

DT 31-JUL-1998 (first entry)
XX
DE Substance P analogue residues 4-11, [D-Pro4,D-Trp7,9,Nle11].
XX
XX Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
KW Substance P; cancer; inhibition; growth hormone releasing factor;
KW spantide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Misc-difference 4 /note= "D-form residue"
FT Misc-difference 6 /note= "D-form residue"
FT Misc-difference 8 /note= "D-form residue"
FT Modified-site /label= Nle
FT /note= "C-terminal amide"
XX
XX EP835662-A2.
PN
XX
XX 15-APR-1998.
PD
XX
XX 11-DEC-1996; 96EP-0309012.
PF
XX
XX 08-OCT-1996; 96US-0727679.
PR
XX 16-AUG-1996; 96IN-0001822.
PR
XX (NAIM-) NAT INST IMMUNOLOGY.
PA
XX
XX Jaggi M, Mukherjee R;
PI
XX
XX WPI; 1998-208959/19.
DR
XX
XX Composition containing analogues of vasoactive intestinal peptide,
PT somatostatin - bombesin and substance P, for treatment of tumours
PT and for inhibiting over-expression of these peptide(s)
XX
PS Disclosure; Page 13; 49pp; English.
XX
XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 AGCKNFFdWKPTNSdC (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.
XX
SQ Sequence 8 AA;

Query Match 63.4%; Score 45; DB 19; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQQWF 9
Db 1 pqqfw 6

RESULT 144
AAR21937
ID AAR21937 standard; Protein; 11 AA.

XX AAR21937;
AC
XX 25-JUN-1992 (first entry)
DT
XX Substance P or (7-11) [Norleucine 11].
DE
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
KW
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 11 /label= OTHER
FT /note= "OTHER - Nle"
FT
XX
XX WO9202248-A.
PN
XX
XX 20-FEB-1992.
PD
XX
XX 29-JUL-1991; 91WO-US05323.
PF
XX
XX 27-JUL-1990; 90US-0559173.
PR
XX (CHIL-) CHILDRENS MED CENT.
PA
XX Yankner BA;
PI
XX
XX WPI; 1992-079804/10.
DR
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 10; Page 21; 35pp; English.
XX
XX The peptide is the tachykinin agonist substance P with a Norleucine
CC residue substituted at position 11. The peptide was synthesised
CC by standard solid phase synthesis. An N-terminal deleted peptide
CC (7-11) with the same substitution was also synthesised. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptides can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
SQ Sequence 11 AA;

Query Match 63.4%; Score 45; DB 13; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.72;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
Db 1 rpkpqffgll 11

RESULT 145
AAR21951
ID AAR21951 standard; Peptide; 11 AA.
XX
XX AAR21951;
AC
XX
XX 25-JUN-1992 (first entry)
DT
XX
XX Substance P [Glu 3].
DE
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
KW

XX OS Synthetic.
XX PN WO9202248-A.
XX PD 20-FEB-1992.
XX PF 29-JUL-1991; 91WO-US05323.
XX PR 27-JUL-1990; 90US-0559173.
XX PA (CHIL-) CHILDRENS MED CENT.
XX PI Yankner BA;
XX DR WPI; 1992-079804/10.
XX PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX PS Claim 10; Page 21; 35pp; English.
XX CC The peptide is the tachykinin agonist substance P with a glutamic
CC acid residue substituted at position 5. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
XX CC See also AAR21932-75.
XX SQ Sequence 11 AA;

Query Match 63.4%; Score 45; DB 13; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.72;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
Db 1 rpkpqffgfm 11
|||||:|

RESULT 146
AAR28445
ID AAR28445 standard; peptide; 11 AA.
XX AC AAR28445;
XX DT 22-MAR-1993 (first entry)
XX DE Neurokinine 1 ligand #3.
XX KW NK1 receptor; tumour; malignant glioma; pheochromocytoma;
XX KW paraganglia; small cell lung cancer; nerve regeneration; lymphoma;
XX KW granuloma; Crohn's disease.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 11 /note= "amidated"
FT
XX PN WO9218536-A.
XX PD 29-OCT-1992.
XX PF 22-APR-1992; 92WO-US03307.
XX PR 22-APR-1991; 91EP-0200955.

XX PA (MLCW) MALLINCKRODT MEDICAL INC.
XX PI Bakker WH, Hagen PM, Krenning EP, Lamberts SWJ, Visser TJ;
XX DR WPI; 1992-382047/46.
XX PF Detection and localisation of tissues with neurokinine-1 receptors
PT - for detecting and treating tumours having neurokinine-1
PT receptors e.g. malignant glioma, small cell lung cancer etc.
XX PS Disclosure; Page 4; 22pp; English.
XX CC This peptide or its Tyr0 deriv. is a preferred peptide having a
CC selective affinity to neurokinine-1 receptors which (when
CC labelled with a radioactive isotope) can be used in imaging methods.
CC A generic formula for preferred peptides is AAR28441. Such peptides
CC are thus useful in diagnosis and treatment of conditions that are
CC related to NK1 receptors and in visualising NK1 receptors on certain
CC tissues. See AAR28442-R28446.
XX SQ Sequence 11 AA;

Query Match 63.4%; Score 45; DB 13; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.72;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
Db 1 rpkpqffgfm 11
|||||:|

RESULT 147
AAR42649
ID AAR42649 standard; peptide; 11 AA.
XX AC AAR42649;
XX DT 19-APR-1994 (first entry)
XX DE Neurokinin 1 receptor affinity-contg. peptide.
XX KW Neurokinin 1; somatostatin; receptor; cytokine; growth factor;
XX KW hormone; intra-operative; tumour; low energy gamma photon;
XX KW radionuclide.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 11 /note= "the C-terminal is amidated"
FT
XX PN WO9318797-A.
XX PD 30-SEP-1993.
XX PF 24-MAR-1993; 93WO-US02772.
XX PR 25-MAR-1992; 92EP-0200848.
XX PA (MLCW) MALLINCKRODT MEDICAL INC.
XX PI Doedens BJ, Ensing GJ, Panek KJ;
XX DR WPI; 1993-320461/40.
XX PT Intra-operatively detecting and locating tumour tissues - using
PT specific peptide(s) labelled with low energy gamma photon
PT emitting radionuclide
XX PS Disclosure; Page 5; 31pp; English.
XX

CC The method of intraoperatively detecting and locating tumoral
CC tissues makes use of peptides having selective neurokinin 1
CC receptor affinity (AAR42644: generic formula; AAR42646-R42650:
CC specific examples), peptides having selective somatostatin
CC receptor affinity (AAR42645: generic formula; AAR42651-R42660:
CC specific examples), and peptides selected from cytokines,
CC growth factors and hormones.

XX Sequence 11 AA;

Query Match 63.4%; Score 45; DB 14; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.72;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPQGFWM 11
|||:|:|
DB 1 rpkpqgfyglm 11

RESULT 148

AAW09003
ID AAW09003 standard; peptide; 11 AA.

XX
AC AAW09003;

XX
DT 03-MAR-1997 (first entry)

XX
DE Substance P analogue, acts as substance P antagonist.

XX
KW Analogue; substance P; spantide; non-peptide bond;
KW competitive inhibitor; receptor; neurogenic inflammation;
KW rheumatoid arthritis; ulcerative colitis; eczema; Crohn's disease;
KW anti-proliferative agent; small cell lung carcinoma; fibroblast.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers

FT Modified-site 6..7
/label= Gln-psi[(CH2-NH)-Phe
/note= "Opt. non-peptide linkage"

FT Modified-site 7..8
/label= Phe-psi[(CH2-NH)-Phe
/note= "Opt. non-peptide linkage"

FT Modified-site 8..9
/label= Phe-psi[(CH2-NH)-Gly
/note= "Opt. non-peptide linkage"

FT Modified-site 9..10
/label= Gly-psi[(CH2-NH)-Leu
/note= "Opt. non-peptide linkage"

FT Modified-site 10..11
/label= Leu-psi[(CH2-NH)-Leu
/note= "Position of claimed non-peptide linkage"

FT Modified-site 11
/note= "Amidated C-terminal"

XX
PN US410019-A.

XX
PD 25-APR-1995.

XX
PF 24-SEP-1987; 87US-0100571.

XX
PR 30-MAR-1992; 92US-0860675.

XX
PR 24-SEP-1987; 87US-0100571.

XX
PR 25-MAR-1988; 88US-0173311.

XX
PR 08-JUN-1988; 88US-0204171.

XX
PR 16-JUN-1988; 88US-0207759.

XX
PR 23-SEP-1988; 88US-0248771.

XX
PR 14-OCT-1988; 88US-0257998.

XX
PR 09-DEC-1988; 88US-028328.

XX
PR 02-MAR-1989; 89US-0317941.

XX
PR 16-AUG-1989; 89US-0394727.

PA (TULA) TULANE EDUCATIONAL FUND.

XX
PI Coy DH, Moreau J;

XX
DR WPI; 1995-169633/22.

XX
PT Novel linear peptide substance P analogues - useful as substance P
antagonists, for treating neurogenic inflammation

XX
PS Claim 3; Column 19; 16pp; English.

XX
CC The sequences given in AAW09003-04 represent analogues of substance P
and spantide, respectively. These analogues comprise a non-peptide
bond between an amino acid residue of the active site, which occurs
in the C-terminal half of the peptide, and an adjacent amino acid
residue. They act as competitive inhibitors of the naturally
occurring peptide by binding to its receptor. These peptides may be
used in the treatment of diseases involving neurogenic inflammation,
e.g. rheumatoid arthritis, ulcerative colitis, eczema and Crohn's
disease. They are also useful as anti-proliferative agents, in
the treatment of small cell lung carcinoma or disorders involving the
proliferation of fibroblasts.

XX
SQ Sequence 11 AA;

Query Match 63.4%; Score 45; DB 16; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.72;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPQGFWM 11
|||:|:|
DB 1 rpkpqgfyglm 11

RESULT 149

AAW33181
ID AAW33181 standard; peptide; 11 AA.

XX
AC AAW33181;

XX
DT 29-JAN-1998 (first entry)

XX
DE Mono-DTPA-Lys1 Substance P.

XX
KW Substance P; radiolabel; diagnostic imaging; therapy;
mono-DTPA-Lys1.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers

FT Modified-site 1
/note= "DTPA-Lys"

FT Modified-site 11
/note= "amidated"

XX
PN WO9640292-A1.

XX
PD 19-DEC-1996.

XX
PF 07-JUN-1996; 96WO-US09706.

XX
PR 07-JUN-1995; 95US-0480372.

XX
PA (MLCW) MALLINCKRODT MEDICAL INC.

XX
PI Srinivasan A;

XX
DR WPI; 1997-087027/08.

XX
PT Prepn. of pure radio-labelled peptide, e.g. for diagnostic imaging -
by combining protected poly(amino:carboxylate) ligand with peptide
and forming complex with radionuclide

XX PS Example 4; Page 12; 20pp; English.

CC Preparing a radiolabelled peptide composition, comprises combining

CC a triamine or diamine chelating agent with a peptide, e.g. the

CC present peptide, in a solid phase peptide synthesiser, and

CC complexing a radionuclide with the chelate-peptide conjugate.

CC Radiolabelled peptides or peptidomimetics can be used as diagnostic

CC imaging agents, or in therapeutic applications, e.g. iodine(111)

CC labelled pentatreotide can be used for somatostatin receptor

CC imaging of neuroendocrine tumours. The radiolabelled products are

CC obtained efficiently and inexpensively in high purity. The

CC protected polyaminocarboxylate ligands can be added to the peptide

CC by standard solution or solid phase peptide synthesis and

CC deprotected with conventional reagents to give only the

CC mono-addition product, free of di-addition product impurities. The

CC deprotected product can be labelled with medically useful

CC radionuclides, e.g. lanthanides or actinides, at any desired

CC location. Pre-derivatisation of individual amino acids is not

CC required.

XX SQ Sequence 11 AA;

Query Match 63.4%; Score 45; DB 18; Length 11;

Best Local Similarity 72.7%; Pred. No. 0.72;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11

Db 1 kpkpqgffgl 11

RESULT 150

AAW79775

ID AAW79775 standard; peptide; 11 AA.

XX

AC AAW79775;

XX

DT 07-JAN-1999 (first entry)

XX

DE Substance P.

XX

KW Tachykinin; neurokinin; NK1; receptor; antagonist; cystic fibrosis;

KW Substance P.

XX

OS Mammalia.

XX

PN US5830854-A.

XX

PD 03-NOV-1998.

XX

PF 14-DEC-1993; 93US-0166437.

XX

PR 14-DEC-1992; 92GB-0026056.

PR 14-DEC-1992; 92GB-0026047.

XX

PA (MERI) MERCK SHARP & DOHME LTD.

XX

FI Hargreaves RJ;

XX

WPI; 1998-609287/51.

XX

PT Treatment of cystic fibrosis - comprises administration of

PT tachykinin receptor antagonist which is a neurokinin-1 receptor

PT antagonist

XX

PS Disclosure; Column 1; 12pp; English.

XX

CC The invention relates to the new use of tachykinin receptor antagonists

CC (particularly NK1 receptor antagonists) for the treatment of cystic

CC fibrosis. The present sequence is that of Substance P, one of three

CC known mammalian tachykinins.

XX SQ Sequence 11 AA;

Query Match 63.4%; Score 45; DB 19; Length 11;

Best Local Similarity 72.7%; Pred. No. 0.72;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11

Db 1 rpkpqgffgl 11

RESULT 151

AAW99689

ID AAW99689 standard; peptide; 11 AA.

XX

AC AAW99689;

XX

DT 03-JUN-1999 (first entry)

XX

DE Substance P analogue #6.

XX

KW Substance P receptor antagonist; analgesic; inhibitor; NMDA blocker;

KW nontoxic N-methyl-D-aspartate receptor antagonist; muscular pain;

KW musculoskeletal pain; chronic pain; neuropathic pain; migraine.

XX

OS Synthetic.

XX

FH Key

FT Modified-site 10..11

FT /note= "Leu-psi(CH2-NH)-Leu"

FT Modified-site 11

FT /note= "amidated"

XX

PN WO9907413-A1.

XX

PD 18-FEB-1999.

XX

PF 26-MAY-1998; 98WO-US10707.

XX

PR 11-AUG-1997; 97US-0055233.

XX

PA (ALGO-) ALGOS PHARM CORP.

XX

PI Caruso FS;

XX

WPI; 1999-167216/14.

XX

PT New analgesic composition comprises - a substance P receptor

PT antagonist with a substance P receptor antagonist potentiator, used

PT for the treatment of pain

XX

PS Claim 3; Page 29; 54pp; English.

XX

CC A method has been developed for treating pain with: (a) a substance P

CC receptor antagonist; and (b) a substance P receptor antagonist

CC potentiator, i.e. N-methyl-D-aspartate (NMDA) receptor antagonist or

CC substance that blocks at least 1 major intracellular consequence of

CC NMDA receptor activation. The method can be used for treating muscular,

CC musculoskeletal, chronic or neuropathic pain, or migraine. The present

CC sequence represents a substance P analogue for use in the method.

XX

SQ Sequence 11 AA;

Query Match 63.4%; Score 45; DB 20; Length 11;

Best Local Similarity 72.7%; Pred. No. 0.72;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11

Db 1 rpkpqgffgl 11

RESULT 152

AAW92679
ID AAW92679 standard; peptide; 11 AA.XX
AC AAW92679;XX
-DT 30-APR-1999 (first entry)XX
DE Human tachykinin agonist beta-amyloid peptide fragment #25.XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.XX
OS Homo sapiens.XX
FN US5876948-A.XX
PD 02-MAR-1999.XX
PF 27-JUL-1991; 91US-0737371.XX
PR 29-JUL-1991; 91US-0737371.XX
PR 27-JUL-1990; 90US-0559173.XX
PA (CHIL-) CHILDRENS MEDICAL CENT.XX
PI Yankner BA;XX
DR WPI; 1999-189630/16.XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cellsXX
PS Disclosure; Column 21-22; 28pp; English.XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage,
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.XX
SQ Sequence 11 AA;

Query Match 63.4%; Score 45; DB 20; Length 11;

Best Local Similarity 72.7%; Pred. No. 0.72;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11

DB 1 RPKPQQWFWM 11

RESULT 153

AAW91402
ID AAW91402 standard; Peptide; 11 AA.XX
AC AAW91402;XX
-DT 22-JUN-2001 (first entry)XX
DE Tachykinins peptide SEQ ID NO:578.XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimide; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
OS Synthetic.
XX WO2000069900-A2.
XX 23-NOV-2000.
XX 17-MAY-2000; 2000WO-US13576.
XX 17-MAY-1999; 99US-0134406.
XX 10-SEP-1999; 99US-0153406.
XX 15-OCT-1999; 99US-0159783.
XX (CONJ-) CONJUCHEM INC.
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX WPI; 2001-112059/12.
XX Modifying and attaching therapeutic peptides to albumin prevents
XX peptidase degradation, useful for increasing length of in vivo activity
XX
XX Disclosure; Page 389; 733pp; English.
XX The present invention describes a modified therapeutic peptide (I)
XX comprising a therapeutically active amino acid region (III) and a
XX reactive group (II) (e.g. succinimide and maleimido groups) attached to
XX a less therapeutically active amino acid region (IV), which covalently
XX bonds with amino/hydroxyl/thiol groups on blood components to form a
XX peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX factors and neurotransmitters, to protect them from peptidase activity
XX in vivo for the treatment of various disorders. Endogenous therapeutic
XX peptides are not suitable as drug candidates as they require frequent
XX administration due to rapid degradation by peptidases in the body.
XX Modifying and attaching therapeutic peptides to albumin prevents or
XX reduces the action of peptidases to increase length of activity (half
XX life) and specificity as bonding to large molecules decreases
XX intracellular uptake and interference with physiological processes.
XX AAB90829 to AAB92441 represent peptides which can be used in the
XX exemplification of the present invention.
XX Sequence 11 AA;

Query Match 63.4%; Score 45; DB 22; Length 11;

Best Local Similarity 72.7%; Pred. No. 0.72;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11

DB 1 RPKPQQWFWM 11

RESULT 154

AAB91409

ID AAB91409 standard; Peptide; 11 AA.

XX
AC AAB91409;XX
-DT 22-JUN-2001 (first entry)XX
DE Tachykinins peptide SEQ ID NO:585.XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimide; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX Homo sapiens.
OS Synthetic.

PN WO200069900-A2.
XX
XX
PD 23-NOV-2000.
XX PF 17-MAY-2000; 2000WO-US13576.
XX
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibautau K;
XX WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX Disclosure; Page 391; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX Sequence 11 AA;
SQ

Query Match 63.4%; Score 45; DB 22; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.72;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPQQWFWM 11
Db 1 rpkpqgfyglm 11
|||||::||
|::|::|

RESULT 155
AAY37217
ID AAY37217 standard; Protein; 455 AA.
XX
XX AAY37217;
XX
XX 07-OCT-1999 (first entry)
DT
XX
XX Amino acid sequence of a Chlamydia trachomatis protein.
DE
XX
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
KW Bartholinitis; pneumonia; venereal lymphogranulomatosis.
XX
XX Chlamydia trachomatis.
OS
XX WO9928475-A2.
PN
XX 10-JUN-1999.
PD
XX

PF 27-NOV-1998; 98WO-IB01939.
XX
XX 04-NOV-1998; 98US-0107077.
PR 28-NOV-1997; 97FR-0015041.
PR 17-DEC-1997; 97FR-0016034.
XX
XX (GEST) GENSET.
XX
XX Griffais R;
XX
XX WPI; 1999-371125/31.
XX
XX Genome sequence of Chlamydia trachomatis
PT
XX Disclosure; Page 981-982; 1755pp; English.
XX
XX AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome
CC of Chlamydia trachomatis (see A201425). The polypeptides can be used as
CC vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
CC can also be used to control growth of the microorganism. Chlamydia
CC trachomatis is responsible for a large number of diseases, e.g. eye
CC diseases such as conventional trachoma, nonendemic trachoma,
CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis;
CC perihhepatitis, Bartholinitis; pneumopathy in breast feeding infants;
CC and venereal lymphogranulomatosis. The polypeptides of the invention
CC may be of use in treating these diseases.
XX
XX Sequence 455 AA;
SQ

Query Match 63.4%; Score 45; DB 20; Length 455;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 KPOQWFWM 10
Db 303 kpeqwiwl 310
||::|||
|::|::|

RESULT 156
AAY92927
ID AAY92927 standard; peptide; 11 AA.
XX
XX AAY92927;
AC
XX 25-OCT-2000 (first entry)
DT
XX
XX Spantide II peptide.
DE
XX
XX Antiinflammatory; antipruritic; hypertensive; antidiarrhetic; analgesic;
KW bradykinin antagonist; plant extract; Ocimum; bradykinin; antagonist;
KW inflammation mediator; substance P; calcitonin gene related peptide;
KW nitric oxide synthase; cytokine; histamine; tumour necrosis factor alpha;
KW sendide; cosmetic; sensitive skin; cutaneous irritation; erythema; pain;
KW dysesthesia; pruritis; vasodilation; hypotension; inflammation;
KW diarrhoea; allergic rhinitis; smooth muscle contraction.
XX
XX Unidentified.
OS
XX

Key Location/Qualifiers
FH Modified-site 1 /note= "nicotiny-Lys; D-form residue"
FT Modified-site 3 /note= "3-pyridylalanine"
FT Modified-site 5 /note= "di-chloro-Phe; D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 11 /label= Nle
FT

FT XX /note= "nor-leucine; C-terminally amidated"

PN WO200027351-A1.

XX 18-MAY-2000.

PD 08-OCT-1999; 99WO-FR02728.

XX 10-NOV-1998; 98FR-0014157.

XX (OREA) L'OREAL SA.

XX Breton L, Martin R;

XX WPI; 2000-387333/33.

XX Cosmetic and pharmaceutical use of an extract of Ocimum in compositions for treating bradykinin synthesis and liberation disorders, especially sensitive skins -

FT PT Disclosure; Page 16; 44pp; French.

XX The invention relates to the use of an extract of a plant of the genus Ocimum in compositions for the treatment of disorders of bradykinin synthesis and/or release. The invention also relates to compositions comprising an extract of Ocimum and at least one compound that decreases the synthesis, release or activity of an inflammation mediator such as antagonists of substance P, and/or calcitonin gene related peptide (CGRP), inhibitors of NO synthase, cytokine, histamine or tumour necrosis factor alpha (TNFa) antagonists. This sequence represents the peptide spantide II which is a substance P antagonist and can be used in the composition of the invention. The extract has cosmetic and pharmaceutical uses. It may be used on sensitive skins to treat or prevent cutaneous irritation, scurf, erythemas, feelings of heat, dysesthesia, and pruritis of the skin and mucous membranes. It may further be used to treat vasodilation, increased vascular permeability, hypotension, pain, proliferation of conjunctive tissue, inflammation, diarrhoea, allergic rhinitis, and smooth muscle contractions of the digestive, respiratory, or uterine tracts.

XX SQ Sequence 11 AA;

Query Match 62.0%; Score 44; DB 21; Length 11;

Best Local Similarity 60.0%; Pred. No. 1;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKQQQFWL 10

:| | | | |

Db 1 kxpfnfwl 10

RESULT 157

AAP30468

ID AAP30468 standard; Protein; 7 AA.

XX AAP30468;

XX 31-MAY-1992 (first entry)

XX Sequence of polypeptide deriv. with antagonistic properties against substance P.

XX Substance P antagonist; chronic pain therapy; high blood pressure; hypertension; hypotensive agent.

XX Key Location/Qualifiers

FT Modified-site 1 /label= Boc-Arg

FT Modified-site 3 /label= D-Trp

FT Modified-site 5 /label= D-Trp

FT

FT Modified-site 7 /label= Met-NH2

FT

PN DE3205991-A.

XX 01-SEP-1983.

PD 16-FEB-1983; 83DE-3467187.

XX 19-FEB-1982; 82DE-3205991.

PR (FERR-) FERRING ARZNEIMITTE.

XX Horig J, Schultheiss H;

PI WPI; 1983-753766/36.

DR Polypeptide derivs. contg. naturally occurring amino acids - antagonists against substance P and for treatment of pain and high blood pressure, including corneal inflammation

FT PT Example; Page 14; 26pp; German.

XX The peptides of the invention can be used to treat chronic pain conditions and high blood pressure, including e.g. chronic inflammations of the cornea caused by various circumstances, e.g. lengthy exposure to UV light, IR-rays or chemicals.

XX SQ Sequence 7 AA;

Query Match 60.6%; Score 43; DB 4; Length 7;

Best Local Similarity 85.7%; Pred. No. 4.3e+05;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QQQFWLM 11

:| | | | |

Db 1 rqwfwlm 7

RESULT 158

AAP50633

ID AAP50633 standard; Peptide; 10 AA.

XX AAP50633;

AC 09-MAR-1992 (first entry)

XX Substance P-like peptide, P2-11.

DE Hair tonic; growth; regeneration.

XX Synthetic.

XX JP60202807-A.

PN 14-OCT-1985.

PD 28-MAR-1984; 84JP-0058390.

PF 28-MAR-1984; 84JP-0058390.

XX (MEIJ) MEIJI SEIKA KAISHA.

XX WPI; 1985-293619/47.

DR Hair tonic compsn. - comprises peptide contg. pyroglutamic acid or other aminoacid(s) residue

PT Disclosure; Page 2; 3pp; Japanese.

XX The C-terminal residues 1-4 may be absent (P6-11, P5-11, P4-11 and P3-11 respectively). The C-terminal is amidated. Substance P

CC (H-RPKPEFFGLM-NH2) or these peptides derived from it can be used in
 CC aq. soln. or suspension to promote hair growth and regeneration.
 CC See also AAP50632 and AAP50634.

XX Sequence 10 AA;

Query Match 60.6%; Score 43; DB 6; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1.3;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPQQWFWM 11
 |||||:| ||
 Db 1 pkpqffglm 10

RESULT 159

AAR21933
 ID AAR21933 standard; Protein; 10 AA.

XX AC AAR21933;

XX DT 25-JUN-1992 (first entry)

XX DE Substance P (2-11) fragment.

XX KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.

XX OS Synthetic.

XX PN WO9202248-A.

XX PD 20-FEB-1992.

XX PF 29-JUL-1991; 91WO-0505323.

XX PR 27-JUL-1990; 90US-0559173.

XX PS (CHIL-) CHILDRENS MED CENT.

XX PI Yankner BA;

XX DR WPI; 1992-079804/10.

XX PT Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX PS Claim 9; Page 21; 35pp; English.

XX CC The peptide is a tachykinin agonist consisting of residues 2-11 of
 CC substance P. The peptide was synthesised by standard solid phase
 CC synthesis. Analogues of the peptide, with N-terminal deletions down
 CC to substance P (7-11) were also synthesised. Neuronal accumulation of
 CC beta-amyloid may be treated by administration of these tachykinin
 CC agonists. The peptides reduce the neurotoxic effects of a beta-
 CC amyloid related polypeptide on cultured neurons. The peptide and
 CC its analogues are useful for controlling diseases characterised by
 CC beta amyloid accumulation in the brain such as Alzheimer's disease
 CC and Down's syndrome.
 CC See also AAR21932-75.

XX Sequence 10 AA;

Query Match 60.6%; Score 43; DB 13; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1.3;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPQQWFWM 11
 |||||:| ||
 Db 1 pkpqffglm 10

RESULT 160

AAW92663

ID AAW92663 standard; peptide; 10 AA.

XX AC AAW92663;

XX DT 30-APR-1999 (first entry)

XX DE Human tachykinin agonist beta-amyloid peptide fragment #9.

XX KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenital angiodysplasia.

XX OS Homo sapiens.

XX PN US5876948-A.

XX PD 02-MAR-1999.

XX PF 27-JUL-1991; 91US-0737371.

XX PR 29-JUL-1991; 91US-0737371.

XX PR 27-JUL-1990; 90US-0559173.

XX PA (CHIL-) CHILDRENS MEDICAL CENT.

XX PI Yankner BA;

XX DR WPI; 1999-189630/16.

XX PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX PS Disclosure; Column 13-14; 28pp; English.

XX CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenital angiodysplasia with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.

XX Sequence 10 AA;

Query Match 60.6%; Score 43; DB 20; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1.3;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPQQWFWM 11
 |||||:| ||
 Db 1 pkpqffglm 10

RESULT 161

AAB91423

ID AAB91423 standard; Peptide; 10 AA.

XX AC AAB91423;

XX DT 22-JUN-2001 (first entry)

XX DE Tachykinins peptide SEQ ID NO:599.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimide; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
OS Synthetic.
XX WO200069900-A2.
XX 23-NOV-2000.
XX 17-MAY-2000; 2000WO-US13576.
XX 17-MAY-1999; 99US-0134406.
XX 10-SEP-1999; 99US-0153406.
XX 15-OCT-1999; 99US-0159783.
XX (CONJ-) CONJUCHEM INC.
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX WPI; 2001-112059/12.
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX Disclosure; Page 395; 733pp; English.
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX Sequence 10 AA;
SQ
Query Match 60.6%; Score 43; DB 22; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPQQWFNL 10
Db 1 rpkpqffgl 10
RESULT 162
AAB91427
ID AAB91427 standard; Peptide; 10 AA.
XX
XX AAB91427;
XX 22-JUN-2001 (first entry)
XX Tachykinins peptide SEQ ID NO:603.
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX Homo sapiens.
OS Synthetic.
XX

PN WO200069900-A2.
XX 23-NOV-2000.
XX 17-MAY-2000; 2000WO-US13576.
XX 17-MAY-1999; 99US-0134406.
XX 10-SEP-1999; 99US-0153406.
XX 15-OCT-1999; 99US-0159783.
XX (CONJ-) CONJUCHEM INC.
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX WPI; 2001-112059/12.
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX Disclosure; Page 396; 733pp; English.
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX Sequence 10 AA;
SQ
Query Match 60.6%; Score 43; DB 22; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPQQWFNL 10
Db 1 rpkpqffgl 10
RESULT 163
AAB91445
ID AAB91445 standard; Peptide; 10 AA.
XX
XX AAB91445;
XX 22-JUN-2001 (first entry)
XX Tachykinins peptide SEQ ID NO:621.
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX Homo sapiens.
OS Synthetic.
XX WO200069900-A2.
XX 23-NOV-2000.
XX

PF 17-MAY-2000; 2000WO-US13576.
XX
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX (CONJ-) CONJUCHEM INC.
PA
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
PI WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX
PS Disclosure; Page 402; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX Sequence 10 AA;
SQ

Query Match 60.6%; Score 43; DB 22; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPQQWFWM 11
Db 1 pkpqffglm 10

RESULT 164
AAR21945
ID AAR21945 standard; Protein; 11 AA.
XX
XX AAR21945;
XX
XX 25-JUN-1992 (first entry)
XX
XX Substance P [Pro 1].
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
XX Synthetic.
XX
XX WO9202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991; 91WO-US05323.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX

PI Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 10; Page 21; 35pp; English.
XX
XX The peptide is the tachykinin agonist substance P with a Proline
CC residue substituted at position 1. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
XX Sequence 11 AA;
SQ

Query Match 60.6%; Score 43; DB 13; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPQQWFWM 11
Db 2 pkpqffglm 11

RESULT 165
AAR21936
ID AAR21936 standard; Protein; 11 AA.
XX
XX AAR21936;
XX
XX 25-JUN-1992 (first entry)
XX
XX Substance P or (7-11) [Ethionine 11].
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 11
FT /label= OTHER
FT /note= "OTHER = Ethionine"
XX
XX WO9202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991; 91WO-US05323.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 10; Page 21; 35pp; English.
XX

CC The peptide is the tachykinin agonist substance P with an Ethionine
 CC residue substituted at position 11. The peptide was synthesised
 CC by standard solid phase synthesis. An N-terminal deleted peptide
 CC (7-11) with the same substitution was also synthesised. Neuronal
 CC accumulation of beta-amyloid may be treated by administration of
 CC tachykinin agonists. The peptides can reduce the neurotoxic effects
 CC of a beta-amyloid related polypeptide on cultured neurons. The
 CC peptide and its analogues are useful for controlling diseases
 CC characterised by beta amyloid accumulation in the brain such as
 CC Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.
 XX Sequence 11 AA;
 SQ

Query Match 60.6%; Score 43; DB 13; Length 11;
 Best Local Similarity 80.0%; Pred. No. 1.4;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWL 10
 |||||:|
 Db 1 rpkpqffgl 10

RESULT 166
 AAR21941
 ID AAR21941 standard; Protein; 11 AA.
 XX

AC AAR21941;

XX 25-JUN-1992 (first entry)

XX Substance P [pGLU 1].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.
 XX

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /label= OTHER
 FT /note= "OTHER = pyro Glu"

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.
 XX

PS Claim 10; Page 21; 35pp; English.

XX The peptide is the tachykinin agonist substance P with a pyro
 CC Glutamic acid residue substituted at position 1. The peptide was
 CC synthesised by standard solid phase synthesis. Neuronal
 CC accumulation of beta-amyloid may be treated by administration of
 CC tachykinin agonists. The peptide can reduce the neurotoxic effects
 CC of a beta-amyloid related polypeptide on cultured neurons. The
 CC peptide and its analogues are useful for controlling diseases
 CC characterised by beta amyloid accumulation in the brain such as
 CC Alzheimer's disease and Down's syndrome.

CC See also AAR21932-75.
 XX Sequence 11 AA;
 SQ

Query Match 60.6%; Score 43; DB 13; Length 11;
 Best Local Similarity 80.0%; Pred. No. 1.4;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPQQWFWL 11
 |||||:|
 Db 2 pkpqffgl 11

RESULT 167

AAR21944

ID AAR21944 standard; Protein; 11 AA.

XX AAR21944;

XX 25-JUN-1992 (first entry)

XX Substance P [Pro 11].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.
 XX

OS Synthetic.

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.
 XX

PS Claim 10; Page 21; 35pp; English.

XX The peptide is the tachykinin agonist substance P with a Proline
 CC residue substituted at position 11. The peptide was
 CC synthesised by standard solid phase synthesis. Neuronal
 CC accumulation of beta-amyloid may be treated by administration of
 CC tachykinin agonists. The peptide can reduce the neurotoxic effects
 CC of a beta-amyloid related polypeptide on cultured neurons. The
 CC peptide and its analogues are useful for controlling diseases
 CC characterised by beta amyloid accumulation in the brain such as
 CC Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.

XX Sequence 11 AA;
 SQ

Query Match 60.6%; Score 43; DB 13; Length 11;
 Best Local Similarity 80.0%; Pred. No. 1.4;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWL 10
 |||||:|
 Db 1 rpkpqffgl 10

RESULT 168

```
AAW92709
ID AAW92709 standard; peptide; 11 AA.
AC AAW92709;
XX
XX 30-APR-1999 (first entry)
DT
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #55.
DE
XX
XX Tachykinin agonist; beta-amyloid; inhibition: neurotoxin; treatment;
KW
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 9
FT /label= Megly
FT /note= "N-methyl-glycine (sarcosine)"
FT
FT Modified-site 11
FT /note= "Residue is Met(O2)"
FT
XX
XX US5876948-A.
PN
XX
XX 02-MAR-1999.
PD
XX
XX 27-JUL-1991; 91US-0737371.
PF
XX
XX 29-JUL-1991; 91US-0737371.
PR
XX 27-JUL-1990; 90US-0559173.
PR
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX PA
XX
XX PI Yankner BA;
XX
XX WPI; 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
PT
XX
XX Disclosure; Column 35-36; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
XX Sequence 11 AA;
SQ
Query Match 60.6%; Score 43; DB 20; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPQQWFWL 10
DB 1 rpkipqffgl 10
RESULT 169
AAW92717
ID AAW92717 standard; peptide; 11 AA.
XX
XX AAW92717;
AC
XX
XX 30-APR-1999 (first entry)
DT
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #63.
DE
XX
XX Tachykinin agonist; beta-amyloid; inhibition: neurotoxin; treatment;
KW
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX
XX Homo sapiens.
OS
XX
XX US5876948-A.
PN
XX
XX 02-MAR-1999.
PD
XX
XX 27-JUL-1991; 91US-0737371.
PF
XX
XX 29-JUL-1991; 91US-0737371.
PR
XX 27-JUL-1990; 90US-0559173.
PR
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX PA
XX
XX PI Yankner BA;
XX
XX WPI; 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
PT
XX
XX Disclosure; Column 37-38; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
XX Sequence 11 AA;
SQ
Query Match 60.6%; Score 43; DB 20; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPQQWFWL 10
DB 1 rpkipqffgl 10
RESULT 170
AAW92718
ID AAW92718 standard; peptide; 11 AA.
XX
XX AAW92718;
AC
XX
XX 30-APR-1999 (first entry)
DT
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #64.
DE
XX
XX Tachykinin agonist; beta-amyloid; inhibition: neurotoxin; treatment;
KW
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX
XX Homo sapiens.
OS
XX
XX US5876948-A.
PN
XX
XX 02-MAR-1999.
PD
XX
XX 27-JUL-1991; 91US-0737371.
PF
XX
XX 29-JUL-1991; 91US-0737371.
PR
XX 27-JUL-1990; 90US-0559173.
PR
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX PA
XX
XX PI Yankner BA;
XX
XX WPI; 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
PT
XX
XX Disclosure; Column 37-38; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
XX Sequence 11 AA;
SQ
Query Match 60.6%; Score 43; DB 20; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPQQWFWL 10
DB 1 rpkipqffgl 10
RESULT 170
AAW92718
ID AAW92718 standard; peptide; 11 AA.
XX
XX AAW92718;
AC
XX
XX 30-APR-1999 (first entry)
DT
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #64.
DE
XX
XX Tachykinin agonist; beta-amyloid; inhibition: neurotoxin; treatment;
KW
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX
XX Homo sapiens.
OS
XX
XX US5876948-A.
PN
XX
XX 02-MAR-1999.
PD
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XX PF 27-JUL-1991; 91US-0737371.
XX PR 29-JUL-1991; 91US-0737371.
XX PR 27-JUL-1990; 90US-0559173.
XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX PI Yankner BA;
XX DR WPI; 1999-189630/16.
XX PT Screening for neurotoxin inhibitors - by testing compounds for their
XX PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX PS Disclosure; Column 37-38; 28pp; English.
XX CC This invention describes a method for screening compounds for inhibiting
XX CC a neurotoxin. The method involves incubating tachykinin agonists with
XX CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
XX CC used for identifying compounds for treating diseases characterised by an
XX CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
XX CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
XX CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
XX CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX CC beta-amyloid peptide fragments.
XX SQ Sequence 11 AA;

Query Match 60.6%; Score 43; DB 20; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RPKPQQWFWL 10
Db 1 rpkpqffgl 10

RESULT 171
AAW92667
ID AAW92667 standard; peptide; 11 AA.
XX AC AAW92667;
XX DT 30-APR-1999 (first entry)
XX DE Human tachykinin agonist beta-amyloid peptide fragment #13.
XX KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Modified-site 11
XX FT /note= "Residue is ethionine"
XX PN US5876948-A.
XX PD 02-MAR-1999.
XX PF 27-JUL-1991; 91US-0737371.
XX PR 29-JUL-1991; 91US-0737371.
XX PR 27-JUL-1990; 90US-0559173.
XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX PI Yankner BA;
XX DR WPI; 1999-189630/16.
XX PT Screening for neurotoxin inhibitors - by testing compounds for their
XX PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX PS Disclosure; Column 37-38; 28pp; English.
XX CC This invention describes a method for screening compounds for inhibiting
XX CC a neurotoxin. The method involves incubating tachykinin agonists with
XX CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
XX CC used for identifying compounds for treating diseases characterised by an
XX CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
XX CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
XX CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
XX CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX CC beta-amyloid peptide fragments.
XX SQ Sequence 11 AA;

Query Match 60.6%; Score 43; DB 20; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RPKPQQWFWL 10
Db 1 rpkpqffgl 10

RESULT 172
AAW92668
ID AAW92668 standard; peptide; 11 AA.
XX AC AAW92668;
XX DT 30-APR-1999 (first entry)
XX DE Human tachykinin agonist beta-amyloid peptide fragment #14.
XX KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Modified-site 11
XX FT /label= Nle
XX PN US5876948-A.
XX PD 02-MAR-1999.
XX PF 27-JUL-1991; 91US-0737371.
XX PR 29-JUL-1991; 91US-0737371.
XX PR 27-JUL-1990; 90US-0559173.
XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX PI Yankner BA;
XX DR WPI; 1999-189630/16.
XX PT Screening for neurotoxin inhibitors - by testing compounds for their
XX PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX PS Disclosure; Column 15-16; 28pp; English.
XX CC This invention describes a method for screening compounds for inhibiting
XX CC a neurotoxin. The method involves incubating tachykinin agonists with
XX CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
XX CC used for identifying compounds for treating diseases characterised by an
XX CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,

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XX Screening for neurotoxin inhibitors - by testing compounds for their
XX PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX PS Disclosure; Column 15-16; 28pp; English.
XX CC This invention describes a method for screening compounds for inhibiting
XX CC a neurotoxin. The method involves incubating tachykinin agonists with
XX CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
XX CC used for identifying compounds for treating diseases characterised by an
XX CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
XX CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
XX CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
XX CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX CC beta-amyloid peptide fragments.
XX SQ Sequence 11 AA;

Query Match 60.6%; Score 43; DB 20; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RPKPQQWFWL 10
Db 1 rpkpqffgl 10

RESULT 172
AAW92668
ID AAW92668 standard; peptide; 11 AA.
XX AC AAW92668;
XX DT 30-APR-1999 (first entry)
XX DE Human tachykinin agonist beta-amyloid peptide fragment #14.
XX KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Modified-site 11
XX FT /label= Nle
XX PN US5876948-A.
XX PD 02-MAR-1999.
XX PF 27-JUL-1991; 91US-0737371.
XX PR 29-JUL-1991; 91US-0737371.
XX PR 27-JUL-1990; 90US-0559173.
XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX PI Yankner BA;
XX DR WPI; 1999-189630/16.
XX PT Screening for neurotoxin inhibitors - by testing compounds for their
XX PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX PS Disclosure; Column 15-16; 28pp; English.
XX CC This invention describes a method for screening compounds for inhibiting
XX CC a neurotoxin. The method involves incubating tachykinin agonists with
XX CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
XX CC used for identifying compounds for treating diseases characterised by an
XX CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,

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CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

XX SQ Sequence 11 AA;

Query Match 60.6%; Score 43; DB 20; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQFWL 10
|||||:|
Db 1 rpkpqffgl 10

RESULT 173
AAW92670
ID AAW92670 standard; peptide; 11 AA.

XX AC AAW92670;

XX DT 30-APR-1999 (first entry)

XX DE Human tachykinin agonist beta-amyloid peptide fragment #16.

XX KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.

XX OS Homo sapiens.

XX XH key Location/Qualifiers

XX FT Modified-site 1 /note= "Residue is ethionine"

XX PN US5876948-A.

XX PD 02-MAR-1999.

XX PF 27-JUL-1991; 91US-0737371.

XX PR 29-JUL-1991; 91US-0737371.

XX PR 27-JUL-1990; 90US-0559173.

XX PA (CHIL-) CHILDRENS MEDICAL CENT.

XX PI Yankner BA;

XX DR WPI; 1999-189630/16.

XX PT Screening for neurotoxin inhibitors - by testing compounds for their
XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX PS Disclosure; Column 17-18; 28pp; English.

XX CC This invention describes a method for screening compounds for inhibiting
XX a neurotoxin. The method involves incubating tachykinin agonists with
XX neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
XX used for identifying compounds for treating diseases characterised by an
XX undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
XX Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
XX with amyloidosis and non-inherited congophilic angiopathy with cerebral
XX haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX beta-amyloid peptide fragments.

XX SQ Sequence 11 AA;

Query Match 60.6%; Score 43; DB 20; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPQQFWL 11
|||||:|
Db 2 pkpqffgl 11

RESULT 174

AAW92672

ID AAW92672 standard; peptide; 11 AA.

XX AC AAW92672;

XX DT 30-APR-1999 (first entry)

XX DE Human tachykinin agonist beta-amyloid peptide fragment #18.

XX KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.

XX OS Homo sapiens.

XX PN US5876948-A.

XX PD 02-MAR-1999.

XX PF 27-JUL-1991; 91US-0737371.

XX PR 29-JUL-1991; 91US-0737371.

XX PR 27-JUL-1990; 90US-0559173.

XX PA (CHIL-) CHILDRENS MEDICAL CENT.

XX PI Yankner BA;

XX DR WPI; 1999-189630/16.

XX PT Screening for neurotoxin inhibitors - by testing compounds for their
XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX PS Disclosure; Column 17-18; 28pp; English.

XX CC This invention describes a method for screening compounds for inhibiting
XX a neurotoxin. The method involves incubating tachykinin agonists with
XX neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
XX used for identifying compounds for treating diseases characterised by an
XX undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
XX Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
XX with amyloidosis and non-inherited congophilic angiopathy with cerebral
XX haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX beta-amyloid peptide fragments.

XX SQ Sequence 11 AA;

Query Match 60.6%; Score 43; DB 20; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPQQFWL 11
|||||:|
Db 2 pkpqffgl 11

RESULT 175

AAW92672

ID AAW92672 standard; peptide; 11 AA.

XX AC AAW92672;

XX DT 20-DEC-2000 (first entry)

XX DE Peptide identified from a databank of polypeptides and polynucleotides.

XX Precursor peptide; polypeptide hormone; peptide identification.
XX Unidentified.
XX

XX Key Location/Qualifiers
XX Modified-site 1 /note= "hydrogen attached"
XX Modified-site 11 /note= "amidated residue"
XX

XX WO200005636-A1.

XX 31-AUG-2000.

XX 24-FEB-2000; 2000WO-FR00460.

XX 25-FEB-1999; 99US-0257525.

XX (SCRS) SCRAS SOC CONSEILS RECH & APPL SCI.
XX (CNRS) CNRS CENT NAT RECH SCI.

XX Camara Ferrer yJA, Thuriel C, Martinez J, Berge G, Goze C;
XX WPI; 2000-572101/53.

XX Identifying peptide with selected function, useful particularly for
XX C-amidated hormones, by screening database for combination of nucleic
XX acid and amino acid sequences -

XX Disclosure; Page 22; 40pp; French.

XX The specification describes a method for identifying a peptide having
XX a particular function. The method comprises preparing a database of
XX polynucleotides and polypeptides of unknown functions, screening the
XX database for a combination of nucleotides or amino acids indicative of
XX the peptide with a particular function, and identifying polynucleotides
XX and proteins which contain the peptide. The method is used to identify
XX precursor peptides with an amidated C-terminus, especially polypeptide
XX hormones, for studying physiologically active substances. The present
XX sequence represents a peptide which was identified using the method of
XX the invention.

XX Sequence 11 AA;

Query Match 60.6%; Score 43; DB 21; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPOQWFWM 11
Db 2 pkpqffglm 11

RESULT 176

AAB99350
ID AAB99350 standard; peptide; 11 AA.

XX AAB99350;

XX 24-AUG-2001 (first entry)

XX Substance P tachykinin-related peptide SEQ ID NO:3.

XX Tachykinin-related peptide; substance P; neurokinin A; neurokinin B;
XX physiologically active; tachykinin; drug; veterinary medicine;
XX agrochemical.

XX Synthetic.

XX Key Location/Qualifiers
XX Modified-site 11

FT /note= "amidated"

XX WO200134637-A1.

XX 17-MAY-2001.

XX 07-NOV-2000; 2000WO-JP07789.

XX 08-NOV-1999; 99JP-0317535.

XX (SUNR) SUNTORY LTD.

XX Ikeda T, Nomoto K, Minakata H;

XX WPI; 2001-329069/34.

XX Synthesis of new physiologically-active peptide analogs of tachykinin,
XX useful as drugs, veterinary medicines and agrochemicals, comprises
XX modifying C-terminal amino-acid residues -

XX Claim 13; Page 23; 36pp; Japanese.

XX The present invention describes a method for producing physiologically
XX active substances. The method comprises converting the amino-acid
XX residue at a specific position in a peptide into another amino-acid
XX residue to provide activity against (in)vertebrates. Also described are:
XX (1) converted unnatural tachykinin-related peptide with tachykinin-like
XX physiological activity against (in)vertebrates which is an amino-acid
XX sequence with the 5 amino-acids at C-terminal as in
XX -Phe-AA1-Gly-AA2-Met-NH2 (1) where AA1 = Val, Ile, Phe, Tyr, His, Met,
XX Thr, Leu, Gly or Gln and AA2 = Ser, Ala, Val, Met, Thr, Pro or Leu; and
XX (2) drugs, veterinary medicines or agrochemicals containing the new
XX tachykinin-related peptide as the active ingredient. The peptide
XX analogues are for use as drugs, veterinary medicines and agrochemicals
XX with activity on vertebrates or invertebrates. By modifying C-terminal
XX amino-acid residues of tachykinin, the activity of tachykinin and its
XX related derivative can therefore be changed from that against
XX vertebrates to that on invertebrates or vice versa. The present sequence
XX represents a specifically claimed tachykinin-related peptide from the
XX present invention.

XX Sequence 11 AA;

Query Match 60.6%; Score 43; DB 22; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQWFWM 10
Db 1 rpqpqffgl 10

RESULT 177

AAW14777

ID AAW14777 standard; Protein; 898 AA.

XX AAW14777;

XX 14-MAY-1997 (first entry)

XX Granulosis virus infectivity protein.

XX Infection; nuclear polyhedrosis virus; Granulosis virus genus.

XX Granulosis virus XGV alpha-4 strain.

XX Key Location/Qualifiers
XX CDS 49..2745
XX /*tag= a

XX JP09009972-A.

PD 14-JAN-1997.
XX
PF 03-JUL-1995; 95JP-0167481.
XX
PR 03-JUL-1995; 95JP-0167481.
XX
XX (NORQ) NORINSUISANSHO NOGYO KENKYU.
PA WPI; 1997-126429/12.
DR N-PSDB; AAT14777.
XX
XX Granulosis virus protein - enhances nuclear polyhedrosis virus
PT Infectious activity
PT
XX
XX Claim 4; Page 10-13; 14pp; Japanese.
XX
XX This sequence represents a protein which has a mol. wt. of ca. 100 KD and
CC which enhances the infectious activity of nuclear polyhedrosis virus.
CC This sequence is originated from a virus of Granulosis virus genus.
CC The protein enhances infectious activity of insecticidal NPV.
XX
XX
SQ Sequence 898 AA;

Query Match 60.6%; Score 43; DB 18; Length 898;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQOWFWLM 11
| | | | |
Db 353 pypqiawlm 362

RESULT 178
AAW14285
ID AAW14285 standard; Protein; 902 AA.
XX
XX AAW14285;
XX
XX
DT 16-JAN-1998 (first entry)
DE
DE H. armigera granulovirus enhancin protein.
XX
XX Enhancin; hybridisation; granulovirus; Trichoplusia ni; insect; midgut;
KW open reading frame; pseudaletia unipuncta; peritrophic membrane protein;
KW insect; absorption; penetration; baculovirus; mortality; pest control.
XX
XX Helicoverpa armigera granulovirus.
OS
XX WO9708197-A1.
XX
XX
PD 06-MAR-1997.
XX
XX 23-AUG-1996; 96WO-0513645.
PF
XX 23-AUG-1996; 96US-0002743.
PR
XX 24-AUG-1995; 95US-0002743.
XX
XX (BOYC-) BOYCE THOMPSON INST PLANT RES.
PA
XX
XX Granados RR;
PI
XX WPI; 1997-179177/16.
DR N-PSDB; AAT79099.
XX
XX DNA encoding the Helicoverpa armigera granulovirus enhancin protein
PT - used to increase infectivity of baculovirus for control of insect
PT pests
XX
XX Claim 1; Page 18-22; 36pp; English.
PS
XX This is the amino acid sequence of the enhancin protein of Helicoverpa
CC armigera granulovirus (HearGV). The protein has a calculated molecular

CC weight of 104.6 kD which is similar to the 104.2 kD of the 901 amino
CC acid enhancin from Pseudaletia unipuncta granulovirus (PsunGV; see patent
CC US5475090). The HearGV enhancin also has 80 and 81% amino acid identity
CC with the Trichoplusia ni granulovirus (TnGV) and PsunGV enhancins
CC respectively. The enhancin proteins disrupt peritrophic membrane
CC proteins in insects so that absorption, penetration and/or uptake of
CC baculovirus in the midgut is increased, leading to higher mortality.
CC They are used in conjunction with a substance toxic to insects for pest
CC control.
XX
XX Sequence 902 AA;
SQ

Query Match 60.6%; Score 43; DB 18; Length 902;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQOWFWLM 11
| | | | |
Db 353 pypqiawlm 362

RESULT 179
AAP30469
ID AAP30469 standard; Protein; 7 AA.
XX
XX AAP30469;
XX
XX 31-MAY-1992 (first entry)
DT
DE Sequence of polypeptide deriv. with antagonistic properties against
DE substance P.
XX
XX Substance P antagonist; chronic pain therapy; high blood pressure;
KW hypertension; hypotensive agent.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 1 /label= H-Pro
FT /note= "This AA may be omitted, in which case AA(2)
FT - Prop. Gln"
FT
FT Modified-site 3 /label= D-Trp
FT Modified-site 5 /label= D-Trp
FT Modified-site 7 /label= Met-NH2
FT
XX DE3205991-A.
XX
XX 01-SEP-1983.
PD
XX 16-FEB-1983; 83DE-3467187.
PF
XX 19-FEB-1982; 82DE-3205991.
PR
XX (FERR-) FERRING ARZNEIMITTE.
PA
XX Horig J, Schultheiss H;
PI
XX WPI; 1983-753766/36.
DR
XX Polypeptide derivs. contg. naturally occurring amino acids -
PT antagonists against substance P and for treatment of pain and
PT high blood pressure, including corneal inflammation
PT
XX Example; Page 16; 26pp; German.
PS
XX The peptides of the invention can be used to treat chronic pain
CC conditions and high blood pressure, including e.g. chronic
CC inflammations of the cornea caused by various circumstances, e.g.
CC lengthy exposure to UV light, IR-rays or chemicals.
XX

SQ Sequence 7 AA;

Query Match 59.2%; Score 42; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. NO. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QWFWLM 11
 |||||
 Db 2 qwfwlm 7

RESULT 180

AAR21960
 ID AAR21960 standard; Peptide; 11 AA.

AC AAR21960;

XX 25-JUN-1992 (first entry)

XX Cyclic substance P [Hcys 5,9].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 5

FT /label= OTHER

FT /note= "OTHER = homocysteine"

FT Misc-difference 9

FT /label= OTHER

FT /note= "OTHER = homocysteine"

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.
 XX Claim 11; Page 22; 35pp; English.

XX The peptide is the tachykinin agonist, substance P with
 CC homocysteine substituted at positions 5 and 9, with a disulphide
 CC bond formed between them making the peptide cyclic. The
 CC peptide was synthesised by standard solid phase synthesis.
 CC Neuronal accumulation of beta-amyloid may be treated by administ-
 CC ration of tachykinin agonists. The peptide can reduce the neuro-
 CC toxic effects of a beta-amyloid related polypeptide on cultured
 CC neurons. The peptide and its analogues are useful for controlling
 CC diseases characterised by beta amyloid accumulation in the brain
 CC such as Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.

XX Sequence 11 AA;

Query Match

Best Local Similarity 59.2%; Score 42; DB 13; Length 11;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
 |||||
 Db 1 rpkipqffxlm 11

RESULT 181

AAR21939
 ID AAR21939 standard; Protein; 11 AA.

XX AAR21939;

XX 25-JUN-1992 (first entry)

XX Substance P [Ile 8].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.
 XX Claim 10; Page 21; 35pp; English.

XX The peptide is the tachykinin agonist substance P with an
 CC isoleucine residue substituted at position 8. The peptide was
 CC synthesised by standard solid phase synthesis. Neuronal
 CC accumulation of beta-amyloid may be treated by administration of
 CC tachykinin agonists. The peptide can reduce the neurotoxic effects
 CC of a beta-amyloid related polypeptide on cultured neurons. The
 CC peptide and its analogues are useful for controlling diseases
 CC characterised by beta amyloid accumulation in the brain such as
 CC Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.

XX Sequence 11 AA;

Query Match

Best Local Similarity 59.2%; Score 42; DB 13; Length 11;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
 |||||
 Db 1 rpkipqffxlm 11

RESULT 182

AAR21949
 ID AAR21949 standard; Protein; 11 AA.

XX AAR21949;

XX 25-JUN-1992 (first entry)

XX Substance P [Pro 3].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.
 XX Synthetic.

OS
 XX WO9202248-A.
 PN
 XX 20-FEB-1992.
 PD
 XX 29-JUL-1991; 91WO-US05323.
 PF
 XX 27-JUL-1990; 90US-0559173.
 PR
 XX (CHIL-) CHILDRENS MED CENT.
 PA
 XX Yankner BA;
 PI
 XX WPI; 1992-079804/10.
 DR

XX Treatment of neuronal accumulation of beta-amyloid - using
 PT Tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.
 XX
 XX Claim 10; Page 21; 35pp; English.
 PS
 XX The peptide is the tachykinin agonist substance P with a Proline
 CC residue substituted at position 3. The peptide was
 CC synthesised by standard solid phase synthesis. Neuronal
 CC accumulation of beta-amyloid may be treated by administration of
 CC tachykinin agonists. The peptide can reduce the neurotoxic effects
 CC of a beta-amyloid related polypeptide on cultured neurons. The
 CC peptide and its analogues are useful for controlling diseases
 CC characterised by beta amyloid accumulation in the brain such as
 CC Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.
 XX
 XX Sequence 11 AA;
 SQ

Query Match 59.2%; Score 42; DB 13; Length 11;
 Best Local Similarity 72.7%; Pred. No. 2;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
 |||||:|:
 Db 1 rpppqif9lm 11

RESULT 183

AAW92683
 ID AAW92683 standard; peptide; 11 AA.
 XX

AC AAW92683;
 XX

DT 30-APR-1999 (first entry)
 XX

DE Human tachykinin agonist beta-amyloid peptide fragment #29.
 XX

KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.

XX Homo sapiens.
 OS

XX Key Location/Qualifiers
 FH Modified-site 5
 FT /note= "Residue is homocysteine"
 FT Modified-site 9
 FT /note= "Residue is homocysteine"
 XX

PN US5876948-A.
 XX

PD 02-MAR-1999.
 XX
 XX 27-JUL-1991; 91US-0737371.
 PF
 XX 29-JUL-1991; 91US-0737371.
 PR
 XX 27-JUL-1990; 90US-0559173.
 PR
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA
 XX Yankner BA;
 PI
 XX WPI; 1999-189630/16.
 XX

XX Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 PT
 XX Disclosure; Column 23-24; 28pp; English.
 PS
 XX

CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.

XX Sequence 11 AA;
 SQ

Query Match 59.2%; Score 42; DB 20; Length 11;
 Best Local Similarity 72.7%; Pred. No. 2;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
 |||||:|:
 Db 1 rpkpxqffxlm 11

RESULT 184

AAW92669
 ID AAW92669 standard; peptide; 11 AA.
 XX

AC AAW92669;
 XX

DT 30-APR-1999 (first entry)
 XX

DE Human tachykinin agonist beta-amyloid peptide fragment #15.
 XX

KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.

XX Homo sapiens.
 OS

XX US5876948-A.
 PN

XX 02-MAR-1999.
 PD

XX 27-JUL-1991; 91US-0737371.
 PF

XX 29-JUL-1991; 91US-0737371.
 PR

XX 27-JUL-1990; 90US-0559173.
 PR

XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA

XX Yankner BA;
 PI

XX WPI; 1999-189630/16.
 XX

XX Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 PT

XX Disclosure; Column 17-18; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX Sequence 11 AA;
SQ

Query Match 59.2%; Score 42; DB 20; Length 11;
Best Local Similarity 72.7%; Pred. No. 2;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RPKPQQWFWM 11
Db 1 rpkpqffglm 11

RESULT 185
AAW92673
ID AAW92673 standard; peptide; 11 AA.
AC AAW92673;
XX
XX 30-APR-1999 (first entry)
XX Human tachykinin agonist beta-amyloid peptide fragment #19.
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX Homo sapiens.
OS
XX US5876948-A.
PN
XX
XX 02-MAR-1999.
XX
XX 27-JUL-1991; 91US-0737371.
XX
XX 29-JUL-1991; 91US-0737371.
XX 27-JUL-1990; 90US-0559173.
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA
XX
XX Yankner BA;
PI
XX
XX
XX WPI; 1999-189630/16.
DR
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Disclosure; Column 17-18; 28pp; English.
XX

XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX Sequence 11 AA;
SQ

Query Match 59.2%; Score 42; DB 20; Length 11;
Best Local Similarity 72.7%; Pred. No. 2;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RPKPQQWFWM 11
Db 1 rpppqffglm 11

RESULT 186
AAB49755
ID AAB49755 standard; peptide; 11 AA.
XX
XX AAB49755;
AC
XX
XX 17-APR-2001 (first entry)
XX Complex sugar bound peptide (SBP) amino acid sequence.
XX Sugar peptide complex; SBP; sugar bound peptide; enzymatically stable.
XX Synthetic.
OS
XX JP2000319297-A.
PN
XX 21-NOV-2000.
PD
XX 30-MAR-1999; 99JP-0088030.
XX 30-MAR-1999; 99JP-0088030.
XX (NOCK) ZH NOGUCHI KENKYUSHO.
XX WPI; 2001-184996/19.
DR
XX A process for preparation of enzymically stable sugar peptide complex
PT
XX
XX Example 2; Page 3; 4pp; Japanese.
PS

XX This invention relates to a process for the preparation of an
CC enzymatically stable sugar peptide complex, and includes an in vivo
CC stable inhibitor of peptide-N-glycanase (EC. 3.5.1.52). The process can
CC be used for the investigation of in vivo reciprocal recognition of
CC cell-cell and substrate-receptor interaction, and their metabolism. The
CC present sequence represents a complex sugar bound peptide (SBP) amino
CC acid sequence prepared by the process of the invention.
XX Sequence 11 AA;
SQ

Query Match 59.2%; Score 42; DB 22; Length 11;
Best Local Similarity 63.6%; Pred. No. 2;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPQQWFWM 11
Db 1 kprpqffglm 11

RESULT 187
AAE04896
ID AAE04896 standard; Protein; 398 AA.
XX
XX AAE04896;
AC
XX
XX 10-SEP-2001 (first entry)
XX Human transporter and ion channel-9 (TRICH-9) protein.
DE
XX Human; transporter and ion channel-9; TRICH-9; vaccine; cystic fibrosis;
KW gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy;
KW

KW hypertension; angina; neurological disorder; asthma; bipolar disorder;
KW dementia; depression; Alzheimer's disease; epilepsy; mood; arrhythmia;
KW Pick's disease; ischaemic cerebrovascular disease; AIDS; anxiety; stroke;
KW Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy;
KW demyelinating disease; mental disorder; Schizophrenia; polymyositis;
KW muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease;
KW dermatomyositis; diabetes mellitus; immunological disorder; psoriasis;
KW rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus;
KW sickle cell anaemia; Wilson's disease; infertility; Cushing's disease;
KW scleroderma; pulmonary artery stenosis; neutropenic; Addison's disease;
KW malabsorption syndrome; hypercholesterolaemia; cancer.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Domain 217..242
FT /label= Transmembrane_domain
FT Domain 247..264
FT /label= Transmembrane_domain
FT Domain 350..368
FT /label= Transmembrane_domain
XX
XX WO200146258-A2.
XX
XX 28-JUN-2001.
XX
XX 22-DEC-2000; 2000WO-US35095.
XX
XX 23-DEC-1999; 99US-0172000.
PR 14-JAN-2000; 2000US-0176083.
PR 21-JAN-2000; 2000US-0177332.
PR 28-JAN-2000; 2000US-0178572.
PR 02-FEB-2000; 2000US-0179758.
PR 10-FEB-2000; 2000US-0181625.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Baughn MR, Burford N, Au-Young J, Lu DAM, Yang J, Reddy R, Lal P;
PI Hillman JL, Azimzai Y, Yue H, Nguyen DB, Yao MG, Gandhi AR;
PI Tang YT, Khan FA;
XX
XX WPI; 2001-418042/44.
DR N-PSDB; AAD09560.
XX
XX Novel human transporter and ion channel proteins useful for treating
PT and preventing transport, neurological, muscle and immunological
PT disorders -
XX
XX Claim 1; Page 121-122; 160pp; English.
XX
XX The present sequence is transporter and ion channel-9 (TRICH-9) protein.
CC TRICH is used as vaccine. TRICH is useful for treating a disease or
CC condition associated with decreased expression of functional TRICH,
CC such as transport disorder including amyotrophic lateral sclerosis,
CC cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth
CC disease, Duchenne muscular dystrophy, angina and hypertension,
CC neurological disorders including Alzheimer's disease, amnesia, bipolar
CC disorder, dementia, depression, epilepsy, ischaemic cerebrovascular
CC disease, stroke, cerebral neoplasms, Pick's disease, Huntington's
CC disease and Parkinson's disease, demyelinating diseases, mental disorders
CC including mood, anxiety, Schizophrenia and seasonal affective disorder,
CC muscle disorder including cardiomyopathy, myocarditis, polymyositis,
CC dermatomyositis, arrhythmias and asthma and immunological disorders
CC including AIDS, adult respiratory distress syndrome (ARDS), allergies,
CC anaemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's
CC syndrome, systemic lupus erythematosus and other diseases including
CC sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary
CC artery stenosis, Grave's disease, Cushing's disease, Addison's disease,
CC glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers
CC psoriasis and viral, bacterial, fungal, helminthic and protozoal
CC infections. TRICH DNA is useful in gene therapy and in diagnostic
CC purposes.
XX

SQ Sequence 398 AA;
Query Match 59.2%; Score 42; DB 22; Length 398;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 4 PQOWFWLM 11
| | | : | | | |
Db 38 pqgyfwll 45
RESULT 188
AAW50976
ID AAW50976 standard; peptide; 8 AA.
XX
XX AAW50976;
XX
XX 31-JUL-1998 (first entry)
XX
XX Substance P analogue residues 4-11, [D-Pro4,D-Trp7,9,10,Val8].
XX
XX Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
KW Substance P; cancer; inhibition; growth hormone releasing factor;
KW spantide.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Misc-difference 4 /note= "D-form residue"
FT Misc-difference 6 /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 8 /note= "D-form residue"
FT Modified-site 8 /note= "C-terminal amide"
XX
XX EP835662-A2.
XX
XX 15-APR-1998.
XX
XX 11-DEC-1996; 96EP-0309012.
XX
XX 08-OCT-1996; 96US-0727679.
XX 16-AUG-1996; 96IN-0001822.
XX
XX (NAIM-) NAT INST IMMUNOLOGY.
XX
XX Jaggi M, Mukherjee R;
PI WPI; 1998-208959/19.
XX
XX Composition containing analogues of vasoactive intestinal peptide,
PT somatostatin - bombesin and substance P, for treatment of tumours
PT and for inhibiting over-expression of these peptide(s)
XX
XX Disclosure; Page 13; 49pp; English.
XX
XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 AGCKNFFQWKPTSDC (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,

CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
 CC cells express receptors for VIP, somatostatin, bombesin and/or substance
 CC P. The present sequence represents a substance P analogue.

XX
 SQ Sequence 8 AA;

Query Match 57.7%; Score 41; DB 19; Length 8;
 Best Local Similarity 75.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQQFWFLM 11
 |||||
 Db 1 pqqvwwvm 8

RESULT 189

AAW92711
 ID AAW92711 standard; peptide; 8 AA.

XX
 AC AAW92711;

XX 30-APR-1999 (first entry)

XX Human tachykinin agonist beta-amyloid peptide fragment #57.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenital angiodysplasia.

XX Homo sapiens.

XX US5876948-A.

XX 02-MAR-1999.

XX 27-JUL-1991; 91US-0737371.

XX 29-JUL-1991; 91US-0737371.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Yankner BA;

XX WPI; 1999-189630/16.

XX Screening for neurotoxin inhibitors - by testing compounds for their
 effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX Disclosure; Column 35-36; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting
 a neurotoxin. The method involves incubating tachykinin agonists with
 neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 used for identifying compounds for treating diseases characterised by an
 undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 with amyloidosis and non-inherited congenital angiodysplasia with cerebral
 haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 beta-amyloid peptide fragments.

XX Sequence 8 AA;

Query Match 57.7%; Score 41; DB 20; Length 8;
 Best Local Similarity 87.5%; Pred. No. 4.3e+05;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQWF 8
 |||||
 Db 1 rpkpqgff 8

RESULT 190

AAR21932

ID AAR21932 standard; peptide; 9 AA.

XX AAR21932;

XX 25-JUN-1992 (first entry)

XX Substance P (1-9) fragment.

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX Claim 9; Page 21; 35pp; English.

XX The peptide is a tachykinin agonist consisting of residues 1-9 of
 substance P. The peptide was synthesised by standard solid phase
 synthesis. Analogues of the peptide, with C-terminal deletions down
 to substance P (1-4) were also synthesised. Neuronal accumulation of
 beta-amyloid may be treated by administration of these tachykinin
 agonists. The peptides reduce the neurotoxic effects of a beta-
 amyloid related polypeptide on cultured neurons. The peptide and
 its analogues are useful for controlling diseases characterised by
 beta amyloid accumulation in the brain such as Alzheimer's disease
 and Down's syndrome.
 CC See also AAR21933-75.

XX Sequence 9 AA;

Query Match 57.7%; Score 41; DB 13; Length 9;
 Best Local Similarity 87.5%; Pred. No. 4.3e+05;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQWF 8
 |||||
 Db 1 rpkpqgff 8

RESULT 191

AAY03162

ID AAY03162 standard; peptide; 9 AA.

XX AAY03162;

XX 10-JUN-1999 (first entry)

XX Substance P fragment P/1-9#.

XX Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
 KW substance P.

OS Synthetic.
 XX US5891842-A.
 PN
 XX
 PD 06-APR-1999.
 XX
 XX 12-APR-1996; 96US-0631434.
 PF
 XX 09-APR-1993; 93US-0044954.
 PR
 XX 12-APR-1996; 96US-0631434.
 XX
 PA (TUFT) TUFTS COLLEGE.
 XX
 XX Kream RM;
 PI
 XX
 XX WPI; 1999-253906/21.
 DR
 XX Synergistic method for enhancing opioid analgesia and anaesthesia
 PT within a human
 XX
 XX Disclosure; Column 14; 20pp; English.
 XX
 CC This sequence is a fragment of substance P used in the method of the
 CC invention. The method is for enhancing opioid analgesia within a human
 CC subject for a duration of 15 minutes comprises concurrent administration
 CC of substance P, or one of its precursors. The method is used to elicit
 CC opioid analgesia and anaesthesia, either prior to or after the occurrence
 CC of a nociceptive event. The components have a synergistic effect. The
 CC method allows use of low doses of opioid that produce little or no
 CC physiological effect reducing conventional risks of toxicity and
 CC addition, and allows the use of low doses of substance P and its related
 CC analogs that limit their in vivo physiological consequences. The
 CC analgesia is naloxone reversible allowing diminishment or complete
 CC elimination of opioid analgesia if desired and on demand. The treatment
 CC provides a durable analgesic effect, but only minimally disturbs and
 CC interrupts the normal metabolic processes of the body.
 XX
 XX Sequence 9 AA;
 SQ

Query Match 57.7%; Score 41; DB 20; Length 9;
 Best Local Similarity 87.5%; Pred. NO. 4.3e+05;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWF 8
 Db | | | | | : |
 1 rpkpqgff 8

RESULT 192
 AAW92665
 ID AAW92665 standard; peptide; 9 AA.
 XX
 XX
 AC AAW92665;
 XX
 DT 17-SEP-2001 (first entry)
 XX
 XX Amino acid sequence of a substance P fragment.
 DE
 XX Clostridial neurotoxin; pain; botulinum toxin; Substance P.
 KW
 XX Unidentified.
 OS
 XX WO200153336-A1.
 PN
 XX 26-JUL-2001.
 PD
 XX 17-JAN-2001; 2001WO-US01529.
 PF
 XX 19-JAN-2000; 2000US-0489667.
 PR
 XX (ALLR) ALLERGAN SALES INC.
 PA
 XX Donovan S;
 PI
 XX WPI; 2001-451900/48.
 DR
 XX Agent useful for treating pain comprises a clostridial neurotoxin (or
 PT component) attached to a targeting moiety -
 XX
 XX Disclosure; Page 72; 77pp; English.
 PS
 XX The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected
 CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin
 CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.

XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA
 XX Yankner BA;
 PI
 XX WPI; 1999-189630/16.
 DR
 XX Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 XX Disclosure; Column 15-16; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 XX Sequence 9 AA;
 SQ

Query Match 57.7%; Score 41; DB 20; Length 9;
 Best Local Similarity 87.5%; Pred. NO. 4.3e+05;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWF 8
 Db | | | | | : |
 1 rpkpqgff 8

RESULT 193
 AAG62780
 ID AAG62780 standard; peptide; 9 AA.
 XX
 XX AAG62780;
 AC
 XX
 DT 17-SEP-2001 (first entry)
 XX
 XX Amino acid sequence of a substance P fragment.
 DE
 XX Clostridial neurotoxin; pain; botulinum toxin; Substance P.
 KW
 XX Unidentified.
 OS
 XX WO200153336-A1.
 PN
 XX 26-JUL-2001.
 PD
 XX 17-JAN-2001; 2001WO-US01529.
 PF
 XX 19-JAN-2000; 2000US-0489667.
 PR
 XX (ALLR) ALLERGAN SALES INC.
 PA
 XX Donovan S;
 PI
 XX WPI; 2001-451900/48.
 DR
 XX Agent useful for treating pain comprises a clostridial neurotoxin (or
 PT component) attached to a targeting moiety -
 XX
 XX Disclosure; Page 72; 77pp; English.
 PS
 XX The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected
 CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin
 CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.

CC The targeting moiety comprises a light chain and an amine end segment of
CC a heavy chain and comprises Substance P as the targeting moiety. The pain
CC alleviating effects persist for 2-6 months. The present sequence
CC represents a substance P fragment, and is used in the course of the
CC invention.
XX
SQ Sequence 9 AA;

Query Match 57.7%; Score 41; DB 22; Length 9;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQWF 8
| | | | | | | |
Db 1 rpkpqgff 8

RESULT 194

AAB98878
ID AAB98878 standard; Peptide; 9 AA.

XX
AC AAB98878;

XX
DT 14-AUG-2001 (first entry)

XX
DE Chimeric analgesic peptide #34.

XX
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Modified-site 9
FT /label= OTHER
FT /note= "C-terminal amide"

XX
FN WO200130371-A2.
XX
PD 03-MAY-2001.

XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.

XX
PA (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

XX
DR WPI; 2001-397593/42.
XX
PS New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group -
PT
XX Claim 10; Page 15; 34pp; English.

XX The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 9 AA;

Query Match 57.7%; Score 41; DB 22; Length 9;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQWF 8
| | | | | | | |

Db 1 rpkpqgff 8
RESULT 195
AAB91444
ID AAB91444 standard; Peptide; 9 AA.
XX
AC AAB91444;

XX
DT 22-JUN-2001 (first entry)

XX
DE Tachykinins peptide SEQ ID NO:620.

XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.

XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.

XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.

XX
PR 15-OCT-1999; 99US-0159783.

XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
PS Disclosure; Page 401; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 9 AA;

Query Match 57.7%; Score 41; DB 22; Length 9;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQWF 8
| | | | | | | |
Db 1 rpkpqgff 8

RESULT 196

AAB91410
ID AAB91410 standard; Peptide; 10 AA.
XX
AC AAB91410;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:586.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
PS Disclosure; Page 391; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 10 AA;

Query Match 57.7%; Score 41; DB 22; Length 10;
Best Local Similarity 87.5%; Pred. No. 2.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOWF 8
Db 1 rpkpqgff 8

RESULT 197
AAB91422
ID AAB91422 standard; Peptide; 10 AA.
XX
AC AAB91422;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:608.

XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:598.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
PS Disclosure; Page 395; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 10 AA;

Query Match 57.7%; Score 41; DB 22; Length 10;
Best Local Similarity 87.5%; Pred. No. 2.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOWF 8
Db 1 rpkpqgff 8

RESULT 198
AAB91432
ID AAB91432 standard; Peptide; 10 AA.
XX
AC AAB91432;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:608.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX WO200069900-A2.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-USI3576.
XX
XX 17-MAY-1999; 99US-0134406.
XX 10-SEP-1999; 99US-0153406.
XX 15-OCT-1999; 99US-0159783.
XX (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
XX WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
XX peptidase degradation, useful for increasing length of in vivo activity
XX
XX Disclosure; Page 398; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
XX comprising a therapeutically active amino acid region (III) and a
XX reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
XX a less therapeutically active amino acid region (IV), which covalently
XX bonds with amino/hydroxyl/thiol groups on blood components to form a
XX peptide stabilised therapeutic peptide composed of 3-50 amino acids.
XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX factors and neurotransmitters, to protect them from peptidase activity
XX in vivo for the treatment of various disorders. Endogenous therapeutic
XX peptides are not suitable as drug candidates as they require frequent
XX administration due to rapid degradation by peptidases in the body.
XX Modifying and attaching therapeutic peptides to albumin prevents or
XX reduces the action of peptidases to increase length of activity (half
XX life) and specificity as bonding to large molecules decreases
XX intracellular uptake and interference with physiological processes.
XX AAB90829 to AAB92441 represent peptides which can be used in the
XX exemplification of the present invention.
XX
XX Sequence 10 AA;
XX
XX Query Match 57.7%; Score 41; DB 22; Length 10;
XX Best Local Similarity 87.5%; Pred. No. 2.6;
XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 RPKPOQWF 8
XX {|||||:
XX Db 1 rpqpqgff 8
XX
XX RESULT 199
XX AAR21940
XX ID AAR21940 standard; Protein: 11 AA.
XX
XX AC AAR21940;
XX
XX DT 25-JUN-1992 (first entry)
XX
XX DE Substance P (Pro 10).
XX
XX KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX KW syndrome; hereditary cerebral haemorrhage.

OS Synthetic.
XX WO9202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991; 91WO-US05323.
XX
XX 27-JUL-1990; 90US-0559173.
XX (CHIL-) CHILDRENS MED CENT.
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 10; Page 21; 35pp; English.
XX
XX The peptide is the tachykinin agonist substance P with a Proline
XX residue substituted at position 10. The peptide was
XX synthesised by standard solid phase synthesis. Neuronal
XX accumulation of beta-amyloid may be treated by administration of
XX tachykinin agonists. The peptide can reduce the neurotoxic effects
XX of a beta-amyloid related polypeptide on cultured neurons. The
XX peptide and its analogues are useful for controlling diseases
XX characterised by beta amyloid accumulation in the brain such as
XX Alzheimer's disease and Down's syndrome.
XX See also AAR21932-75.
XX
XX Sequence 11 AA;
XX
XX Query Match 57.7%; Score 41; DB 13; Length 11;
XX Best Local Similarity 87.5%; Pred. No. 2.9;
XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 RPKPOQWF 8
XX {|||||:
XX Db 1 rpqpqgff 8
XX
XX RESULT 200
XX AAW92716
XX ID AAW92716 standard; peptide; 11 AA.
XX
XX AC AAW92716;
XX
XX DT 30-APR-1999 (first entry)
XX
XX DE Human tachykinin agonist beta-amyloid peptide fragment #62.
XX
XX KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX
XX OS Homo sapiens.
XX
XX PN US5876948-A.
XX
XX PD 02-MAR-1999.
XX
XX PF 27-JUL-1991; 91US-0737371.
XX
XX PR 29-JUL-1991; 91US-0737371.
XX PR 27-JUL-1990; 90US-0559173.
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX Yankner BA;
XX

XX WPI; 1999-189630/16.
 XX Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 XX Disclosure; Column 37-38; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 SQ Sequence 11 AA;

Query Match 57.7%; Score 41; DB 20; Length 11;
 Best Local Similarity 87.5%; Pred. No. 2.9;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RPKPQWF 8
 |||||
 Db 1 rpkpqff 8

Search completed: April 1, 2002, 16:18:23
 Job time: 54 sec

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OM protein - protein search, using sw model

Run on: April 1, 2002, 16:18:44 ; Search time 20.12 Seconds
(without alignments)
12.303 Million cell updates/sec

Title: US-09-988-792-2
Perfect score: 71
Sequence: 1 RPKQQWFWM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 192

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 50%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pcp.*
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4: /cgn2_6/ptodata/2/iaa/6B.COMB.pcp.*
5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pcp.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pcp.*

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	100.0	11	6	5441935-5
2	68	95.8	11	6	5441935-2
3	61	85.9	11	6	5441935-3
4	54	76.1	8	6	5441935-10
5	49	69.0	11	2	US-07-737-371E-12
6	48	67.6	8	6	5441935-6
7	48	67.6	11	1	US-07-934-553-1
8	48	67.6	11	1	US-08-184-935-12
9	48	67.6	11	1	US-08-269-288-2
10	48	67.6	11	1	US-08-338-484-1
11	48	67.6	11	1	US-08-175-432-1
12	48	67.6	11	1	US-08-225-474-1
13	48	67.6	11	1	US-08-391-910-2
14	48	67.6	11	1	US-08-418-994-2
15	48	67.6	11	1	US-08-480-505-3
16	48	67.6	11	1	US-08-391-814-2
17	48	67.6	11	1	US-08-167-870-1
18	48	67.6	11	1	US-08-255-272-6
19	48	67.6	11	1	US-08-441-591-6
20	48	67.6	11	1	US-08-303-362A-6
21	48	67.6	11	1	US-08-462-859A-1
22	48	67.6	11	1	US-08-123-659A-1
23	48	67.6	11	1	US-08-462-415-2
24	48	67.6	11	1	US-08-463-874-2
25	48	67.6	11	1	US-08-464-247A-1
26	48	67.6	11	1	US-08-464-248A-1
27	48	67.6	11	1	US-08-444-135-2

28	48	67.6	11	1	US-08-318-391-2	Sequence 2, Appli
29	48	67.6	11	2	US-08-796-598-11	Sequence 11, Appl
30	48	67.6	11	2	US-08-447-175A-11	Sequence 11, Appl
31	48	67.6	11	2	US-07-737-371E-21	Sequence 21, Appl
32	48	67.6	11	2	US-07-737-371E-22	Sequence 22, Appl
33	48	67.6	11	2	US-07-737-371E-24	Sequence 24, Appl
34	48	67.6	11	2	US-07-737-371E-27	Sequence 27, Appl
35	48	67.6	11	2	US-07-737-371E-65	Sequence 65, Appl
36	48	67.6	11	2	US-07-737-371E-77	Sequence 77, Appl
37	48	67.6	11	2	US-08-848-766A-1	Sequence 1, Appli
38	48	67.6	11	3	US-08-927-128-17	Sequence 17, Appl
39	48	67.6	11	4	US-08-257-966-2	Sequence 2, Appli
40	48	67.6	11	5	PCT-US95-05600-23	Sequence 23, Appl
41	48	67.6	11	6	5441935-1	Patent No. 5441935
42	48	67.6	11	6	5441935-8	Patent No. 5441935
43	48	67.6	12	1	US-08-441-591-7	Sequence 7, Appli
44	48	67.6	12	1	US-08-303-362A-7	Sequence 7, Appli
45	48	67.6	12	4	US-08-505-250-27	Sequence 27, Appl
46	48	67.6	12	4	US-08-505-250-53	Sequence 53, Appl
47	48	67.6	12	5	PCT-US92-06532-4	Sequence 4, Appli
48	48	67.6	12	5	PCT-US95-05600-24	Sequence 24, Appl
49	48	67.6	20	3	US-08-890-157A-2	Sequence 2, Appli
50	48	67.6	20	4	US-08-505-250-50	Sequence 50, Appl
51	48	67.6	126	6	5268359-5	Patent No. 5268359
52	48	67.6	130	6	5268359-2	Patent No. 5268359
53	48	67.6	487	1	US-08-462-859A-9	Sequence 9, Appli
54	48	67.6	487	1	US-08-123-659A-9	Sequence 9, Appli
55	48	67.6	487	1	US-08-464-247A-9	Sequence 9, Appli
56	48	67.6	487	1	US-08-464-248A-9	Sequence 9, Appli
57	48	67.6	492	1	US-08-462-859A-7	Sequence 7, Appli
58	48	67.6	492	1	US-08-123-659A-7	Sequence 7, Appli
59	48	67.6	492	1	US-08-464-247A-7	Sequence 7, Appli
60	48	67.6	492	1	US-08-464-248A-7	Sequence 7, Appli
61	47	66.2	11	2	US-07-737-371E-20	Sequence 20, Appl
62	46	64.8	11	2	US-07-737-371E-17	Sequence 17, Appl
63	46	64.8	11	2	US-07-737-371E-23	Sequence 23, Appl
64	45	63.4	9	1	US-08-346-849-7	Sequence 7, Appli
65	45	63.4	9	2	US-08-293-284A-7	Sequence 7, Appli
66	45	63.4	11	1	US-07-899-205-1	Sequence 1, Appli
67	45	63.4	11	2	US-08-490-118-1	Sequence 1, Appli
68	45	63.4	11	2	US-07-737-371E-25	Sequence 25, Appl
69	45	63.4	11	5	PCT-US92-06532-1	Sequence 1, Appli
70	43	60.6	10	2	US-07-737-371E-9	Sequence 9, Appli
71	43	60.6	11	1	US-08-031-325A-26	Sequence 26, Appl
72	43	60.6	11	2	US-07-737-371E-13	Sequence 13, Appl
73	43	60.6	11	2	US-07-737-371E-16	Sequence 16, Appl
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75	43	60.6	11	2	US-07-737-371E-18	Sequence 18, Appl
76	43	60.6	11	2	US-07-737-371E-55	Sequence 55, Appl
77	43	60.6	11	2	US-07-737-371E-61	Sequence 61, Appl
78	43	60.6	11	2	US-07-737-371E-63	Sequence 63, Appl
79	43	60.6	11	2	US-07-737-371E-64	Sequence 64, Appl
80	43	60.6	11	2	US-07-737-371E-66	Sequence 66, Appl
81	43	60.6	11	2	US-08-747-137-34	Sequence 34, Appl
82	43	60.6	11	4	US-08-505-250-34	Sequence 34, Appl
83	43	60.6	902	1	US-08-701-846-2	Sequence 2, Appli
84	42	59.2	11	1	US-08-428-488-15	Sequence 15, Appl
85	42	59.2	11	2	US-07-737-371E-15	Sequence 15, Appl
86	42	59.2	11	2	US-07-737-371E-19	Sequence 19, Appl
87	42	59.2	11	2	US-07-737-371E-57	Sequence 29, Appl
88	41	57.7	8	2	US-07-737-371E-59	Sequence 57, Appl
89	41	57.7	9	2	US-07-737-371E-11	Sequence 11, Appl
90	41	57.7	11	2	US-07-737-371E-26	Sequence 26, Appl
91	41	57.7	11	2	US-07-737-371E-62	Sequence 62, Appl
92	41	57.7	11	2	US-07-737-371E-67	Sequence 67, Appl
93	41	57.7	17	3	US-08-890-157A-1	Sequence 1, Appli
94	40	56.3	11	2	US-07-737-371E-28	Sequence 28, Appl
95	40	56.3	104	4	US-09-060-726A-6	Sequence 6, Appli
96	40	56.3	411	4	US-09-236-080-2	Sequence 2, Appli
97	40	56.3	411	4	US-09-236-080-6	Sequence 6, Appli
98	40	56.3	1333	1	US-08-447-411-76	Sequence 76, Appl
99	40	56.3	1333	2	US-08-662-227-34	Sequence 34, Appl
100	40	56.3	1333	4	US-09-017-947-34	Sequence 34, Appl

101	39	54.9	11	1	US-08-462-413-2	Sequence 2, Appl	174	38	53.5	1528	1	US-08-326-117B-2	Sequence 2, Appl
102	39	54.9	11	2	US-07-737-371E-34	Sequence 34, Appl	175	38	53.5	1528	3	US-08-982-129-2	Sequence 2, Appl
103	39	54.9	299	5	PCT-US91-00899-6	Sequence 6, Appl	176	38	53.5	1721	3	US-08-700-651-5	Sequence 5, Appl
104	39	54.9	361	1	US-07-814-281-2	Sequence 2, Appl	177	38	53.5	1721	3	US-08-928-361B-6	Sequence 6, Appl
105	39	54.9	361	1	US-08-393-246-2	Sequence 2, Appl	178	38	53.5	1837	3	US-08-928-361B-5	Sequence 5, Appl
106	39	54.9	361	1	US-08-273-411-3	Sequence 3, Appl	179	37	52.1	11	2	US-07-737-371E-3	Sequence 3, Appl
107	39	54.9	361	1	US-08-525-058A-2	Sequence 2, Appl	180	37	52.1	11	2	US-07-737-371E-30	Sequence 30, Appl
108	39	54.9	361	2	US-08-696-731-2	Sequence 2, Appl	181	37	52.1	11	2	US-07-737-371E-32	Sequence 32, Appl
109	39	54.9	361	4	US-09-042-531-2	Sequence 2, Appl	182	37	52.1	22	1	US-08-468-514-11	Sequence 11, Appl
110	39	54.9	361	5	PCT-US91-00899-7	Sequence 7, Appl	183	37	52.1	272	1	US-08-690-095-1	Sequence 1, Appl
111	39	54.9	374	1	US-07-514-281-11	Sequence 11, Appl	184	37	52.1	272	3	US-09-113-789-1	Sequence 1, Appl
112	39	54.9	374	1	US-08-393-246-11	Sequence 11, Appl	185	37	52.1	365	3	US-09-028-934-35	Sequence 35, Appl
113	39	54.9	374	1	US-08-525-058A-11	Sequence 11, Appl	186	36	50.7	9	2	US-07-737-371E-60	Sequence 60, Appl
114	39	54.9	374	2	US-08-696-731-11	Sequence 11, Appl	187	36	50.7	11	2	US-07-737-371E-2	Sequence 2, Appl
115	39	54.9	374	4	US-09-042-531-11	Sequence 11, Appl	188	36	50.7	13	1	US-07-712-828B-5	Sequence 5, Appl
116	39	54.9	747	2	US-08-816-693A-51	Sequence 51, Appl	189	36	50.7	359	3	US-09-082-089-3	Sequence 3, Appl
117	39	54.9	747	3	US-08-885-291-53	Sequence 53, Appl	190	36	50.7	363	3	US-09-082-089-5	Sequence 5, Appl
118	39	54.9	747	4	US-09-496-672-51	Sequence 51, Appl	191	36	50.7	372	3	US-09-082-089-2	Sequence 2, Appl
119	39	54.9	816	2	US-08-785-310A-8	Sequence 8, Appl	192	36	50.7	611	2	US-08-677-049-2	Sequence 2, Appl
120	39	54.9	816	2	US-08-816-693A-53	Sequence 53, Appl							
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122	39	54.9	816	4	US-09-496-672-53	Sequence 53, Appl							
123	39	54.9	824	2	US-08-785-310A-7	Sequence 7, Appl							
124	39	54.9	824	2	US-08-816-693A-52	Sequence 52, Appl							
125	39	54.9	824	3	US-08-885-291-52	Sequence 52, Appl							
126	39	54.9	824	4	US-09-496-672-52	Sequence 52, Appl							
127	39	54.9	846	3	US-08-885-291-55	Sequence 55, Appl							
128	39	54.9	846	3	US-09-107-847-2	Sequence 2, Appl							
129	39	54.9	846	4	US-09-496-672-55	Sequence 55, Appl							
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131	39	54.9	855	3	US-08-885-291-2	Sequence 2, Appl							
132	39	54.9	855	4	US-09-496-672-2	Sequence 2, Appl							
133	38	53.5	6	6	5441935-7	Patent No. 5441935							
134	38	53.5	11	2	US-07-737-371E-54	Sequence 54, Appl							
135	38	53.5	91	3	US-08-700-651-14	Sequence 14, Appl							
136	38	53.5	91	3	US-08-928-361B-19	Sequence 19, Appl							
137	38	53.5	113	1	US-08-326-117B-8	Sequence 8, Appl							
138	38	53.5	113	3	US-08-982-129-8	Sequence 8, Appl							
139	38	53.5	124	3	US-08-700-651-11	Sequence 11, Appl							
140	38	53.5	124	3	US-08-928-361B-16	Sequence 16, Appl							
141	38	53.5	128	3	US-08-700-651-7	Sequence 7, Appl							
142	38	53.5	128	3	US-08-928-361B-12	Sequence 12, Appl							
143	38	53.5	130	3	US-08-700-651-8	Sequence 8, Appl							
144	38	53.5	130	3	US-08-700-651-9	Sequence 9, Appl							
145	38	53.5	130	3	US-08-928-361B-13	Sequence 13, Appl							
146	38	53.5	130	3	US-08-928-361B-14	Sequence 14, Appl							
147	38	53.5	138	3	US-08-700-651-10	Sequence 10, Appl							
148	38	53.5	138	3	US-08-928-361B-15	Sequence 15, Appl							
149	38	53.5	150	3	US-08-928-361B-18	Sequence 18, Appl							
150	38	53.5	159	3	US-08-928-361B-9	Sequence 9, Appl							
151	38	53.5	159	3	US-08-928-361B-28	Sequence 28, Appl							
152	38	53.5	162	3	US-08-700-651-13	Sequence 13, Appl							
153	38	53.5	175	3	US-08-700-651-12	Sequence 12, Appl							
154	38	53.5	175	3	US-08-928-361B-17	Sequence 17, Appl							
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156	38	53.5	249	3	US-08-928-361B-20	Sequence 20, Appl							
157	38	53.5	270	2	US-09-055-095-4	Sequence 4, Appl							
158	38	53.5	270	2	US-08-809-494A-2	Sequence 2, Appl							
159	38	53.5	270	4	US-09-352-302-2	Sequence 2, Appl							
160	38	53.5	273	2	US-09-055-095-3	Sequence 3, Appl							
161	38	53.5	273	2	US-08-809-494A-4	Sequence 4, Appl							
162	38	53.5	273	4	US-08-809-494A-6	Sequence 6, Appl							
163	38	53.5	273	4	US-09-352-302-4	Sequence 4, Appl							
164	38	53.5	273	4	US-09-352-302-6	Sequence 6, Appl							
165	38	53.5	357	5	PCT-US91-00899-14	Sequence 14, Appl							
166	38	53.5	405	1	US-07-514-281-8	Sequence 8, Appl							
167	38	53.5	405	1	US-08-393-246-8	Sequence 8, Appl							
168	38	53.5	405	1	US-08-525-058A-8	Sequence 8, Appl							
169	38	53.5	405	2	US-08-483-151-4	Sequence 4, Appl							
170	38	53.5	405	2	US-08-696-731-8	Sequence 8, Appl							
171	38	53.5	405	4	US-09-042-531-8	Sequence 8, Appl							
172	38	53.5	1184	2	US-08-518-914-1	Sequence 1, Appl							
173	38	53.5	1184	3	US-08-996-083-3	Sequence 3, Appl							

ALIGNMENTS

RESULT 1

5441935-5

Patent No. 5441935

APPLICANT: Rozenqurt, Enrique; Zachary, Ian; Woll, Penella

TITLE OF INVENTION: ROWTH FACTOR RECEPTORS

NUMBER OF SEQUENCES:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/939,587

FILING DATE: 03-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 814,064

FILING DATE: 23-DEC-1991

APPLICATION NUMBER: 411,536

FILING DATE: 29-NOV-1989

SEQ ID NO: 5

LENGTH: 11

5441935-5

Query Match 100.0%; Score 71; DB 6; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.6e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11

Db 1 RPKPQQWFWM 11

RESULT 2

5441935-2

Patent No. 5441935

APPLICANT: Rozenqurt, Enrique; Zachary, Ian; Woll, Penella

TITLE OF INVENTION: ROWTH FACTOR RECEPTORS

NUMBER OF SEQUENCES:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/939,587

FILING DATE: 03-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 814,064

FILING DATE: 23-DEC-1991

APPLICATION NUMBER: 411,536

FILING DATE: 29-NOV-1989

SEQ ID NO: 2

LENGTH: 11

5441935-2

Query Match 95.8%; Score 68; DB 6; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.0001;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RPKPQQFWLL 11

RESULT 3
5441935-3
; Patent No. 5441935
; APPLICANT: Rozenqurt, Enrique; Zachary, Ian; Woll, Penella
; TITLE OF INVENTION: ROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,587
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 814,064
; FILING DATE: 23-DEC-1991
; APPLICATION NUMBER: 411,536
; FILING DATE: 29-NOV-1989
; SEQ ID NO: 3:
; LENGTH: 11
5441935-3

Query Match 85.9%; Score 61; DB 6; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0012;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFWLM 11
|||||

Db 1 RPKPQQFWLM 11

RESULT 4
5441935-10
; Patent No. 5441935
; APPLICANT: Rozenqurt, Enrique; Zachary, Ian; Woll, Penella
; TITLE OF INVENTION: ROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,587
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 814,064
; FILING DATE: 23-DEC-1991
; APPLICATION NUMBER: 411,536
; FILING DATE: 29-NOV-1989
; SEQ ID NO: 10:
; LENGTH: 8
5441935-10

Query Match 76.1%; Score 54; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQQFWLM 11
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Db 1 PQQFWLM 8

RESULT 5
US-07-737-371E-12
; Sequence 12, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-12

Query Match 69.0%; Score 49; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.072;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQFWLM 11
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Db 1 RPKPQYFGLM 11

RESULT 6
5441935-6
; Patent No. 5441935
; APPLICANT: Rozenqurt, Enrique; Zachary, Ian; Woll, Penella
; TITLE OF INVENTION: ROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,587
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 814,064
; FILING DATE: 23-DEC-1991
; APPLICATION NUMBER: 411,536
; FILING DATE: 29-NOV-1989
; SEQ ID NO: 6:
; LENGTH: 8
5441935-6

Query Match 67.6%; Score 48; DB 6; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQFWLM 11
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Db 1 PQQFWLM 8

RESULT 7

US-07-934-553-1
; Sequence 1, Application US/07934553
; Patent No. 5314690
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, ROY
; APPLICANT: HARRIS, KATHLEEN E
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE
; TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TILTON, FALLON, LUNGWUS & CHESTNUT
; STREET: 100 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/07/934,553
; APPLICATION DATE: 19920821
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705,071
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTRESS, SUSAN B
; REGISTRATION NUMBER: 31,327
; REFERENCE/DOCKET NUMBER: NU-90333CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/456-8000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-07-934-553-1

Query Match 67.68; Score 48; DB 1; Length 11;
Best Local Similarity 81.88; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
1111111111
Db 1 RPKPQQFFGLM 11

RESULT 8
US-08-184-935-12
; Sequence 12, Application US/08184935
; Patent No. 5476770
; GENERAL INFORMATION:
; APPLICANT: PRADELLES, PHILIPPE
; TITLE OF INVENTION: IMMUNOMETRIC DETERMINATION OF AN ANTIGEN
; TITLE OF INVENTION: OR HAPTEN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,935
FILING DATE: 24-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5476770man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 846-286-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: /note= "C-terminal amide"
US-08-184-935-12

Query Match 67.68; Score 48; DB 1; Length 11;
Best Local Similarity 81.88; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
1111111111
Db 1 RPKPQQFFGLM 11

RESULT 9
US-08-269-288-2
; Sequence 2, Application US/08269288
; Patent No. 5491140
; GENERAL INFORMATION:
; APPLICANT: Bruns, Robert F.
; APPLICANT: Gehlert, Donald R.
; APPLICANT: Howbert, James J.
; APPLICANT: Lunn, William H.W.
; TITLE OF INVENTION: NAPHTHYL TACHYKININ RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/1104
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/269,288
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9715
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-269-288-2

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQWFWM 11
|||||:||
Db 1 RPKPOQFFGLM 11

RESULT 10

US-08-338-484-1
; Sequence 1, Application US/08338484
; Patent No. 5494926

; GENERAL INFORMATION:

; APPLICANT: Owens, Andrew P.
; APPLICANT: Teall, Martin R.
; APPLICANT: Williams, Brian J.
; TITLE OF INVENTION: 2/3-(HETEROCYCLIC ALKYL
; TITLE OF INVENTION: AMINO)-1-(SUBSTITUTED PHENYL-METHOXY)-ETHANES/PROPANES AS
; TITLE OF INVENTION: TACHYKININ RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Robert J. No. 5494926th
; STREET: 126 E. Lincoln Ave., P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338.484
FILING DATE: 18-NOV-1994
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: No. 5494926th, Robert J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1158
TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-7262

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-338-484-1

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQWFWM 11
|||||:||
Db 1 RPKPOQFFGLM 11

RESULT 11

US-08-175-432-1
; Sequence 1, Application US/08175432

; Patent No. 5495047
; GENERAL INFORMATION:
; APPLICANT: Saari, Walfred S. B.
; APPLICANT: Van Niel, Monique B.
; APPLICANT: Williams, Brian J.
; TITLE OF INVENTION: FUSED TRICYCLIC COMPOUNDS,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR USE
; TITLE OF INVENTION: IN THERAPY
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NORTH, ROBERT J.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175.432
FILING DATE: 07-JAN-1994
CLASSIFICATION: 560
ATTORNEY/AGENT INFORMATION:
NAME: No. 5495047th, Robert J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1152Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-175-432-1

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQWFWM 11
|||||:||
Db 1 RPKPOQFFGLM 11

RESULT 12

US-08-225-474-1
; Sequence 1, Application US/08225474
; Patent No. 5360915

; GENERAL INFORMATION:

; APPLICANT: Patterson, Roy
; APPLICANT: Harris, Kathleen E.
; TITLE OF INVENTION: Method and Composition for Treating
; TITLE OF INVENTION: Ige Mediated Allergies
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 S. Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,474
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,553
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705,071
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tilton, Timothy L.
REGISTRATION NUMBER: 16,926
REFERENCE/DOCKET NUMBER: NU 9033-CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)-456-8000
TELEFAX: (312)-456-7776
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-225-474-1

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
|||||:|
Db 1 RPKPQQFFGLM 11

RESULT 13
US-08-391-910-2
Sequence 2, Application US/08391910
Patent No. 5563133
GENERAL INFORMATION:
APPLICANT: Hipskind, Philip A.
TITLE OF INVENTION: HEXAMETHYLENIMINYL TACHYKININ RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,910
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9979
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-391-910-2

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
|||||:|
Db 1 RPKPQQFFGLM 11

RESULT 14
US-08-418-994-2
Sequence 2, Application US/08418994
Patent No. 5565568
GENERAL INFORMATION:
APPLICANT: Cho, Sung-Yong S.
APPLICANT: Hipskind, Philip A.
APPLICANT: Howbert, J. J.
APPLICANT: Muehl, Brian S.
APPLICANT: Nixon, James A.
TITLE OF INVENTION: 2-ACYLAMINOPROPANAMIDES AS TACHYKININ
TITLE OF INVENTION: RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,994
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-8252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-418-994-2

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
|||||:|
Db 1 RPKPQQFFGLM 11

RESULT 15
US-08-480-505-3

; Sequence 3, Application US/08480505
; Patent No. 5601821
; GENERAL INFORMATION:
; APPLICANT: STANNORTH, DENIS R
; APPLICANT: LEWIN, IAN V
; APPLICANT: NAYYAR, SARITA
; APPLICANT: JONES, VALERIE
; TITLE OF INVENTION: IMMUNOACTIVE PEPTIDES AND ANTIBODIES AND
; TITLE OF INVENTION: THEIR USE IN ANTI-ALLERGY TREATMENT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 14TH FLOOR, 2200 CLARENDON BOULEVARD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-3360
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,505
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/08/102,692
; FILING DATE:
; APPLICATION NUMBER: US 07/776,380
; FILING DATE: 26-NOV-1991
; APPLICATION NUMBER: GB 8913737.6
; FILING DATE: 15-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB90/00926
; FILING DATE: 15-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 875-0400
; TELEFAX: (703) 525-3468
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Neuropeptide "Substance P"
; US-08-480-505-3

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQWFWM 11
DB 1 RPKPOQFFGLM 11

RESULT 16
US-08-391-814-2
; Sequence 2, Application US/08391814
; Patent No. 5607947
; GENERAL INFORMATION:
; APPLICANT: Hipskind, Phillip A.
; TITLE OF INVENTION: PYRROLIDINYL TACHYKININ RECEPTOR

; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,814
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0736
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-391-814-2

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQWFWM 11
DB 1 RPKPOQFFGLM 11

RESULT 17
US-08-167-870-1
; Sequence 1, Application US/08167870
; Patent No. 5610183
; GENERAL INFORMATION:
; APPLICANT: OWENS, ANDREW P.
; APPLICANT: WILLIAMS, BRIAN J.
; TITLE OF INVENTION: AROMATIC COMPOUNDS, COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM AND THEIR USE IN THERAPY
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBERT J. NORTH
; STREET: P. O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,870
; FILING DATE: 17-DEC-1993
; CLASSIFICATION: 544
; ATTORNEY/AGENT INFORMATION:
; NAME: NORTH, ROBERT J.
; REGISTRATION NUMBER: 27,366
; REFERENCE/DOCKET NUMBER: T-1151Y

TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-7262
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-167-870-1

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:| |
Db 1 RPKPQQFFGLM 11

RESULT 18
US-08-255-272-6
Sequence 6, Application US/08255272
Patent No. 5627268
GENERAL INFORMATION:
APPLICANT: Kumar, Ramesh
APPLICANT: Sharma, Ajay
APPLICANT: Khoury-Christianson, Anastasia
APPLICANT: M.
TITLE OF INVENTION: Production of Therapeutic Peptides in
TITLE OF INVENTION: Transgenic Animals as a Fusion with Hemoglobin
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,272
FILING DATE:
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 435
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 6794-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-255-272-6

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:| |
Db 1 RPKPQQFFGLM 11

RESULT 19
US-08-441-591-6
Sequence 6, Application US/08441591
Patent No. 5637682
GENERAL INFORMATION:
APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.
TITLE OF INVENTION: HIGH-AFFINITY
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
TITLE OF INVENTION: TO THE TACHYKININ
TITLE OF INVENTION: SUBSTANCE P
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,591
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,362
FILING DATE: 9-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21/C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-441-591-6

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:| |

Db 1 RPKPQQFFGLM 11

RESULT 20

US-08-303-362A-6

; Sequence 6, Application US/08303362A

; Patent No. 5648214

; GENERAL INFORMATION:

; APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.

; TITLE OF INVENTION: HIGH-AFFINITY

; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS

; TITLE OF INVENTION: TO THE TACHYKININ

; TITLE OF INVENTION: SUBSTANCE P

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Swanson & Bratschun, L.L.C.

; STREET: 8400 E. Prentice Avenue, Suite 200

; CITY: Englewood

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/303,362A

; FILING DATE: 9-SEPTEMBER-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/714,131

; FILING DATE: 10-JUNE-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/931,473

; FILING DATE: 17-AUGUST-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/117,991

; FILING DATE: 8-SEPTEMBER 1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/536,428

; FILING DATE: 11-JUNE-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/964,624

; FILING DATE: 21-OCTOBER-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Barry J. Swanson

; REGISTRATION NUMBER: 33,215

; REFERENCE/DOCKET NUMBER: NEX21

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 793-3333

; TELEFAX: (303) 793-3433

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-303-362A-6

Query Match

Best Local Similarity 67.6%; Score 48; DB 1; Length 11;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11

Db 1 RPKPQQFFGLM 11

RESULT 21

US-08-462-859A-1

; Sequence 1, Application US/08462859A

; Patent No. 5652092

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vitek, M. P.

; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: One Cyanamid Plaza

; CITY: Wayne

; STATE: New Jersey

; COUNTRY: United States

; ZIP: 07470-8426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,859A

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Barnhard, Elizabeth M.

; REGISTRATION NUMBER: 31,088

; REFERENCE/DOCKET NUMBER: 31,844-04

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (201)831-3246

; TELEFAX: (201)831-3305

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-462-859A-1

Query Match 67.6%; Score 48; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.1;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11

Db 1 RPKPQQFFGLM 11

RESULT 22

US-08-123-659A-1

; Sequence 1, Application US/08123659A

; Patent No. 5656477

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vitek, M. P.

; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Anne Rosenblum

; STREET: 163 Delaware Avenue, Suite 212

; CITY: Delmar

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 12054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.
; REGISTRATION NUMBER: 30,419
; REFERENCE/DOCKET NUMBER: 31,844-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (518)475-0611
; TELEFAX: (518)475-0619
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-123-659A-1

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|
Db 1 RPKPQQFFGLM 11

RESULT 23
US-08-462-415-2
; Sequence 2, Application US/08462415
; Patent No. 5670499
; GENERAL INFORMATION:
; APPLICANT: Cho, Sung Y.
; APPLICANT: Crowell, Thomas A.
; APPLICANT: Gitter, Bruce D.
; APPLICANT: Hipskind, Philip A.
; APPLICANT: Howbert, Jeffrey J.
; APPLICANT: Krushinski, Joseph H.
; APPLICANT: Lobb, Karen L.
; APPLICANT: Muehl, Brian S.
; APPLICANT: Nixon, James A.
; TITLE OF INVENTION: HETEROCYCLIC TACHYKININ RECEPTOR
; TITLE OF INVENTION: ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Division
; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,415
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X8849B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-0756
; TELEFAX: 317-276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-462-415-2

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|
Db 1 RPKPQQFFGLM 11

RESULT 24
US-08-463-874-2
; Sequence 2, Application US/08463874
; Patent No. 5684033
; GENERAL INFORMATION:
; APPLICANT: Cho, Sung Y.
; APPLICANT: Crowell, Thomas A.
; APPLICANT: Gitter, Bruce D.
; APPLICANT: Hipskind, Philip A.
; APPLICANT: Howbert, Jeffrey J.
; APPLICANT: Krushinski, Joseph H.
; APPLICANT: Lobb, Karen L.
; APPLICANT: Muehl, Brian S.
; APPLICANT: Nixon, James A.
; TITLE OF INVENTION: NON-PEPTIDE TACHYKININ RECEPTOR
; TITLE OF INVENTION: ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Division
; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,874
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X8849C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-0756
; TELEFAX: 317-276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-463-874-2

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|
Db 1 RPKPQQFFGLM 11


```
RESULT 25
US-08-464-247A-1
; Sequence 1, Application US/08464247A
; Patent No. 5693478
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,247A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-247A-1

Query Match 67.68; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
|11111111
Db 1 RPKPQQFFGLM 11

RESULT 26
US-08-464-248A-1
; Sequence 1, Application US/08464248A
; Patent No. 5703209
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,135
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/955,380
; FILING DATE: 01-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jarkovsky, Issac
; REGISTRATION NUMBER: 22,713
; REFERENCE/DOCKET NUMBER: 7754-003-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
```

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,248A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-248A-1

Query Match 67.68; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
|11111111
Db 1 RPKPQQFFGLM 11

RESULT 27
US-08-444-135-2
; Sequence 2, Application US/08444135
; Patent No. 5723575
; GENERAL INFORMATION:
; APPLICANT: Gilson, Chaim
; APPLICANT: Zelinger, Zvi
; TITLE OF INVENTION: Backbone Cyclic Peptides, Processes For
; TITLE OF INVENTION: Their Preparation and Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Them
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,135
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/955,380
; FILING DATE: 01-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jarkovsky, Issac
; REGISTRATION NUMBER: 22,713
; REFERENCE/DOCKET NUMBER: 7754-003-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
```

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-444-135-2

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RPKPQQWFWM 11
Db 1 RPKPQQFFGLM 11

RESULT 28
US-08-318-391-2
Sequence 2, Application US/08318391
Patent No. 5744482
GENERAL INFORMATION:
APPLICANT: Cohen, Marlene L.
APPLICANT: Johnson, Kirk W.
APPLICANT: Phebus, Lee A.
TITLE OF INVENTION: USE OF A SEROTONIN AGONIST IN
COMBINATION WITH A TACHIKININ RECEPTOR ANTAGONIST IN THE
TREATMENT OR PREVENTION OF MIGRAINE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,391
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9664
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-318-391-2

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RPKPQQWFWM 11
Db 1 RPKPQQFFGLM 11

RESULT 29
US-08-796-598-11
Sequence 11, Application US/08796598
Patent No. 5827659
GENERAL INFORMATION:
APPLICANT: PATTERSON, DALE H.
APPLICANT: TARR, GEORGE E.
TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
POLYMERS WITH A STATISTICAL CERTAINTY USING MASS SPECTROMETRY.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administrator - Testa, Hurwitz &
ADDRESSEE: Thibeault
STREET: High Street Tower, 125 High Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,598
FILING DATE: 07-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,055
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FLYNN Esq., Kerry A.
REGISTRATION NUMBER: 33,693
REFERENCE/DOCKET NUMBER: SYP-115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-796-598-11

Query Match 67.6%; Score 48; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RPKPQQWFWM 11
Db 1 RPKPQQFFGLM 11

RESULT 30
US-08-447-175A-11
Sequence 11, Application US/08447175A
Patent No. 5869240
GENERAL INFORMATION:
APPLICANT: PATTERSON, DALE H.
TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
POLYMERS WITH A STATISTICAL CERTAINTY USING MASS
SPECTROMETRY.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administrator - Testa, Hurwitz &
ADDRESSEE: Thibeault, LLP
STREET: High Street Tower, 125 High Street
CITY: Boston
STATE: MA
COUNTRY: USA

Query Match 67.6%; Score 48; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RPKPQQWFWM 11
Db 1 RPKPQQFFGLM 11

ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,175A
FILING DATE: 19-MAY-1995
CLASSIFICATION: 422
ATTORNEY/AGENT INFORMATION:
NAME: RAUSCHENBACH, Kurt
REGISTRATION NUMBER: 40,137
REFERENCE/DOCKET NUMBER: SYP-114
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-447-175A-11

Query Match 67.6%; Score 48; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RPKPQQQFWLM 11
Db 1 RPKPQQQFGLM 11

RESULT 31
US-07-737-371E-21
Sequence 21, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 9...9
OTHER INFORMATION: where Xaa at position 9 is D-Ala
US-07-737-371E-21

Query Match 67.6%; Score 48; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RPKPQQQFWLM 11
Db 1 RPKPQQQFGLM 11

RESULT 32
US-07-737-371E-22
Sequence 22, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 9...9
OTHER INFORMATION: where Xaa at position 9 is Sar
US-07-737-371E-22

Query Match 67.6%; Score 48; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RPKPQQQFWLM 11

Db 1 RPKPQQFFXLM 11
|||||:||||

RESULT 33

US-07-737-371E-24
; Sequence 24, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 9...9
; OTHER INFORMATION: where Xaa at position 9 is D-Pro

US-07-737-371E-24

Query Match 67.6%; Score 48; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPQQFFXLM 11
|||||:||||
Db 1 RPKPQQFFXLM 11

RESULT 34

US-07-737-371E-27
; Sequence 27, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 9...9
; OTHER INFORMATION: where Xaa at position 9 is Me-Gly

US-07-737-371E-27

Query Match 67.6%; Score 48; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPQQFFXLM 11
|||||:||||
Db 1 RPKPQQFFXLM 11

RESULT 35

US-07-737-371E-65
; Sequence 65, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990

CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 9...9
OTHER INFORMATION: where Xaa at position 9 is Me-Gly
US-07-737-371E-27

Query Match 67.6%; Score 48; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQFFXLM 11
|||||:||||
Db 1 RPKPQQFFXLM 11

RESULT 35

US-07-737-371E-65
; Sequence 65, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990

ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 9...9
OTHER INFORMATION: where Xaa at position 9 is Me-Gly
US-07-737-371E-65

Query Match 67.6%; Score 48; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQQFWFLM 11
| | | | | | | | | |
Db 1 RPKPQQQFFXLM 11

RESULT 36

US-07-737-371E-77
Sequence 77, Application US/07737371E
Patent No. 5876948

GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

COMPUTER READABLE FORM:
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-77

Query Match 67.6%; Score 48; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQQFWFLM 11
| | | | | | | | | |
Db 1 RPKPQQQFFGLM 11

RESULT 37

US-08-848-766A-1
Sequence 1, Application US/08848766A
Patent No. 5932551

GENERAL INFORMATION:
APPLICANT: Caldwell, Charles G.
APPLICANT: Chapman, Kevin T.
APPLICANT: Durette, Philippe L.
APPLICANT: Esser, Craig K.
APPLICANT: Hagmann, William K.
APPLICANT: Kopka, Ihor E.
APPLICANT: Polo, Scott A.
APPLICANT: Sahoo, Soumya P.
TITLE OF INVENTION: SUBSTITUTED N-CARBOXYALKYLPEPTIDYL
DERIVATIVES AS ANTIDEGENERATIVE ACTIVE AGENTS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,766A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/873,905
FILING DATE: 24-APR-1992

ATTORNEY/AGENT INFORMATION:
NAME: Panzer, Curtis C
REGISTRATION NUMBER: 33,752
REFERENCE/DOCKET NUMBER: 183551A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3199
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-848-766A-1

Query Match 67.6%; Score 48; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQQFWFLM 11
| | | | | | | | | |
Db 1 RPKPQQQFFGLM 11

RESULT 38

US-08-927-128-17
; Sequence 17, Application US/08927128
; Patent No. 6127150
; GENERAL INFORMATION:
; APPLICANT: Coolidge, Thomas
; APPLICANT: Wagner, Fred
; APPLICANT: ven Heeke, Gino
; APPLICANT: Schuster, Sheldon
; APPLICANT: Stout, Jay
; APPLICANT: Wylie, Dwane
; TITLE OF INVENTION: PURIFICATION DIRECTED CLOSING OF PEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 6127150west Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,128
; FILING DATE: 05-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/680,004
; FILING DATE: 15-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.2USD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/332-5300
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-927-128-17

Query Match 67.6%; Score 48; DB 3; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 RPKPQQWFWM 11
|||||:11
Db 1 RPKPQQFFGLM 11

RESULT 39
US-08-257-966-2
; Sequence 2, Application US/08257966
; Patent No. 6175013
; GENERAL INFORMATION:
; APPLICANT: Hipskind, Philip A.
; APPLICANT: Howbert, James J.
; APPLICANT: Muehl, Brian S.
; TITLE OF INVENTION: IMIDAZOLINYL TACHYKININ RECEPTOR
; ANTAGONISTS
; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/1104
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,966
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9197
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-257-966-2

Query Match 67.6%; Score 48; DB 4; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 RPKPQQWFWM 11
|||||:11
Db 1 RPKPQQFFGLM 11

RESULT 40
PCT-US95-05600-23
; Sequence 23, Application PC/TUS9505600
; GENERAL INFORMATION:
; APPLICANT: GOLD, LARRY
; APPLICANT: NIEUWLANDT, DAN
; APPLICANT: WECKER, MATTHEW
; APPLICANT: SCHNEIDER, DANIEL J.
; APPLICANT: FEIGON, JULI
; APPLICANT: ALLEN, PATRICK
; APPLICANT: SULLENGER, BRUCE A.
; APPLICANT: DOUDNA, JENNIFER, A.
; TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF
; INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE
; P. HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
; MEDIUM TYPE: storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05600

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,863
; FILING DATE: 06-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/248,632
; FILING DATE: 24-MAY-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,362
; FILING DATE: 09-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/361,795
; FILING DATE: 21-DECEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 08-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX17/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US95-05600-23

Query Match 67.6%; Score 48; DB 5; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11
Db 1 RPKPQOWFWLM 11

RESULT 41
5441935-1
; Patent No. 5441935
; APPLICANT: Rozengurt, Enrique; Zachary, Ian; Woll, Penella
; TITLE OF INVENTION: ROTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,587
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 814,064
; FILING DATE: 23-DEC-1991
; APPLICATION NUMBER: 411,536
; FILING DATE: 29-NOV-1989
; SEQ ID NO: 1;

; LENGTH: 11
5441935-1

Query Match 67.6%; Score 48; DB 6; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11
Db 1 RPKPQOWFWLM 11

RESULT 42
5441935-8
; Patent No. 5441935
; APPLICANT: Rozengurt, Enrique; Zachary, Ian; Woll, Penella
; TITLE OF INVENTION: ROTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,587
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 814,064
; FILING DATE: 23-DEC-1991
; APPLICATION NUMBER: 411,536
; FILING DATE: 29-NOV-1989
; SEQ ID NO: 8;
; LENGTH: 11
5441935-8

Query Match 67.6%; Score 48; DB 6; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11
Db 1 RPKPQOWFWLM 11

RESULT 43
US-08-441-591-7
; Sequence 7, Application US/08441591
; Patent No. 5637682
; GENERAL INFORMATION:
; APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.
; TITLE OF INVENTION: HIGH-AFFINITY
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
; TITLE OF INVENTION: TO THE TACHYKININ
; TITLE OF INVENTION: SUBSTANCE P
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,591
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,362
; FILING DATE: 9-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131

;
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX21/C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-441-591-7

Query Match 67.6%; Score 48; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.11;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Caps 0;

QY 1 RPKPQOWFWLM 11
Db 1 RPKPQOWFWLM 11

RESULT 44
US-08-303-362A-7
; Sequence 7, Application US/08303362A
; Patent No. 5648214
; GENERAL INFORMATION:
; APPLICANT: NIEWLANDT, D., GOLD, L. AND WECKER, M.
; TITLE OF INVENTION: HIGH-AFFINITY
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
; TITLE OF INVENTION: TO THE TACHYKININ
; TITLE OF INVENTION: SUBSTANCE P
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,362A
; FILING DATE: 9-SEPTEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991

;
; FILING DATE: 8-SEPTEMBER 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-303-362A-7

Query Match 67.6%; Score 48; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.11;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Caps 0;

QY 1 RPKPQOWFWLM 11
Db 1 RPKPQOWFWLM 11

RESULT 45
US-08-505-250-27
; Sequence 27, Application US/08505250
; Patent No. 6183983
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kokichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Sakagami, Makoto
; APPLICANT: Taniguchi, Makoto
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
; FILE REFERENCE: 110-511
; CURRENT APPLICATION NUMBER: US/08/505,250
; CURRENT FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: PCT/JP95/00298
; EARLIER FILING DATE: 1995-02-27
; EARLIER APPLICATION NUMBER: JP 198187/94
; EARLIER FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
; US-08-505-250-27

Query Match 67.6%; Score 48; DB 4; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.11;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Caps 0;

QY 1 RPKPQOWFWLM 11
Db 2 RPKPQOWFWLM 12

RESULT 46

US-08-505-250-53
; Sequence 53, Application US/08505250
; Patent No. 6183983
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kokichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Sakagami, Masahiro
; APPLICANT: Taniguchi, Makoto
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
; FILE REFERENCE: 110-511
; CURRENT APPLICATION NUMBER: US/08/505,250
; EARLIER FILING DATE: 1995-11-29
; EARLIER FILING DATE: 1995-02-27
; EARLIER APPLICATION NUMBER: JP 198187/94
; EARLIER FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-08-505-250-53

Query Match 67.6%; Score 48; DB 4; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.11;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
Db 2 RPKPQQFFGLM 12

RESULT 47
PCT-US92-06532-4
; Sequence 4, Application PC/TUS9206532
; GENERAL INFORMATION:
; APPLICANT: Krause, James E.
; TITLE OF INVENTION: Human Substance P Receptor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SD
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: U.S.A
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06532
; FILING DATE: 19920805
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(776)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 12
; OTHER INFORMATION: /label= amide
PCT-US92-06532-4

Query Match 67.6%; Score 48; DB 5; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.11;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
Db 2 RPKPQQFFGLM 12

RESULT 48
PCT-US95-05600-24
; Sequence 24, Application PC/TUS9505600
; GENERAL INFORMATION:
; APPLICANT: GOLD, LARRY
; APPLICANT: NIEUWLANDT, DAN
; APPLICANT: WECKER, MATTHEW
; APPLICANT: SCHNEIDER, DANIEL J.
; APPLICANT: FEIGON, JULI
; APPLICANT: ALLEN, PATRICK
; APPLICANT: SULLENGER, BRUCE A.
; APPLICANT: DOUDNA, JENNIFER, A.
; TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF
; TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE
; TITLE OF INVENTION: P. HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
; MEDIUM TYPE: storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05600
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,863
; FILING DATE: 06-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/248,632
; FILING DATE: 24-MAY-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,362
; FILING DATE: 09-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/361,795
; FILING DATE: 21-DECEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 08-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX17/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-05600-24

Query Match 67.6%; Score 48; DB 5; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.11;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|
DB 1 RPKPQQFFGLM 11

RESULT 49

US-08-890-157A-2
Sequence 2, Application US/08890157A
Patent No. 6063758
GENERAL INFORMATION:
APPLICANT: Douglas A. Lappi and Ronald G. Wiley
TITLE OF INVENTION: Substance P-Saporin (SP-SAP) Conjugates And
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,157A
FILING DATE: 09-JUL-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Phillips, Peter J.
REGISTRATION NUMBER: 29,691
REFERENCE/DOCKET NUMBER: 53984
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)331-0526
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-157A-2

Query Match 67.6%; Score 48; DB 3; Length 20;
Best Local Similarity 81.8%; Pred. No. 0.18;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|
DB 10 RPKPQQFFGLM 20

RESULT 50

US-08-505-250-50
Sequence 50, Application US/08505250
Patent No. 6183983
GENERAL INFORMATION:
APPLICANT: Sato, Haruya
APPLICANT: Yamamoto, Keiji
APPLICANT: Suzuki, Kokichi
APPLICANT: Ikeda, Masahiro
APPLICANT: Sakagami, Masahiro
APPLICANT: Taniguchi, Makoto
TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
FILE REFERENCE: 110-511
CURRENT APPLICATION NUMBER: US/08/505,250
CURRENT FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: PCT/JP95/00298
EARLIER FILING DATE: 1995-02-27
EARLIER APPLICATION NUMBER: JP 198187/94
EARLIER FILING DATE: 1994-08-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50
LENGTH: 20
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-08-505-250-50

Query Match 67.6%; Score 48; DB 4; Length 20;
Best Local Similarity 81.8%; Pred. No. 0.18;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|
DB 2 RPKPQQFFGLM 12

RESULT 51

5268359-5
Patent No. 5268359
APPLICANT: HARMAR, ANTHONY J.; PASCALL, JOHN; MCKEOWN, ANN
TITLE OF INVENTION: HUMAN TACHYKININS AND THEIR PRECURSOR
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/285,964
FILING DATE: 03-JUN-1987
SEQ ID NO: 51
LENGTH: 126
5268359-5

Query Match 67.6%; Score 48; DB 6; Length 126;
Best Local Similarity 81.8%; Pred. No. 1.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|
DB 58 RPKPQQFFGLM 68

RESULT 52

5268359-2

; APPLICANT: HARMAR, ANTHONY J.; PASCALL, JOHN; MCKEOWN, ANN
; TITLE OF INVENTION: HUMAN TACHYKININS AND THEIR PRECURSOR
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/285.964
; FILING DATE: 03-JUN-1987
; SEQ ID NO: 2:
; LENGTH: 130
5268359-2

Query Match 67.6%; Score 48; DB 6; Length 130;
Best Local Similarity 81.8%; Pred. No. 1.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQWFGLM 11

|||||: ||

Db 58 RPKPOQWFGLM 68

RESULT 53

US-08-462-859A-9

; Sequence 9, Application US/08462859A

; Patent No. 5652092

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vittek, M. P.

; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: One Cyanamid Plaza

; CITY: Wayne

; STATE: New Jersey

; COUNTRY: United States

; ZIP: 07470-8426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462.859A

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Barnhard, Elizabeth M.

; REGISTRATION NUMBER: 31,088

; REFERENCE/DOCKET NUMBER: 31,844-04

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (201)831-3246

; TELEFAX: (201)831-3305

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 487 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-462-859A-9

Query Match

Best Local Similarity 67.6%; Score 48; DB 1; Length 487;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQWFGLM 11

|||||: ||

Db 362 RPKPOQWFGLM 372

RESULT 54

US-08-123-659A-9

; Sequence 9, Application US/08123659A

; Patent No. 5656477

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vittek, M. P.

; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Anne Rosenblum

; STREET: 163 Delaware Avenue, Suite 212

; CITY: Delmar

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 12054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/123.659A

; FILING DATE: 20-SEP-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Rosenblum, Anne M.

; REGISTRATION NUMBER: 30,419

; REFERENCE/DOCKET NUMBER: 31,844-01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (518)475-0611

; TELEFAX: (518)475-0619

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 487 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-123-659A-9

Query Match

67.6%; Score 48; DB 1; Length 487;

Best Local Similarity 81.8%; Pred. No. 4.1;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQWFGLM 11

|||||: ||

Db 362 RPKPOQWFGLM 372

RESULT 55

US-08-464-247A-9

; Sequence 9, Application US/08464247A

; Patent No. 5693478

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vittek, M. P.

; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: One Campus Drive

; CITY: Parsippany

; STATE: New Jersey

; COUNTRY: United States

; ZIP: 07054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-9

Query Match 67.6%; Score 48; DB 1; Length 487;
Best Local Similarity 81.8%; Pred. No. 4.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|
Db 362 RPKPQQFFGLM 372

RESULT 56

US-08-464-248A-9
Sequence 9, Application US/08464248A
Patent No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-464-248A-9

Query Match 67.6%; Score 48; DB 1; Length 487;
Best Local Similarity 81.8%; Pred. No. 4.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|
Db 362 RPKPQQFFGLM 372

RESULT 57

US-08-462-859A-7
Sequence 7, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-7

Query Match 67.6%; Score 48; DB 1; Length 492;
Best Local Similarity 81.8%; Pred. No. 4.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|
Db 362 RPKPQQFFGLM 372

RESULT 58

US-08-123-659A-7
Sequence 7, Application US/08123659A
Patent No. 5656477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of

;; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
;; TITLE OF INVENTION: of B-Amyloid Peptide
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Anne Rosenblum
;; STREET: 163 Delaware Avenue, Suite 212
;; CITY: Delmar
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 12054
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA: US/08/123,659A
;; FILING DATE: 20-SEP-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rosenblum, Anne M.
;; REGISTRATION NUMBER: 30,419
;; REFERENCE/DOCKET NUMBER: 31,844-01
;; TELEPHONE: (518)475-0611
;; TELEFAX: (518)475-0619
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 492 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-123-659A-7

Query Match 67.6%; Score 48; DB 1; Length 492;
Best Local Similarity 81.8%; Pred. No. 4.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
Db 362 RPKPQQFFGLM 372

RESULT 59
US-08-464-247A-7
; Sequence 7, Application US/08464247A
; Patent No. 5693478
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.

;; REGISTRATION NUMBER: 31,088
;; REFERENCE/DOCKET NUMBER: 31,844-03
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201-683-2158
;; TELEFAX: 201-683-4117
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 492 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-464-247A-7

Query Match 67.6%; Score 48; DB 1; Length 492;
Best Local Similarity 81.8%; Pred. No. 4.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
Db 362 RPKPQQFFGLM 372

RESULT 60
US-08-464-248A-7
; Sequence 7, Application US/08464248A
; Patent No. 5703209
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 492 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-248A-7

Query Match 67.6%; Score 48; DB 1; Length 492;
Best Local Similarity 81.8%; Pred. No. 4.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
Db 362 RPKPQQFFGLM 372

```
RESULT 61
US-07-737-371E-20
; Sequence 20, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-20

Query Match 66.2%; Score 47; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.14;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 RPKPQQWFWM 11
Db 1 RPKPQQFFALM 11

RESULT 62
US-07-737-371E-17
; Sequence 17, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-17

Query Match 64.8%; Score 46; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
Db 1 RPKPQQMFGLM 11

RESULT 63
US-07-737-371E-23
; Sequence 23, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
```

; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-23

Query Match 64.8%; Score 45; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.2;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQWFWM 11
Db 1 RPKPQFFPLM 11

RESULT 64
US-08-346-849-7
; Sequence 7, Application US/08346849
; Patent No. 5670483
; GENERAL INFORMATION:
; APPLICANT: Zhang, Shuguang
; APPLICANT: Lockshin, Curtis
; APPLICANT: Rich, Alexander
; APPLICANT: Holmes, Todd
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,849
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008
; TELEPHONE: (617) 861-9540
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-346-849-7

Query Match 63.4%; Score 45; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQW 7
Db 1 RPKPQW 7

RESULT 65
US-08-293-284A-7
; Sequence 7, Application US/08293284A
; Patent No. 5955343
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd
; APPLICANT: Zhang, Shuguang
; APPLICANT: Rich, Alexander
; APPLICANT: DiPersio, C. Michael
; APPLICANT: Lockshin, Curtis
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,284A
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-293-284A-7

Query Match 63.4%; Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQW 7
Db 1 RPKPQW 7

RESULT 66
US-07-899-205-1
; Sequence 1, Application US/07899205
; Patent No. 5288730
; GENERAL INFORMATION:
; APPLICANT: Baker, Raymond
; APPLICANT: Teall, Martin R.
; APPLICANT: Swain, Christopher J.
; APPLICANT: Williams, Brian J.
; TITLE OF INVENTION: AZABICYCLIC COMPOUNDS PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS CONTAINING THEM AND THEIR USE IN THERAPY
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/899,205
FILING DATE: 19920616
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Polk, Manfred
REGISTRATION NUMBER: 27,102
REFERENCE/DOCKET NUMBER: T-1106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4285
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-899-205-1

Query Match 63.4%; Score 45; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.29;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
Db 1 RPKPQEFFGLM 11

RESULT 67
US-08-496-118-1
Sequence 1, Application US/08496118
Patent No. 5830854
GENERAL INFORMATION:
APPLICANT: Hargreaves, Richard J.
TITLE OF INVENTION: THERAPEUTIC USE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robert J. No. 5830854th
STREET: 126 E. Lincoln Avenue - P. O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,118
FILING DATE: 27-JUNE-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5830854th, Robert J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1213CA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-496-118-1

Query Match 63.4%; Score 45; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.29;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
Db 1 RPKPQEFFGLM 11

RESULT 68
US-07-737-371E-25
Sequence 25, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-25

Query Match 63.4%; Score 45; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.29;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
Db 1 RPKPQEFFGLM 11

RESULT 69

PCT-US92-06532-1
; Sequence 1, Application PC/TUS9206532
; GENERAL INFORMATION:
; APPLICANT: Krause, James E.
; TITLE OF INVENTION: Human Substance P Receptor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SD
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: U.S.A
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06532
; FILING DATE: 19920805
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(776)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /label= amide
PCT-US92-06532-1

Query Match 63.4%; Score 45; DB 5; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.29;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFILM 11
||||:|:|
Db 1 RPKPEQFFGLM 11

RESULT 70
US-07-737-371E-9
; Sequence 9, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-9

Query Match 60.6%; Score 43; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.52;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RPKQQWFILM 11
||||:|:|
Db 1 RPKQOFFGLM 10

RESULT 71
US-08-031-325A-26
; Sequence 26, Application US/08031325A
; Patent No. 5369094
; GENERAL INFORMATION:
; APPLICANT: Schally, Andrew V.
; APPLICANT: Cai, Renzhi
; TITLE OF INVENTION: POLYPEPTIDE BOMBESIN ANTAGONISTS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OMRI M. BEHR, ESQ
; STREET: 325 PIERSON AVENUE
; CITY: EDISON
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 08837
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/031,325A
; FILING DATE: 15-MAR-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/619,747
; FILING DATE: 29-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BEHR, OMRI M.
; REGISTRATION NUMBER: 22,940
; REFERENCE/DOCKET NUMBER: SHAL3.0-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 494-5240
; TELEFAX: (908) 494-0428
; TELEX: 511642 BEPATEDIN
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 11
;; OTHER INFORMATION: /note= "Res 11 - Met-NH2"
US-08-031-325A-26

Query Match 60.6%; Score 43; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 0.58;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFGL 10
|||||:|
Db 1 RPKPQQFFGL 10

RESULT 72
US-07-737-371E-13
; Sequence 13, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 11...11
; OTHER INFORMATION: where xaa at position 11 is ethionine

Query Match 60.6%; Score 43; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 0.58;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFGL 10
|||||:|
Db 1 RPKPQQFFGL 10

RESULT 73
US-07-737-371E-14
; Sequence 14, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 11...11
; OTHER INFORMATION: where xaa at position 11 is Nle

Query Match 60.6%; Score 43; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 0.58;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFGL 10
|||||:|
Db 1 RPKPQQFFGL 10

RESULT 74
US-07-737-371E-16
; Sequence 16, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA

Query Match 60.6%; Score 43; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 0.58;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQFWL 10
| | | | | : | |
Db 1 RPKPQQFFXL 10

RESULT 77

US-07-737-371E-61
; Sequence 61, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 10...10
; OTHER INFORMATION: where Xaa at location 10 is Me-Leu
US-07-737-371E-61

Query Match 60.6%; Score 43; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.58;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQFWLM 11
| | | | | : | |
Db 1 RPKPQQFFGXM 11

RESULT 78

US-07-737-371E-63
; Sequence 63, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.

; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 11...11
; OTHER INFORMATION: where Xaa at position 11 is Me-Met
US-07-737-371E-63

Query Match 60.6%; Score 43; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 0.58;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQFWL 10
| | | | | : | |
Db 1 RPKPQQFFGL 10

RESULT 79

US-07-737-371E-64
; Sequence 64, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-64

Query Match 60.6%; Score 43; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 0.58;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQWFNL 10
| | | | | | | |
Db 1 RPKPOQFGL 10

RESULT 80
US-07-737-371E-66
; Sequence 66, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 10...10
; OTHER INFORMATION: where xaa at position 10 is Me-Leu
US-07-737-371E-66

Query Match 60.6%; Score 43; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.58;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQWFNL 11
| | | | | | | | | |
Db 1 RPKPOQFFGX 11

RESULT 81
US-08-747-137-34
; Sequence 34, Application US/08747137
; Patent No. 5945033
; GENERAL INFORMATION:
; APPLICANT: YEN, Richard C.K.
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,137
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,546
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,831
; FILING DATE: 01-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,560
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/641,720
; FILING DATE: 15-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016197-00084005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /product= "Met-Amide"
US-08-747-137-34

Query Match 60.6%; Score 43; DB 2; Length 11;

Best Local Similarity 80.0%; Pred. No. 0.58;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRPQOQFWL 10
|||||:|
Db 1 RRPQOQFGL 10

RESULT 82

US-08-505-250-34

; Sequence 34, Application US/08505250
; Patent No. 6183983
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kokichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Sakagami, Masahiro
; APPLICANT: Taniguchi, Makoto
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
; FILE REFERENCE: 110-511
; CURRENT APPLICATION NUMBER: US/08/505,250
; CURRENT FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: PCT/JP95/00298
; EARLIER FILING DATE: 1995-02-27
; EARLIER APPLICATION NUMBER: JP 198187/94
; EARLIER FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide

US-08-505-250-34

Query Match 60.6%; Score 43; DB 4; Length 11;

Best Local Similarity 80.0%; Pred. No. 0.58;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRPQOQFWL 10
|||||:|
Db 2 RRPQOQFGL 11

RESULT 83

US-08-701-846-2

; Sequence 2, Application US/08701846

; Patent No. 5717069

; GENERAL INFORMATION:

; APPLICANT: Granados, Robert R.

; TITLE OF INVENTION: DNA SEQUENCE CODING FOR A POLYPEPTIDE

; TITLE OF INVENTION: WHICH ENHANCES VIRUS INFECTION OF HOST INSECTS

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Barnard, Brown & Michaels

; STREET: 306 E. State St., Suite 220

; CITY: Ithaca,

; STATE: NY

; COUNTRY: USA

; ZIP: 14850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/701,846

; FILING DATE: 23-AUG-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/002,743

; FILING DATE: 24-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Michaels, Christopher A.

; REGISTRATION NUMBER: 34,390

; REFERENCE/DOCKET NUMBER: BTI-32

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (607)273-1711

; TELEFAX: (607)273-2609

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 902 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-701-846-2

Query Match 60.6%; Score 43; DB 1; Length 902;

Best Local Similarity 70.0%; Pred. No. 41;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQOQFWL 11

|||||

Db 353 PYQIWAFLM 362

RESULT 84

US-08-428-488-15

; Sequence 15, Application US/08428488

; Patent No. 5624894

; GENERAL INFORMATION:

; APPLICANT: BODOR, Nicholas S.

; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE

; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM

; NUMBER OF SEQUENCES: 107

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P. O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/428,488

; FILING DATE: 27-APR-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Baumeister, Mary Katherine

; REGISTRATION NUMBER: 26,254

; REFERENCE/DOCKET NUMBER: 028724-087

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 1

; OTHER INFORMATION: /note= "Position 1 = H-Arg."

; FEATURE:

; NAME/KEY: Modified-site

LOCATION: 5
OTHER INFORMATION: /note= "Position 5 = Glu-NH2."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /note= "Position 6 = Glu-NH2."
US-08-428-488-15

Query Match 59.2%; Score 42; DB 1; Length 11;
Best Local Similarity 63.6%; Pred. No. 0.81;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
| | | | | | | | | | |
Db 1 RPKPEEFGLM 11

RESULT 85
US-07-737-371E-15
Sequence 15, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-15

Query Match 59.2%; Score 42; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.81;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
| | | | | | | | | | |
Db 1 RPKPQQFGLM 11

RESULT 86

US-07-737-371E-19
Sequence 19, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-19

Query Match 59.2%; Score 42; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.81;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
| | | | | | | | | | |
Db 1 RPKPQQFGLM 11

RESULT 87
US-07-737-371E-29
Sequence 29, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95

```
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 5...5
; OTHER INFORMATION: where Xaa at position 5 is homocysteine
; LOCATION: 9...9
; OTHER INFORMATION: where Xaa at position 9 is homocysteine
; US-07-737-371E-29

Query Match 59.2%; Score 42; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.81;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRPQQWF 11
Db 1 RRPXQFFXLM 11

RESULT 88
US-07-737-371E-57
; Sequence 57, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-737-371E-57
```

```
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-737-371E-57

Query Match 57.7%; Score 41; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQQWF 8
Db 1 RRPQQFF 8

RESULT 89
US-07-737-371E-11
; Sequence 11, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-737-371E-11

Query Match 57.7%; Score 41; DB 2; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQQWF 8
Db 1 RRPQQFF 8

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
```


RESULT 90
US-07-737-371E-26
; Sequence 26, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 8...8
; OTHER INFORMATION: where Xaa at position 8 is Me-Phe
US-07-737-371E-26

Query Match 57.7%; Score 41; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPQQFWLM 11
Db 1 RPKPQQFXGLM 11

RESULT 91
US-07-737-371E-62
; Sequence 62, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US

ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-62

Query Match 57.7%; Score 41; DB 2; Length 11;
Best Local Similarity 87.5%; Pred. No. 1.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQWF 8
Db 1 RPKPQQFF 8

RESULT 92
US-07-737-371E-67
; Sequence 67, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 11..11
OTHER INFORMATION: where xaa at position 11 is Me-Met
US-07-737-371E-67

Query Match 57.7%; Score 41; DB 2; Length 11;
Best Local Similarity 87.5%; Pred. No. 1.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWF 8
|||||:|
Db 1 RPKPQQFF 8

RESULT 93
US-08-890-157A-1
Sequence 1, Application US/08890157A
Patent No. 6063758
GENERAL INFORMATION:
APPLICANT: Douglas A. Iappi and Ronald G. Wiley
TITLE OF INVENTION: Substance P-Saporin (SP-SAP) Conjugates And
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,157A
FILING DATE: 09-JUL-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Phillips, Peter J.
REGISTRATION NUMBER: 29,691
REFERENCE/DOCKET NUMBER: 53984
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-157A-1

Query Match 57.7%; Score 41; DB 3; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWF 8
|||||:|
Db 10 RPKPQQFF 17

RESULT 94
US-07-737-371E-28
Sequence 28, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-28

Query Match 56.3%; Score 40; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 1.6;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|
Db 1 RPKPQQFFCLM 11

RESULT 95
US-09-060-726A-6
Sequence 6, Application US/09060726A
Patent No. 6225530
GENERAL INFORMATION:
APPLICANT: Weigel, Detlef
APPLICANT: Salk Institute
TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
TITLE OF INVENTION: MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
FILE REFERENCE: SALKINS 026A
CURRENT APPLICATION NUMBER: US/09/060,726A
CURRENT FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 104
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-060-726A-6

Query Match 56.3%; Score 40; DB 4; Length 104;
Best Local Similarity 40.0%; Pred. No. 14;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KPQQWFWM 11
|:|:|:|:
Db 44 PSPREHVV 53

RESULT 96
US-09-236-080-2
; Sequence 2, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236.080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-080-2

Query Match 56.3%; Score 40; DB 4; Length 411;
Best Local Similarity 55.6%; Pred. No. 54;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQQWFWM 11
|:|:|:|:
Db 271 KPVVWFIL 279

RESULT 97
US-09-236-080-6
; Sequence 6, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236.080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-236-080-6

Query Match 56.3%; Score 40; DB 4; Length 411;
Best Local Similarity 55.6%; Pred. No. 54;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQQWFWM 11
|:|:|:|:
Db 271 KPVVWFIL 279

RESULT 98
US-08-447-411-76
; Sequence 76, Application US/08447411
; Patent No. 5773243

; GENERAL INFORMATION:
; APPLICANT: FRITZINGER, DAVID C.
; APPLICANT: BREDEHORST, REINHARD
; APPLICANT: VOGEL, CARL-WILHELM
; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,411
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/043,747
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5773243man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-101-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1333 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-447-411-76

Query Match 56.3%; Score 40; DB 1; Length 1333;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQQWFWM 11
|:|:|:|:
Db 435 PESWLWM 442

RESULT 99
US-08-662-227-34
; Sequence 34, Application US/08662227
; Patent No. 592320
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; APPLICANT: BREDEHORST, REINHORST
; APPLICANT: KOCK, MICHAEL
; APPLICANT: FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/662,227
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-0107-0X
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1333 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-662-227-34

Query Match 56.3%; Score 40; DB 2; Length 1333;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQQFWLW 11
I: I I I I
DB 435 PESWLWLM 442

RESULT 100
US-09-017-947-34
; Sequence 34, Application US/09017947
; Patent No. 6303754
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; APPLICANT: BREDEHORST, REINHORST
; APPLICANT: KOCK, MICHAEL
; APPLICANT: FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,947
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/662,227
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-0107-0X
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1333 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-017-947-34

Query Match 56.3%; Score 40; DB 4; Length 1333;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQQFWLW 11
I: I I I I
DB 435 PESWLWLM 442

RESULT 101
US-08-462-413-2
; Sequence 2, Application US/08462413
; Patent No. 5530009
; GENERAL INFORMATION:
; APPLICANT: Cho, Sung Y.
; APPLICANT: Copp, James D.
; APPLICANT: Ginah, Francis O.
; APPLICANT: Hansen, Guy J.
; APPLICANT: Hipskind, Phillip A.
; APPLICANT: Huff, Bret E.
; APPLICANT: Martineili, Michael J.
; APPLICANT: Staszak, Michael A.
; APPLICANT: Tharp-Taylor, Roger W.
; TITLE OF INVENTION: PROCESS FOR PREPARING NON-PEPTIDYL
; TITLE OF INVENTION: TACHYKININ RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,413
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,708
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9475
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-462-413-2

Query Match 54.9%; Score 39; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 2.3;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
||| ||: ||
Db 1 RPKRQQPFGLM 11

RESULT 102

US-07-737-371E-34
; Sequence 34, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07737371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 5...5
; OTHER INFORMATION: where Xaa at position 5 is D-Cys
US-07-737-371E-34

Query Match 54.9%; Score 39; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
|||| | ||
Db 1 RPKPQQCFGLM 11

RESULT 103

PCT-US91-00899-6
; Sequence 6, Application PC/TUS9100899
; GENERAL INFORMATION:
; APPLICANT: Lowe, John B.
; TITLE OF INVENTION: Method and Products For the Synthesis of
; TITLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids,
; TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned
; TITLE OF INVENTION: Genetic Sequences That Determine These Structures
; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00899
; FILING DATE: 19910214
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavallee Ph.D., Jean-Paul
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-021-55 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-5940
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 299 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Blood
; CELL LINE: A431
; PCT-US91-00899-6

Query Match 54.9%; Score 39; DB 5; Length 299;
Best Local Similarity 55.6%; Pred. No. 56;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 9
||: ||: ||
Db 64 RPKPQQWFWM 72

RESULT 104

US-07-914-281-2
; Sequence 2, Application US/07914281
; Patent No. 5324663
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/914,281
FILING DATE: 19920720
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-914-281-2

Query Match 54.9%; Score 39; DB 1; Length 361;
Best Local Similarity 55.6%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
||:|:|:|
Db 126 RPOGQRWI 134

RESULT 105
US-08-393-246-2
Sequence 2, Application US/08393246
Patent No. 559590
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.,
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,246
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,433
FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids

TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-393-246-2
Query Match 54.9%; Score 39; DB 1; Length 361;
Best Local Similarity 55.6%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 RPKPQQWF 9
||:|:|:|
Db 126 RPOGQRWI 134
RESULT 106
US-08-273-411-3
Sequence 3, Application US/08273411
Patent No. 5625124
GENERAL INFORMATION:
APPLICANT: Falk, Per
APPLICANT: Gordon, Jeffrey I.
TITLE OF INVENTION: Animal Model for Gastro-Intestinal
Disease
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,411
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..361
OTHER INFORMATION: /note= "GDP-L-fucose:beta-D-N-acetylglucosaminide-3,4-alp
PUBLICATION INFORMATION:
AUTHORS: Kukowska-Latallo, et al.
JOURNAL: Genes & Development
VOLUME: 4
PAGES: 1288-1303
DATE: 1990
RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 TO 361
US-08-273-411-3
Query Match 54.9%; Score 39; DB 1; Length 361;

Best Local Similarity 55.6%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQOWFW 9
||:|:|:|
Db 126 RPQQRWIW 134

RESULT 107
US-08-525-058A-2
; Sequence 2, Application US/08525058A
; Patent No. 5770420
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,058A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-525-058A-2

Query Match 54.9%; Score 39; DB 1; Length 361;
Best Local Similarity 55.6%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQOWFW 9
||:|:|:|
Db 126 RPQQRWIW 134

RESULT 108
US-08-696-731-2
; Sequence 2, Application US/08696731
; Patent No. 595347
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,731
; FILING DATE: 14-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/393,246
; FILING DATE:
; APPLICATION NUMBER: US 08/220,433
; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-696-731-2

Query Match 54.9%; Score 39; DB 2; Length 361;
Best Local Similarity 55.6%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQOWFW 9
||:|:|:|
Db 126 RPQQRWIW 134

RESULT 109
US-09-042-531-2
; Sequence 2, Application US/09042531
; Patent No. 6268193
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/042,531
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/393,246
;; FILING DATE:
;; APPLICATION NUMBER: US 08/220,433
;; FILING DATE: 30-MAR-1994
;; APPLICATION NUMBER: US 07/914,281
;; FILING DATE: 20-JUL-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lavalleye, Jean-Paul M. P.
;; REGISTRATION NUMBER: 31,451
;; REFERENCE/DOCKET NUMBER: 2363-060-55
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703)521-4500
;; TELEFAX: (703)486-2347
;; TELEX: 248855 OPAT UR
;; INFORMATION FOR SEQ ID NO: 2:
;; LENGTH: 361 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-09-042-531-2

Query Match 54.9%; Score 39; DB 4; Length 361;
Best Local Similarity 55.6%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
||: ||: ||
Db 126 RPOGQRW 134

RESULT 110
PCT-US91-00899-7
;; Sequence 7, Application PC/TUS9100899
;; GENERAL INFORMATION:
;; APPLICANT: Lowe, John B.
;; TITLE OF INVENTION: Method and Products For the Synthesis of
;; TITLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids,
;; TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned
;; TITLE OF INVENTION: Genetic Sequences That Determine These Structures
;; NUMBER OF SEQUENCES: 16
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;; ADDRESSEE: P.C.
;; STREET: 1755 Jefferson Davis Highway, Suite 400
;; CITY: Arlington
;; STATE: Virginia
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US91/00899
;; FILING DATE: 19910214
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lavalleye Ph.D., Jean-Paul
;; REGISTRATION NUMBER: 31,451
;; REFERENCE/DOCKET NUMBER: 2363-021-55 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703)521-5940
;; TELEFAX: (703)486-2347
;; TELEX: 248855 OPAT UR
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 361 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: YES
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; TISSUE TYPE: Blood
;; CELL LINE: A431
PCT-US91-00899-7

Query Match 54.9%; Score 39; DB 5; Length 361;
Best Local Similarity 55.6%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
||: ||: ||
Db 126 RPOGQRW 134

RESULT 111
US-07-914-281-11
;; Sequence 11, Application US/07914281
;; Patent No. 5324663
;; GENERAL INFORMATION:
;; APPLICANT: LOWE, JOHN B.
;; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
;; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
;; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
;; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;; ADDRESSEE: P.C.
;; STREET: 1755 Jefferson Davis Highway, Fourth Floor
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: U.S.A.
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/914,281
;; FILING DATE: 19920720
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lavalleye, Jean-Paul M. P.
;; REGISTRATION NUMBER: 31,451
;; REFERENCE/DOCKET NUMBER: 2363-060-55
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703)521-4500
;; TELEFAX: (703)486-2347
;; TELEX: 248855 OPAT UR
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 374 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-07-914-281-11

Query Match 54.9%; Score 39; DB 1; Length 374;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
||: ||: ||
Db 139 RPOGQRW 147

; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-696-731-11

Query Match 54.9%; Score 39; DB 2; Length 374;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
||: ||: ||
Db 139 RPOGQRWI 147

RESULT 115
US-09-042-531-11
; Sequence 11, Application US/09042531
; Patent No. 6268193
; GENERAL INFORMATION:
; APPLICANT: LONE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,531
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,246
; FILING DATE:
; APPLICATION NUMBER: US 08/220,433
; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-042-531-11

Query Match 54.9%; Score 39; DB 4; Length 374;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
||: ||: ||
Db 139 RPOGQRWI 147

RESULT 116
US-08-816-693A-51
; Sequence 51, Application US/08816693A
; Patent No. 5874241
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S
; APPLICANT: Turek, Fred W
; APPLICANT: Pinto, Lawrence H
; TITLE OF INVENTION: Clock Gene and Gene Product
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,693A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5874241thrup, Thomas E
; REGISTRATION NUMBER: 33,268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 747 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-816-693A-51

Query Match 54.9%; Score 39; DB 2; Length 747;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWF 10
| || |
Db 316 KGOQW 323

RESULT 117
US-08-885-291-51
; Sequence 51, Application US/08885291A
; Patent No. 6057125
; GENERAL INFORMATION:

APPLICANT: Takahashi, Joseph S.
APPLICANT: Turek, Fred W.
APPLICANT: Pinto, Lawrence H.
TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
FILE REFERENCE: 0290-5
CURRENT APPLICATION NUMBER: US/08/885,291A
CURRENT FILING DATE: 1997-06-30
EARLIER APPLICATION NUMBER: 08/816,693
EARLIER FILING DATE: 1997-03-13
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51
LENGTH: 747
TYPE: PRT
ORGANISM: Mus musculus
US-08-885-291-51

Query Match 54.9%; Score 39; DB 3; Length 747;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQQWFNL 10
| ||| ||
Db 316 KGQQWIL 323

RESULT 118

US-09-496-672-51
Sequence 51, Application US/09496672
Patent No. 6291429

GENERAL INFORMATION:
APPLICANT: Takahashi, Joseph S.
APPLICANT: Turek, Fred W.
APPLICANT: Pinto, Lawrence H.
TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
FILE REFERENCE: 0290-5
CURRENT APPLICATION NUMBER: US/09/496,672
CURRENT FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 08/885,291
PRIOR FILING DATE: 1997-06-30
PRIOR APPLICATION NUMBER: 08/816,693
PRIOR FILING DATE: 1997-03-13
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51
LENGTH: 747
TYPE: PRT
ORGANISM: Mus musculus
US-09-496-672-51

Query Match 54.9%; Score 39; DB 4; Length 747;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQQWFNL 10
| ||| ||
Db 316 KGQQWIL 323

RESULT 119

US-08-785-310A-8
Sequence 8, Application US/08785310A
Patent No. 5840532

GENERAL INFORMATION:
APPLICANT: McKnight, Steven L.
APPLICANT: Russell, David W.
TITLE OF INVENTION: Neuronal PAS Domain Protein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/785,310A
APPLICATION NUMBER: US/08/785,310A
FILING DATE: 21-JAN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UTSD:1226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-785-310A-8

Query Match 54.9%; Score 39; DB 2; Length 816;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQQWFNL 10
| ||| ||
Db 319 KGQQWIL 326

RESULT 120

US-08-816-693A-53
Sequence 53, Application US/08816693A
Patent No. 5874241

GENERAL INFORMATION:
APPLICANT: Takahashi, Joseph S.
APPLICANT: Turek, Fred W.
APPLICANT: Pinto, Lawrence H.
TITLE OF INVENTION: Clock Gene and Gene Product
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/816,693A
APPLICATION NUMBER: US/08/816,693A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5874241thrup, Thomas E.
REGISTRATION NUMBER: 33,268
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5400
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:

; LENGTH: 816 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-816-693A-53

Query Match 54.9%; Score 39; DB 2; Length 816;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFWL 10
| ||| ||
DB 319 KGQQWIL 326

RESULT 121

US-08-885-291-53
; Sequence 53, Application US/08885291A
; Patent No. 6057125
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S.
; APPLICANT: Turek, Fred W.
; TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
; FILE REFERENCE: 0290-5
; CURRENT APPLICATION NUMBER: US/08/885,291A
; CURRENT FILING DATE: 1997-06-30
; EARLIER APPLICATION NUMBER: 08/816,693
; EARLIER FILING DATE: 1997-03-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-885-291-53

Query Match 54.9%; Score 39; DB 3; Length 816;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFWL 10
| ||| ||
DB 319 KGQQWIL 326

RESULT 122

US-09-496-672-53
; Sequence 53, Application US/09496672
; Patent No. 6291429
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S.
; APPLICANT: Turek, Fred W.
; APPLICANT: Pinto, Lawrence H.
; TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
; FILE REFERENCE: 0290-5
; CURRENT APPLICATION NUMBER: US/09/496,672
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 08/885,291
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 08/816,693
; PRIOR FILING DATE: 1997-03-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-496-672-53

Query Match 54.9%; Score 39; DB 4; Length 816;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFWL 10
| ||| ||
DB 319 KGQQWIL 326

RESULT 123

US-08-785-310A-7
; Sequence 7, Application US/08785310A
; Patent No. 5840532
; GENERAL INFORMATION:
; APPLICANT: McKnight, Steven L.
; APPLICANT: Russell, David W.
; TITLE OF INVENTION: Neuronal PAS Domain Protein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,310A
; FILING DATE: 21-JAN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UTSD:1226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 824 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-785-310A-7

Query Match 54.9%; Score 39; DB 2; Length 824;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFWL 10
| ||| ||
DB 319 KGQQWIL 326

RESULT 124

US-08-816-693A-52
; Sequence 52, Application US/08816693A
; Patent No. 5874241
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S
; APPLICANT: Turek, Fred W
; APPLICANT: Pinto, Lawrence H
; TITLE OF INVENTION: Clock Gene and Gene Product
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz

; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816.693A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5874241thrup, Thomas E
; REGISTRATION NUMBER: 33,268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 824 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-816-693A-52

Query Match 54.9%; Score 39; DB 2; Length 824;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQOWFWL 10
| ||| ||
Db 319 KGQOWIWL 326

RESULT 125
US-08-885-291-52
; Sequence 52, Application US/08885291A
; Patent No. 6057125
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S.
; APPLICANT: Turek, Fred W.
; TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
; FILE REFERENCE: 0290-5
; CURRENT APPLICATION NUMBER: US/08/885.291A
; CURRENT FILING DATE: 1997-06-30
; EARLIER APPLICATION NUMBER: 08/816.693
; EARLIER FILING DATE: 1997-03-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-885-291-52

Query Match 54.9%; Score 39; DB 3; Length 824;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQOWFWL 10
| ||| ||
Db 319 KGQOWIWL 326

RESULT 126
US-09-496-672-52

; Sequence 52, Application US/09496672
; Patent No. 6291429
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S.
; APPLICANT: Turek, Fred W.
; TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
; FILE REFERENCE: 0290-5
; CURRENT APPLICATION NUMBER: US/09/496.672
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 08/885.291
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 08/816.693
; PRIOR FILING DATE: 1997-03-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-496-672-52

Query Match 54.9%; Score 39; DB 4; Length 824;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQOWFWL 10
| ||| ||
Db 319 KGQOWIWL 326

RESULT 127
US-08-885-291-55
; Sequence 55, Application US/08885291A
; Patent No. 6057125
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S.
; APPLICANT: Turek, Fred W.
; TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
; FILE REFERENCE: 0290-5
; CURRENT APPLICATION NUMBER: US/08/885.291A
; CURRENT FILING DATE: 1997-06-30
; EARLIER APPLICATION NUMBER: 08/816.693
; EARLIER FILING DATE: 1997-03-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 846
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-885-291-55

Query Match 54.9%; Score 39; DB 3; Length 846;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQOWFWL 10
| ||| ||
Db 344 KGQOWIWL 351

RESULT 128
US-09-107-847-2
; Sequence 2, Application US/09107847
; Patent No. 6100062
; GENERAL INFORMATION:
; APPLICANT: DUCKWORTH, DAVID
; APPLICANT: MICHALOVICH, DAVID
; TITLE OF INVENTION: NOVEL USE
; NUMBER OF SEQUENCES: 2

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Ratner & Prestia
;; STREET: P.O. Box 980
;; CITY: Valley Forge
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19482
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FASTSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/107,847
;; FILING DATE: 30-JUN-1998
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 97304996.8
;; FILING DATE: 08-JUL-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Prestia, Paul F
;; REGISTRATION NUMBER: 23,031
;; REFERENCE/DOCKET NUMBER: GH-30003
;; TELEPHONE: 610-407-0700
;; TELEFAX: 610-407-0701
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 846 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-107-847-2

Query Match 54.9%; Score 39; DB 3; Length 846;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQFWL 10
| | | | |
DB 344 KGOQIWL 351

RESULT 129
US-09-496-672-55
;; Sequence 55, Application US/09496672
;; Patent No. 6291429
;; GENERAL INFORMATION:
;; APPLICANT: Takahashi, Joseph S.
;; APPLICANT: Turek, Fred W.
;; TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
;; FILE REFERENCE: 0290-5
;; CURRENT APPLICATION NUMBER: US/09/496,672
;; PRIOR APPLICATION NUMBER: 2000-02-03
;; PRIOR FILING DATE: 1997-06-30
;; PRIOR APPLICATION NUMBER: 08/816,693
;; PRIOR FILING DATE: 1997-03-13
;; NUMBER OF SEQ ID NOS: 55
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 55
;; LENGTH: 846
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-496-672-55

Query Match 54.9%; Score 39; DB 4; Length 846;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 KPOQFWL 10
| | | | |
DB 344 KGOQIWL 351

RESULT 130
US-08-816-693A-2
;; Sequence 2, Application US/08816693A
;; Patent No. 5874241
;; GENERAL INFORMATION:
;; APPLICANT: Takahashi, Joseph S
;; APPLICANT: Turek, Fred W
;; APPLICANT: Pinto, Lawrence H
;; TITLE OF INVENTION: Clock Gene and Gene Product
;; NUMBER OF SEQUENCES: 53
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
;; STREET: Two Prudential Plaza, Suite 4700
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60601
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/816,693A
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5874241thrup, Thomas E
;; REGISTRATION NUMBER: 33,268
;; TELEPHONE: 312-616-5400
;; TELEFAX: 312-616-5460
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 855 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-816-693A-2

Query Match 54.9%; Score 39; DB 2; Length 855;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQFWL 10
| | | | |
DB 344 KGOQIWL 351

RESULT 131
US-08-885-291-2
;; Sequence 2, Application US/08885291A
;; Patent No. 6057125
;; GENERAL INFORMATION:
;; APPLICANT: Takahashi, Joseph S.
;; APPLICANT: Turek, Fred W.
;; APPLICANT: Pinto, Lawrence H.
;; TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
;; FILE REFERENCE: 0290-5
;; CURRENT APPLICATION NUMBER: US/08/885,291A
;; CURRENT FILING DATE: 1997-06-30
;; EARLIER FILING DATE: 1997-03-13
;; NUMBER OF SEQ ID NOS: 55
;; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-885-291-2

Query Match 54.9%; Score 39; DB 3; Length 855;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPQQWFWL 10
| | | | |
DB 344 KGQQWFWL 351

RESULT 132

US-09-496-672-2
; Sequence 2, Application US/09496672
; Patent No. 6291429

; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S.
; APPLICANT: Turek, Fred W.
; APPLICANT: Pinto, Lawrence H.
; TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
; FILE REFERENCE: 0290-5
; CURRENT APPLICATION NUMBER: US/09/496,672
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 08/885,291
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 08/816,693
; PRIOR FILING DATE: 1997-03-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-496-672-2

Query Match 54.9%; Score 39; DB 4; Length 855;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPQQWFWL 10
| | | | |
DB 344 KGQQWFWL 351

RESULT 133

5441935-7
; Patent No. 5441935

; APPLICANT: Rozenqurt, Enrique; Zachary, Ian; Woll, Penella
; TITLE OF INVENTION: ROTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,587
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 814,064
; FILING DATE: 23-DEC-1991
; APPLICATION NUMBER: 411,536
; FILING DATE: 29-NOV-1989
; SEQ ID NO: 7
; LENGTH: 6
5441935-7

Query Match 53.5%; Score 38; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 QWFWLM 11
: | | | | |
DB 1 RWFWM 6

RESULT 134

US-07-737-371E-54

; Sequence 54, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 7...7
; OTHER INFORMATION: where xaa at position 7 is p-Chloro-Phe
; LOCATION: 8...8
; OTHER INFORMATION: where xaa at position 8 is p-Chloro-Phe
US-07-737-371E-54

Query Match 53.5%; Score 38; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWFWLM 11
| | | | |
DB 1 RPKPQQXXGLM 11

RESULT 135

US-08-700-651-14
; Sequence 14, Application US/08700651B
; Patent No. 6015882

; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: LEECH, JAMES
; APPLICANT: NELSON, RICHARD, C.
; APPLICANT: GUT, JIRI

;; TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
;; TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum

;; FILE REFERENCE: 480.19-4(HV)
;; CURRENT APPLICATION NUMBER: US/08/700.651B
;; CURRENT FILING DATE: 1997-08-14
;; EARLIER APPLICATION NUMBER: 08/415.751
;; EARLIER FILING DATE: 1995-04-03
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 14
;; LENGTH: 91
;; TYPE: PRT
;; ORGANISM: Cryptosporidium parvum
;; FEATURE:
;; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-14

Query Match 53.5%; Score 38; DB 3; Length 91;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPOQWFWL 10
||:| ||
Db 83 KPDEWCWL 90

RESULT 136

US-08-928-361B-19
; Sequence 19, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: SPECIES INFECTIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana

REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELEPHONE: 650-324-1677
TELEFAX: 650-324-1677

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-928-361B-19

Query Match 53.5%; Score 38; DB 3; Length 91;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPOQWFWL 10
||:| ||
Db 83 KPDEWCWL 90

RESULT 137

US-08-326-117B-8
; Sequence 8, Application US/08326117B
; Patent No. 5693491
; GENERAL INFORMATION:
; APPLICANT: BULLA, LEE A.
; APPLICANT: JI, TAE
; TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS
; TITLE OF INVENTION: TOXIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326,117B
FILING DATE: 19-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.

REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 7112-0037.00
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-326-117B-8

Query Match 53.5%; Score 38; DB 1; Length 113;
Best Local Similarity 71.4%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQQWFWL 10
|:| | ||
Db 57 PQQWFWL 63

RESULT 138

US-08-982-129-8
; Sequence 8, Application US/08982129
; Patent No. 6007981
; GENERAL INFORMATION:
; APPLICANT: BULLA, LEE A.
; APPLICANT: JI, TAE
; TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS
; TITLE OF INVENTION: TOXIN
; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/982,129
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/326,117
; FILING DATE: 19-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 7112-0037.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-982-129-8

Query Match 53.5%; Score 38; DB 3; Length 113;
Best Local Similarity 71.4%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQQWFWL 10
| | | | |
DB 57 PQQWFWL 63

RESULT 139
US-08-700-651-11
; Sequence 11, Application US/08700651B
; Patent No. 6015882
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: LEECH, JAMES
; APPLICANT: NELSON, RICHARD, C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
; TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
; FILE REFERENCE: 480.19-4(HV)
; CURRENT APPLICATION NUMBER: US/08/700,651B
; CURRENT FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: 08/415,751
; EARLIER FILING DATE: 1995-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
; FEATURE:
; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-11

Query Match 53.5%; Score 38; DB 3; Length 124;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPQQWFWL 10
| | : | |
DB 116 KPDEWCWL 123

RESULT 140
US-08-928-361B-16
; Sequence 16, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: SPECIES INFECTIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,361B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,062
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verdy, Hana
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480.76-1(HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-1677
; TELEFAX: 650-324-1678
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-928-361B-16

Query Match 53.5%; Score 38; DB 3; Length 124;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPQQWFWL 10
| | : | |
DB 116 KPDEWCWL 123

RESULT 141
US-08-700-651-7
; Sequence 7, Application US/08700651B
; Patent No. 6015882
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: LEECH, JAMES
; APPLICANT: NELSON, RICHARD, C.

;; APPLICANT: GUT, JIRI
;; TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
;; TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
;; TITLE OF INVENTION: INFECTIONS
;; FILE REFERENCE: 480.19-4(HV)
;; CURRENT APPLICATION NUMBER: US/08/700,651B
;; CURRENT FILING DATE: 1997-08-14
;; EARLIER APPLICATION NUMBER: 08/415,751
;; EARLIER FILING DATE: 1995-04-03
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 7
;; LENGTH: 128
;; TYPE: PRT
;; ORGANISM: Cryptosporidium parvum
;; FEATURE:
;; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-7

Query Match 53.5%; Score 38; DB 3; Length 128;
Best Local Similarity 62.5%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWEWL 10
|| : ||
Db 120 KPDEWCWL 127

RESULT 142
US-08-928-361B-12
; Sequence 12, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: SPECIES INFECTIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,361B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,062
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verny, Hana
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480.76-1(HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-1677
; TELEFAX: 650-324-1678
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-928-361B-12

Query Match 53.5%; Score 38; DB 3; Length 128;
Best Local Similarity 62.5%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWEWL 10
|| : ||
Db 120 KPDEWCWL 127

RESULT 143
US-08-700-651-8
; Sequence 8, Application US/08700651B
; Patent No. 6015882
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: LEECH, JAMES
; APPLICANT: NELSON, RICHARD, C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
; TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
; TITLE OF INVENTION: INFECTIONS
; FILE REFERENCE: 480.19-4(HV)
; CURRENT APPLICATION NUMBER: US/08/700,651B
; CURRENT FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: 08/415,751
; EARLIER FILING DATE: 1995-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
; FEATURE:
; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-8

Query Match 53.5%; Score 38; DB 3; Length 130;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWEWL 10
|| : ||
Db 122 KPDEWCWL 129

RESULT 144
US-08-700-651-9
; Sequence 9, Application US/08700651B
; Patent No. 6015882
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: LEECH, JAMES
; APPLICANT: NELSON, RICHARD, C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
; TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
; TITLE OF INVENTION: INFECTIONS
; FILE REFERENCE: 480.19-4(HV)
; CURRENT APPLICATION NUMBER: US/08/700,651B
; CURRENT FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: 08/415,751
; EARLIER FILING DATE: 1995-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
; FEATURE:

; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-9

Query Match 53.5%; Score 38; DB 3; Length 130;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFWL 10
||:|:|
Db 122 KPDEWCWL 129

RESULT 145

US-08-928-361B-13
; Sequence 13, Application US/08928361B
; Patent No. 6071518

; GENERAL INFORMATION:

; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: SPECIES INFECTIONS

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PETERS, VERNY, JONES & BIKSA

; STREET: 385 Sherman Avenue, Suite 6

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306-1840

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/928,361B

; FILING DATE: 12-SEP-1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/026,062

; FILING DATE: 13-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: VERNY, HANA

; REGISTRATION NUMBER: 30,518

; REFERENCE/DOCKET NUMBER: 480.76-1(HV)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-324-1677

; TELEFAX: 650-324-1678

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 130 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-928-361B-13

Query Match 53.5%; Score 38; DB 3; Length 130;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFWL 10
||:|:|
Db 122 KPDEWCWL 129

RESULT 146

US-08-928-361B-14

; Sequence 14, Application US/08928361B

; Patent No. 6071518

; GENERAL INFORMATION:

; APPLICANT: Petersen, Carolyn

; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,

; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS

; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM

; TITLE OF INVENTION: SPECIES INFECTIONS

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PETERS, VERNY, JONES & BIKSA

; STREET: 385 Sherman Avenue, Suite 6

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306-1840

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/928,361B

; FILING DATE: 12-SEP-1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/026,062

; FILING DATE: 13-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: VERNY, HANA

; REGISTRATION NUMBER: 30,518

; REFERENCE/DOCKET NUMBER: 480.76-1(HV)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-324-1677

; TELEFAX: 650-324-1678

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 130 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-928-361B-14

Query Match 53.5%; Score 38; DB 3; Length 130;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFWL 10
||:|:|
Db 122 KPDEWCWL 129

RESULT 147

US-08-700-651-10

; Sequence 10, Application US/08700651B

; Patent No. 6015882

; GENERAL INFORMATION:

; APPLICANT: PETERSEN, CAROLYN

; APPLICANT: LEECH, JAMES

; APPLICANT: NELSON, RICHARD, C.

; APPLICANT: GUT, JIRI

; TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS

; TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum

; TITLE OF INVENTION: INFECTIONS

; FILE REFERENCE: 480.19-4(HV)

; CURRENT APPLICATION NUMBER: US/08/700,651B

; CURRENT FILING DATE: 1997-08-14

; EARLIER APPLICATION NUMBER: 08/415,751

; EARLIER FILING DATE: 1995-04-03

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10

; LENGTH: 138

; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
; FEATURE:
; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-10

Query Match 53.5%; Score 38; DB 3; Length 138;
Best Local Similarity 62.5%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQQWFWL 10
||:|
Db 130 KPDEWCWL 137

RESULT 148

US-08-928-361B-15
; Sequence 15, Application US/08928361B
; Patent No. 6071518

; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: SPECIES INFECTIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,361B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,062
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verny, Hana
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480.76-1(HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-1677
; TELEFAX: 650-324-1678
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-928-361B-15

Query Match 53.5%; Score 38; DB 3; Length 138;
Best Local Similarity 62.5%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQQWFWL 10
||:|
Db 130 KPDEWCWL 137

RESULT 149

US-08-928-361B-18
; Sequence 18, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: SPECIES INFECTIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,361B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,062
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verny, Hana
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480.76-1(HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-1677
; TELEFAX: 650-324-1678
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-928-361B-18

Query Match 53.5%; Score 38; DB 3; Length 150;
Best Local Similarity 62.5%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQQWFWL 10
||:|
Db 142 KPDEWCWL 149

RESULT 150

US-08-928-361B-9
; Sequence 9, Application US/08928361B
; Patent No. 6071518

; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: SPECIES INFECTIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840

Query Match 53.5%; Score 38; DB 3; Length 150;
Best Local Similarity 62.5%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQQWFWL 10
||:|
Db 142 KPDEWCWL 149

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928.361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: VERNY, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELEPHONE: 650-324-1677
TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-928-361B-9

Query Match 53.5%; Score 38; DB 3; Length 159;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQOWFWL 10
||:|
Db 8 KPDEWCWL 15

RESULT 151
US-08-928-361B-28
; Sequence 28, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: SPECIES INFECTIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928.361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: VERNY, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-324-1677
TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-928-361B-28

Query Match 53.5%; Score 38; DB 3; Length 159;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQOWFWL 10
||:|
Db 8 KPDEWCWL 15

RESULT 152
US-08-700-651-13
; Sequence 13, Application US/08700651B
; Patent No. 6015882
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: LEECH, JAMES
; APPLICANT: NELSON, RICHARD, C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
; TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORIDIUM PARVUM
; TITLE OF INVENTION: INFECTIONS
; FILE REFERENCE: 480.19-4(HV)
; CURRENT APPLICATION NUMBER: US/08/700.651B
; CURRENT FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: 08/415,751
; EARLIER FILING DATE: 1995-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
; FEATURE:
; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-13

Query Match 53.5%; Score 38; DB 3; Length 162;
Best Local Similarity 62.5%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQOWFWL 10
||:|
Db 154 KPDEWCWL 161

RESULT 153
US-08-700-651-12
; Sequence 12, Application US/08700651B
; Patent No. 6015882
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: LEECH, JAMES
; APPLICANT: NELSON, RICHARD, C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
; TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORIDIUM PARVUM
; TITLE OF INVENTION: INFECTIONS
; FILE REFERENCE: 480.19-4(HV)
; CURRENT APPLICATION NUMBER: US/08/700.651B
; CURRENT FILING DATE: 1997-08-14

; EARLIER APPLICATION NUMBER: 08/415,751
; EARLIER FILING DATE: 1995-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
; FEATURE:
; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-12

Query Match 53.5%; Score 38; DB 3; Length 175;
Best Local Similarity 62.5%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQFWL 10
|| : ||
Db 167 KPDEWCWL 174

RESULT 154
US-08-928-361B-17
; Sequence 17, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS.
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: SPECIES INFECTIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,361B
; FILING DATE: 12-SEP-1997

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,062
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verny, Hana
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480.76-1(HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-1677
; TELEFAX: 650-324-1678
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-928-361B-17

Query Match 53.5%; Score 38; DB 3; Length 175;
Best Local Similarity 62.5%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQFWL 10
|| : ||
Db 167 KPDEWCWL 174
RESULT 155
US-08-700-651-15
; Sequence 15, Application US/08700651B
; Patent No. 6015882
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: LEECH, JAMES
; APPLICANT: NELSON, RICHARD, C.
; TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
; TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
; TITLE OF INVENTION: INFECTIONS
; FILE REFERENCE: 480.19-4(HV)
; CURRENT APPLICATION NUMBER: US/08/700,651B
; CURRENT FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: 08/415,751
; EARLIER FILING DATE: 1995-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
; FEATURE:
; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-15

Query Match 53.5%; Score 38; DB 3; Length 249;
Best Local Similarity 62.5%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQFWL 10
|| : ||
Db 241 KPDEWCWL 248

RESULT 156
US-08-928-361B-20
; Sequence 20, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: SPECIES INFECTIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,361B
; FILING DATE: 12-SEP-1997

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,062
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verny, Hana
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480.76-1(HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-1677
; TELEFAX: 650-324-1678
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-928-361B-17

NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-928-361B-20

Query Match 53.5%; Score 38; DB 3; Length 249;
Best Local Similarity 62.5%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPQOWFWL 10
||:|:|:
DB 241 KPDEWCWL 248

RESULT 157
US-09-055-095-4
; Sequence 4, Application US/09055095
; Patent No. 5945308
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Patterson, Chandra
; APPLICANT: Corley, Neil C.
; APPLICANT: Sather, Susan
; TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/055,095
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0500 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1902982
US-09-055-095-4

Query Match 53.5%; Score 38; DB 2; Length 270;
Best Local Similarity 62.5%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQOWFW 9
|:|:|:
DB 139 PCPQDWLW 146

RESULT 158
US-08-809-494A-2
; Sequence 2, Application US/08809494A
; Patent No. 5962260
; GENERAL INFORMATION:
; APPLICANT: Sawamura, Tatsuya
; APPLICANT: Masaki, Tomoo
; TITLE OF INVENTION: Modified Low-Density Lipoprotein
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAulay Fisher Nissen Goldberg & Kiel
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,494A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-321705
; FILING DATE: 30-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-214206
; FILING DATE: 31-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E.
; REGISTRATION NUMBER: 24408
; REFERENCE/DOCKET NUMBER: JG-YY-4363PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 986-4090
; TELEFAX: 212 818-9479
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-494A-2

Query Match 53.5%; Score 38; DB 2; Length 270;
Best Local Similarity 62.5%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQOWFW 9
|:|:|:
DB 139 PCPQDWLW 146

RESULT 159
US-09-352-302-2
; Sequence 2, Application US/09352302
; Patent No. 6197937
; GENERAL INFORMATION:
; APPLICANT: Sawamura, Tatsuya

APPLICANT: Masaki, Tomoo
TITLE OF INVENTION: Modified Low-Density Lipoprotein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAulay Fisher Nissen Goldberg & Kiel
STREET: 261 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/352,302
FILING DATE: 12-JUL-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules E
REGISTRATION NUMBER: 24408
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D
TELEPHONE: 212 986-4090
TELEFAX: 212 818-9479
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-352-302-2

Query Match 53.5%; Score 38; DB 4; Length 270;
Best Local Similarity 62.5%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 PKPQQWFV 9
| | | | |
Db 139 PCPQDWLW 146

RESULT 160
US-09-055-095-3
Sequence 3, Application US/09055095
Patent No. 5945308
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Patterson, Chandra
APPLICANT: Corley, Neil C.
APPLICANT: Sather, Susan
TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/055,095
FILING DATE: Filed Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0500 US
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1902984
US-09-055-095-3

Query Match 53.5%; Score 38; DB 2; Length 273;
Best Local Similarity 62.5%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQQWFV 9
| | | | |
Db 143 PCPQDWLW 150

RESULT 161
US-08-809-494A-4
Sequence 4, Application US/08809494A
Patent No. 5962260
GENERAL INFORMATION:
APPLICANT: Sawamura, Tatsuya
APPLICANT: Masaki, Tomoo
TITLE OF INVENTION: Modified Low-Density Lipoprotein
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAulay Fisher Nissen Goldberg & Kiel
STREET: 261 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,494A
FILING DATE: 24-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules E
REGISTRATION NUMBER: 24408
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT
TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212 986-4090
; TELEFAX: 212 818-9479
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-494A-4

Query Match 53.5%; Score 38; DB 2; Length 273;
Best Local Similarity 62.5%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQQWFV 9
| | | | |
DB 142 PCPQDWLW 149

RESULT 162
US-08-809-494A-6
; Sequence 6, Application US/08809494A
; Patent No. 5962260
; GENERAL INFORMATION:
; APPLICANT: Sawamura, Tatsuya
; APPLICANT: Masaki, Tomoo
; TITLE OF INVENTION: Modified Low-Density Lipoprotein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAulay Fisher Nissen Goldberg & Kiel
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,494A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-321705
; FILING DATE: 30-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-214206
; FILING DATE: 31-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; REGISTRATION NUMBER: 24408
; REFERENCE/DOCKET NUMBER: JG-YY-4363PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 986-4090
; TELEFAX: 212 818-9479
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-494A-6

Query Match 53.5%; Score 38; DB 2; Length 273;
Best Local Similarity 62.5%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQQWFV 9

DB 143 PCPQDWLW 150
| | | | |

RESULT 163
US-09-352-302-4
; Sequence 4, Application US/09352302
; Patent No. 6197937
; GENERAL INFORMATION:
; APPLICANT: Sawamura, Tatsuya
; APPLICANT: Masaki, Tomoo
; TITLE OF INVENTION: Modified Low-Density Lipoprotein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAulay Fisher Nissen Goldberg & Kiel
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/352,302
; FILING DATE: 12-JUL-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-321705
; FILING DATE: 30-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-214206
; FILING DATE: 31-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; REGISTRATION NUMBER: 24408
; REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 986-4090
; TELEFAX: 212 818-9479
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-352-302-4

Query Match 53.5%; Score 38; DB 4; Length 273;
Best Local Similarity 62.5%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQQWFV 9
| | | | |
DB 142 PCPQDWLW 149

RESULT 164
US-09-352-302-6
; Sequence 6, Application US/09352302
; Patent No. 6197937
; GENERAL INFORMATION:
; APPLICANT: Sawamura, Tatsuya
; APPLICANT: Masaki, Tomoo
; TITLE OF INVENTION: Modified Low-Density Lipoprotein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAulay Fisher Nissen Goldberg & Kiel

STREET: 261 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/352.302
FILING DATE: 12-JUL-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules E.
REGISTRATION NUMBER: 24408
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
TELEFAX: 212 818-9479
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-352-302-6

Query Match 53.5%; Score 38; DB 4; Length 273;
Best Local Similarity 62.5%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQWF 9
| | | |
Db 143 PCPDWIW 150

RESULT 165
PCT-US91-00899-14
Sequence 14, Application PC/TUS9100899
GENERAL INFORMATION:
APPLICANT: Lowe, John B.
TITLE OF INVENTION: Method and Products For the Synthesis of
TITLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids,
TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned
TITLE OF INVENTION: Genetic Sequences That Determine These Structures
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00899
FILING DATE: 19910214
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye Ph.D., Jean-Paul

REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-021-55 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-5940
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: C-terminal
PCT-US91-00899-14

Query Match 53.5%; Score 38; DB 5; Length 357;
Best Local Similarity 50.0%; Pred. No. 95;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKQWF 10
| | | |
Db 110 RPKQWF 119

RESULT 166
US-07-914-281-8
Sequence 8, Application US/07914281
Patent No. 5324663
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/914,281
FILING DATE: 19920720
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 405 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-914-281-8

Query Match 53.5%; Score 38; DB 1; Length 405;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKQQQFWL 10
|||l:l|:
Db 161 RPPGQRWVM 170

RESULT 167
US-08-393-246-8
; Sequence 8, Application US/08393246
; Patent No. 5595900
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,246
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/220,433
; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-393-246-8

Query Match 53.5%; Score 38; DB 1; Length 405;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKQQQFWL 10
|||l:l|:
Db 161 RPPGQRWVM 170

RESULT 168
US-08-525-058A-8
; Sequence 8, Application US/08525058A
; Patent No. 5770420
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,

; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,058A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-525-058A-8

Query Match 53.5%; Score 38; DB 1; Length 405;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKQQQFWL 10
|||l:l|:
Db 161 RPPGQRWVM 170

RESULT 169
US-08-483-151-4
; Sequence 4, Application US/08483151
; Patent No. 5858752
; GENERAL INFORMATION:
; APPLICANT: Seed, Brian
; APPLICANT: Holgerisson, Jan
; TITLE OF INVENTION: FUCOSYLTRANSFERASE GENES AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,151
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238

REFERENCE/DOCKET NUMBER: 00786/278001
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 405 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-151-4

Query Match 53.5%; Score 38; DB 2; Length 405;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQOWFWL 10
|||::|||
Db 161 RPRKRWVM 170

RESULT 170

US-08-696-731-8
Sequence 8, Application US/08696731
Patent No. 5953347

GENERAL INFORMATION:

APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/696,731
FILING DATE: 14-AUG-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/393,246
FILING DATE:

APPLICATION NUMBER: US 08/220,433
FILING DATE: 30-MAR-1994

APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-JUL-1992

ATTORNEY/AGENT INFORMATION:

NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451

REFERENCE/DOCKET NUMBER: 2363-060-55

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 405 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-696-731-8

Query Match 53.5%; Score 38; DB 2; Length 405;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQOWFWL 10
|||::|||
Db 161 RPRKRWVM 170

RESULT 171

US-09-042-531-8
Sequence 8, Application US/09042531
Patent No. 6288193

GENERAL INFORMATION:

APPLICANT: LOWE, JOHN B.

TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/042,531
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/393,246
FILING DATE:

APPLICATION NUMBER: US 08/220,433
FILING DATE: 30-MAR-1994

APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-JUL-1992

ATTORNEY/AGENT INFORMATION:

NAME: Lavalleye, Jean-Paul M. P.

REGISTRATION NUMBER: 31,451

REFERENCE/DOCKET NUMBER: 2363-060-55

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)521-4500

TELEFAX: (703)486-2347

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 405 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-09-042-531-8

Query Match 53.5%; Score 38; DB 4; Length 405;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQOWFWL 10
|||::|||
Db 161 RPRKRWVM 170

RESULT 172
US-08-918-914-1
; Sequence 1, Application US/08918914
; Patent No. 5876963
; GENERAL INFORMATION:
; APPLICANT: Mitchell, Peter
; APPLICANT: Hutchinson, Nancy
; APPLICANT: Lawton, Michael
; APPLICANT: Magna, Holly
; APPLICANT: Vocum, Sue
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN NUCLEOTIDE PYROPHOSPHORYLASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,914
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1184 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: ???
; CLONE: 422069
US-08-918-914-1

Query Match 53.5%; Score 38; DB 2; Length 1184;
Best Local Similarity 44.4%; Pred. No. 3e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQWF 9
Db 335 KRPDKYFW 343

RESULT 173
US-08-996-083-3
; Sequence 3, Application US/08996083A
; Patent No. 6124095
; GENERAL INFORMATION:
; APPLICANT: Magna, Holly
; APPLICANT: Schaffer, Paul
; APPLICANT: Lawton, Michael
; APPLICANT: Vocum, Sue
; APPLICANT: Mitchell, Peter
; APPLICANT: Hutchinson, Nancy
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN NUCLEOTIDE PYROPHOSPHORYLASE-2

; FILE REFERENCE: PF-0420 US
; CURRENT APPLICATION NUMBER: US/08/996,083A
; CURRENT FILING DATE: 1997-12-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte Clone No. 6124095: 422069
; PUBLICATION INFORMATION:
US-08-996-083-3

Query Match 53.5%; Score 38; DB 3; Length 1184;
Best Local Similarity 44.4%; Pred. No. 3e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQWF 9
Db 335 KRPDKYFW 343

RESULT 174
US-08-326-117B-2
; Sequence 2, Application US/08326117B
; Patent No. 5693491
; GENERAL INFORMATION:
; APPLICANT: BULLA, LEE A.
; TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS
; TITLE OF INVENTION: TOXIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/326,117B
; FILING DATE: 19-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 7112-0037.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1528 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-326-117B-2

Query Match 53.5%; Score 38; DB 1; Length 1528;
Best Local Similarity 71.4%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQQWF 10

Db 233 PNQMWL 239
| | | |

RESULT 175

US-08-982-129-2
; Sequence 2, Application US/08982129
; Patent No. 6007981
; GENERAL INFORMATION:
; APPLICANT: BULLA, LEE A.
; APPLICANT: JI, TAE
; TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS
; TITLE OF INVENTION: TOXIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/982,129
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/326,117
; FILING DATE: 19-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 7112-0037.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1528 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-982-129-2

Query Match 53.5%; Score 38; DB 3; Length 1528;
Best Local Similarity 71.4%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQQWFWL 10
| | | |
Db 233 PNQMWL 239

RESULT 176

US-08-700-651-5
; Sequence 5, Application US/08700651B
; Patent No. 6015882
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: LEECH, JAMES
; APPLICANT: NELSON, RICHARD, C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
; TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
; FILE REFERENCE: 480.19-4(HV)
; CURRENT APPLICATION NUMBER: US/08/700,651B

; CURRENT FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: 08/415,751
; EARLIER FILING DATE: 1995-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1721
; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-08-700-651-5

Query Match 53.5%; Score 38; DB 3; Length 1721;
Best Local Similarity 62.5%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPQQWFWL 10
| | | |
Db 415 KPDEWCWL 422

RESULT 177

US-08-928-361B-6
; Sequence 6, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: SPECIES INFECTIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,361B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,062
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verny, Hana
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480.76-1(HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-1677
; TELEFAX: 650-324-1678
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1721 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-928-361B-6

Query Match 53.5%; Score 38; DB 3; Length 1721;
Best Local Similarity 62.5%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPQQWFWL 10

Db 415 KPDEWCWL 422
|| : | | |

RESULT 178

US-08-928-361B-5

; Sequence 5, Application US/08928361B

; Patent No. 6071518

; GENERAL INFORMATION:

; APPLICANT: Petersen, Carolyn

; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,

; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS

; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM

; TITLE OF INVENTION: SPECIES INFECTIONS

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PETERS, VERNY, JONES & BIKSA

; STREET: 385 Sherman Avenue, Suite 6

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306-1840

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/928,361B

; FILING DATE: 12-SEP-1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/026,062

; FILING DATE: 13-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Verny, Hana

; REGISTRATION NUMBER: 30,518

; REFERENCE/DOCKET NUMBER: 480,76-1(HV)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-324-1677

; TELEFAX: 650-324-1678

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1837 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-928-361B-5

Query Match 53.5%; Score 38; DB 3; Length 1837;

Best Local Similarity 62.5%; Pred. No. 4.6e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFVL 10

|| : | | |

Db 532 KPDEWCWL 539

RESULT 179

US-07-737-371E-3

; Sequence 3, Application US/07737371E

; Patent No. 5876948

; GENERAL INFORMATION:

; APPLICANT: Yankner, Bruce A.

; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 1...1
; OTHER INFORMATION: where xaa at position 1 is D-Arg
; LOCATION: 7...7
; OTHER INFORMATION: where xaa at position 7 is D-Trp
; LOCATION: 9...9
; OTHER INFORMATION: where xaa at position 9 is D-Trp
US-07-737-371E-3

Query Match

52.1%; Score 37; DB 2; Length 11;

Best Local Similarity 70.0%; Pred. No. 4.6;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOQWFVLM 11

||||| |:

Db 2 PKPOQXFLL 11

RESULT 180

US-07-737-371E-30

; Sequence 30, Application US/07737371E

; Patent No. 5876948

; GENERAL INFORMATION:

; APPLICANT: Yankner, Bruce A.

; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/737,371E

; FILING DATE: 29-JUL-1991

; CLASSIFICATION: 536

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/559,172
;; FILING DATE: 27-JUL-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Freeman, John W.
;; REGISTRATION NUMBER: 29,066
;; REFERENCE/DOCKET NUMBER: 00108/028002
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-542-5070
;; TELEFAX: 617-542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 30:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FEATURE:
;; LOCATION: 5...5
;; OTHER INFORMATION: where xaa at position 5 is homocysteine
;; LOCATION: 10...10
;; OTHER INFORMATION: where xaa at position 10 is homocysteine
;; US-07-737-371E-30

Query Match 52.1%; Score 37; DB 2; Length 11;
Best Local Similarity 63.6%; Pred. No. 4.6;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQFWLM 11
|||||:|:|
Db 1 RPKPXQFFGX 11

RESULT 181
US-07-737-371E-32
; Sequence 32, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; NUMBER OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids

;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FEATURE:
;; LOCATION: 5...5
;; OTHER INFORMATION: where xaa at position 5 is homocysteine
;; LOCATION: 11...11
;; OTHER INFORMATION: where xaa at position 11 is homocysteine
;; US-07-737-371E-32

Query Match 52.1%; Score 37; DB 2; Length 11;
Best Local Similarity 70.0%; Pred. No. 4.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQFWL 10
|||||:|:|
Db 1 RPKPXQFFGL 10

RESULT 182
US-08-468-514-11
; Sequence 11, Application US/08468514
; Patent No. 5576296
; GENERAL INFORMATION:
; APPLICANT: Bartfal, Tamas
; APPLICANT: Hofkfelt, Tomas
; APPLICANT: Langel, Ulo
; APPLICANT: Ahren, Bo
; APPLICANT: Lindskog, Stefan
; APPLICANT: Consolo, Silvana
; APPLICANT: Land, Tilt
; APPLICANT: Wiesenfeld-Hallin, Zsuzsanna
; TITLE OF INVENTION: GALANIN ANTAGONIST
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,514
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,139
; FILING DATE: 12-NOV-1993
; APPLICATION NUMBER: PCT/SE92/00316
; FILING DATE: 14-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9101472-0
; FILING DATE: 15-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Steiner Ph.D., Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8783
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO


```
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 22
; OTHER INFORMATION: /note= "amide"
US-08-468-514-11

Query Match          52.1%; Score 37; DB 1; Length 22;
Best Local Similarity 70.0%; Pred. No. 8.9;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 RPKPQQWFWM 11
DB      13 PPQQFFGLM 22

RESULT 183
US-08-690-095-1
Sequence 1, Application US/08690095
Patent No. 5792648
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Suriya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,789
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/690,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0110 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: MPHGN0T03
CLONE: 513418
US-08-690-095-1

Query Match          52.1%; Score 37; DB 1; Length 272;
Best Local Similarity 44.4%; Pred. No. 1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0;

QY      1 RPKPQQWFW 9
DB      131 KPCCPRRWI 139

RESULT 185
US-09-028-934-35
Sequence 35, Application US/09028934
Patent No. 6117670
GENERAL INFORMATION:
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight S.
APPLICANT: Lam, Steven T.
APPLICANT: Hammer, Philip E.
APPLICANT: van Pee, Karl-Heinz
APPLICANT: Kirner, Sabine
APPLICANT: Young, Thomas R.
TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6117670artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
```

STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,934
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/729,214
FILING DATE: 09-OCT-1996
PRIOR APPLICATION DATA: US 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1506/CIP7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 565 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-028-934-35

Query Match 52.1%; Score 37; DB 3; Length 565;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
||| |||
Db 227 KPGQRWRW 235

RESULT 186
US-07-737-371E-60
Sequence 60, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 2...2
OTHER INFORMATION: where xaa at position 2 is D-Pro
LOCATION: 7...7
OTHER INFORMATION: where xaa at position 7 is D-Trp
LOCATION: 9...9
OTHER INFORMATION: where xaa at position 9 is D-Trp

REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-60

Query Match 50.7%; Score 36; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.6e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQFWLM 11
||||| |||
Db 1 KPOQFGLM 9

RESULT 187
US-07-737-371E-2
Sequence 2, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 2...2
OTHER INFORMATION: where xaa at position 2 is D-Pro
LOCATION: 7...7
OTHER INFORMATION: where xaa at position 7 is D-Trp
LOCATION: 9...9
OTHER INFORMATION: where xaa at position 9 is D-Trp

US-07-737-371E-2

Query Match 50.7%; Score 36; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11
| | | | | | | |
Db 1 RXPQOXFXLM 11

RESULT 188

US-07-712-828B-5

; Sequence 5, Application US/07712828B
; Patent No. 5235039

; GENERAL INFORMATION:

; APPLICANT: Heath et al.

; TITLE OF INVENTION: Assay Method for Hydrolytic

; TITLE OF INVENTION: Enzymes

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Eli Lilly and Company

; STREET: Lilly Corporate Center

; CITY: Indianapolis

; STATE: IN.

; COUNTRY: U.S.A.

; ZIP: 46285

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage

; COMPUTER: Macintosh

; OPERATING SYSTEM: Macintosh

; SOFTWARE: Microsoft Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07712.828B

; FILING DATE: 19010610

; CLASSIFICATION: 530

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-07-712-828B-5

Query Match 50.7%; Score 36; DB 1; Length 13;
Best Local Similarity 63.6%; Pred. No. 7.6;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11
| | | | | | | |
Db 1 RRRPQOFFGLM 11

RESULT 189

US-09-082-089-3

; Sequence 3, Application US/09082089
; Patent No. 6100060

; GENERAL INFORMATION:

; APPLICANT: BARNES, MICHAEL

; APPLICANT: TESTA, TANIA

; APPLICANT: KELSELL, DAVID

; TITLE OF INVENTION: No. 6100060e1 Compounds

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082.089
; FILING DATE: 20-MAY-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9710737.9
; FILING DATE: 23-MAY-1997
; APPLICATION NUMBER: GB 9803981.1
; FILING DATE: 25-FEB-1998
; APPLICATION NUMBER: GB 9804007.4
; FILING DATE: 25-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F.
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-30166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 359 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-082-089-3

Query Match 50.7%; Score 36; DB 3; Length 359;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 RPK--PQOWFW 9
| | | | | | | |
Db 148 RPKDLPDOWLM 158

RESULT 190

US-09-082-089-5

; Sequence 5, Application US/09082089
; Patent No. 6100060

; GENERAL INFORMATION:

; APPLICANT: BARNES, MICHAEL

; APPLICANT: TESTA, TANIA

; APPLICANT: KELSELL, DAVID

; TITLE OF INVENTION: No. 6100060e1 Compounds

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/082.089

; FILING DATE: 20-MAY-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9710737.9

; FILING DATE: 23-MAY-1997

; APPLICATION NUMBER: GB 9803981.1

; FILING DATE: 25-FEB-1998

; APPLICATION NUMBER: GB 9804007.4
; FILING DATE: 25-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F.
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-30166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-082-089-5

Query Match 50.7%; Score 36; DB 3; Length 363;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 RPK--PQQWF 9
Db 152 RPKDLPDRLW 162

RESULT 191
US-09-082-089-2
; Sequence 2, Application US/09082089
; Patent No. 6100060
; GENERAL INFORMATION:
; APPLICANT: BARNES, MICHAEL
; APPLICANT: TESTA, TANIA
; APPLICANT: KELSELL, DAVID
; TITLE OF INVENTION: No. 6100060e1 Compounds
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,089
; FILING DATE: 20-MAY-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9710737.9
; FILING DATE: 23-MAY-1997
; APPLICATION NUMBER: GB 9803981.1
; FILING DATE: 25-FEB-1998
; APPLICATION NUMBER: GB 9804007.4
; FILING DATE: 25-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F.
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-30166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-082-089-2

Query Match 50.7%; Score 36; DB 3; Length 372;
Best Local Similarity 54.5%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 RPK--PQQWF 9
Db 161 RPKDLPDRLW 171

RESULT 192
US-08-677-049-2
; Sequence 2, Application US/08677049
; Patent No. 5858707
; GENERAL INFORMATION:
; APPLICANT: Guimaraes, M. Jorge
; APPLICANT: Bazan, J. Fernando
; APPLICANT: McClanahan, Terrill K.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: PURIFIED MAMMALIAN NUCLEOBASE PERMEASES;
; TITLE OF INVENTION: NUCLEIC ACIDS; ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,049
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,788
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Egwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0511
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 611 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-677-049-2

Query Match 50.7%; Score 36; DB 2; Length 611;
Best Local Similarity 55.6%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PKPQQWF 10
Db 296 PSDAPFWL 304

Mon Apr 1 16:34:29 2002

us-09-988-792-2.50pct.ra1

Page 71

Search completed: April 1, 2002, 16:18:46
Job time: 77 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run On: April 1, 2002, 16:19:17 ; Search time 23.26 seconds
(without alignments)
36.024 Million cell updates/sec

Title: US-09-988-792-2
Perfect score: 71
Sequence: 1 RPKPQQWFWM 11

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 147

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

(Post-processing: Minimum Match 50%

Maximum Match 100%
Listing first 1000 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	67.6	11	1 SPHO	substance P - hors
2	48	67.6	11	1 A60654	substance P - guin
3	48	67.6	63	2 JC2412	tachykinin gamma c
4	48	67.6	72	2 I62742	tachykinin A gamma
5	48	67.6	72	2 JC5455	preprotachykinin-A
6	48	67.6	97	2 SI2958	tachykinin delta p
7	48	67.6	112	1 SPRTA	substance P alpha
8	48	67.6	115	1 SPRBG	substance P gamma
9	48	67.6	115	2 S47039	tachykinin 1 precu
10	48	67.6	129	1 SHUB	neurokinin 1 precu
11	48	67.6	130	1 SPRTB	substance P beta p
12	48	67.6	130	1 SPBOB	neurokinin 1 precu
13	48	67.6	130	2 S47038	tachykinin 1 precu
14	48	67.6	130	2 IS2526	neurokinin 1 precu
15	45	63.4	11	2 JN0023	substance P - chic
16	45	63.4	453	2 F81720	lipid A biosynthes
17	45	63.4	455	2 E71569	probable acyltrans
18	44	62.0	437	1 B29336	ubiquinol--cytochr
19	43	60.6	365	2 C81050	cytochrome c oxida
20	43	60.6	365	2 F81826	probable cytochrom
21	42	59.2	378	1 A40004	histidine decarbox
22	41	57.7	55	2 T11538	H+-transporting AT
23	41	57.7	158	2 H70028	conserved hypothet
24	41	57.7	159	2 D71500	hypothetical prote
25	41	57.7	261	2 C83157	hypothetical prote
26	41	57.7	286	2 B82564	acetylxlylan estera
27	41	57.7	291	1 S76015	hypothetical prote
28	41	57.7	304	2 A84353	acetyltransferase
29	41	57.7	529	2 S76167	hypothetical prote

30	40	56.3	273	2 C82182	hypothetical prote
31	40	56.3	289	2 D81085	HtrB/Msbb family p
32	40	56.3	289	2 B81857	probable acetyltra
33	40	56.3	290	2 E71631	lipid A biosynthes
34	40	56.3	318	2 G82350	lipid A biosynthes
35	40	56.3	343	2 T42129	probable acyltrans
36	40	56.3	363	2 S74814	hypothetical prote
37	40	56.3	665	2 S52072	DMCNGC protein - f
38	39	55.6	548	2 B75427	hypothetical prote
39	39	54.9	55	2 T11768	H+-transporting AT
40	39	54.9	99	2 JQ1632	HCLFI protein - hu
41	39	54.9	208	2 S76097	hypothetical prote
42	39	54.9	341	2 B86503	acyltransferase li
43	39	54.9	361	2 A36669	galactoside 3(4)-L
44	39	54.9	374	2 A42270	alpha (1,3) fucosy
45	39	54.9	412	2 D71803	ubiquinol--cytochr
46	39	54.9	416	2 F83010	probable oxidoredu
47	39	54.9	440	1 B29413	ubiquinol--cytochr
48	39	54.9	452	2 F81436	probable integral
49	39	54.9	462	2 E81551	lipid A biosynthes
50	39	54.9	467	2 B72119	acyltransferase -
51	39	54.9	480	2 E72682	hypothetical prote
52	39	54.9	525	2 H71365	probable licc prot
53	39	54.9	1015	2 T13062	CLOCK protein - fr
54	39	54.9	1023	2 T13068	CLOCK protein - fr
55	39	54.9	1027	2 T13071	CLOCK protein - fr
56	38	53.5	105	2 D83242	hypothetical prote
57	38	53.5	323	2 A85798	suppressor of htrB
58	38	53.5	323	2 A42608	(Kdo)2-(lauroyl)-1
59	38	53.5	328	2 A46521	52K phosphoprotein
60	38	53.5	330	2 A30533	lymphocyte-specifi
61	38	53.5	330	2 I57835	lymphocyte-specifi
62	38	53.5	363	2 JE0111	lectin-like oxidiz
63	38	53.5	373	2 B82697	rod shape-determin
64	38	53.5	400	2 JC4591	alpha-1,3 fucosyl
65	38	53.5	405	2 B36340	alpha(1,3)-fucosyl
66	38	53.5	412	2 C64712	ubiquinol--cytochr
67	38	53.5	421	2 C96806	unknown protein T5
68	38	53.5	433	2 A57596	alpha-1,3-fucosyl
69	38	53.5	455	2 T04448	hypothetical prote
70	38	53.5	533	2 S62489	hypothetical prote
71	38	53.5	789	2 I59550	aryl hydrocarbon r
72	38	53.5	901	1 WNVNVT	104K glycoprotein
73	38	53.5	909	2 S76899	hypothetical prote
74	38	53.5	1184	2 T09484	cartilage intermed
75	38	53.5	1832	2 T31113	mucin-like glycopr
76	37.5	52.8	298	2 D69351	hypothetical prote
77	37.5	52.8	375	2 JQ0846	DNA-binding protei
78	37.5	52.8	1196	1 DNBEV1	major DNA-binding
79	37.5	52.8	1196	1 DNBEKS	DNA-binding protei
80	37.5	52.8	1196	1 DNBEHF	DNA-binding protei
81	37.5	52.8	1197	1 A48350	DNA-binding protei
82	37.5	52.8	1204	1 DNBE29	DNA-binding protei
83	37.5	52.8	1208	2 T42574	DNA-binding protei
84	37.5	52.8	1209	1 DNBECA	DNA-binding protei
85	37	52.1	11	2 S23308	substance p - rain
86	37	52.1	175	2 S50061	DNA binding protei
87	37	52.1	274	2 T39087	hypothetical prote
88	37	52.1	342	2 A54057	alpha(1,3)-fucosyl
89	37	52.1	365	2 S55498	alpha(1,3/4)-fucos
90	37	52.1	403	2 H64861	hypothetical prote
91	37	52.1	404	1 S25953	ubiquinol--cytochr
92	37	52.1	436	2 B82147	conserved hypothet
93	37	52.1	536	2 C82433	methyl-accepting c
94	37	52.1	655	1 A54306	proprotein convert
95	37	52.1	662	1 TOBPU	transposase - phag
96	37	52.1	681	2 I78558	hypothetical Brach
97	37	52.1	747	2 I39444	AMP deaminase (EC
98	37	52.1	1002	2 T34252	deep orange protei
99	37	52.1	1239	2 G02750	DNA-directed DNA p
100	37	52.1	1384	2 T26656	hypothetical prote
101	37	52.1	1635	2 T32452	hypothetical prote
102	37	52.1	2458	2 T17420	probable polyketid

103 36.5 51.4 537 2 JC4534 cytochrome P450 4F
104 36.5 51.4 659 2 S77658 hypothetical prote
105 36.5 51.4 1186 1 DNBBEG DNA-binding protei
106 36 50.7 11 2 S23306 substance P - Atla
107 36 50.7 55 2 S45489 H+-transporting AT
108 36 50.7 103 2 S77270 hypothetical prote
109 36 50.7 154 2 C75435 hypothetical prote
110 36 50.7 171 2 E83140 phosphatidylglycer
111 36 50.7 187 2 S43177 p18 protein - lels
112 36 50.7 268 2 T16544 hypothetical prote
113 36 50.7 280 2 A82185 glycerol-3-phospha
114 36 50.7 287 2 A75511 conserved hypothet
115 36 50.7 318 2 I64053 membrane-bound lyt
116 36 50.7 330 2 S76408 hypothetical prote
117 36 50.7 347 2 S44995 pectate lyase - Er
118 36 50.7 353 4 I59347 hypothetical gluta
119 36 50.7 360 2 S34173 wnt-5c protein - A
120 36 50.7 365 2 A48914 proto-oncogene Wnt
121 36 50.7 372 2 S75038 hypothetical prote
122 36 50.7 379 2 E36470 Wnt-5b protein - m
123 36 50.7 379 2 D36470 Wnt-5a protein - m
124 36 50.7 380 2 A71390 ubiquinol--cytochr
125 36 50.7 380 2 S70394 ubiquinol--cytochr
126 36 50.7 381 2 S59093 citrate synthase p
127 36 50.7 473 2 T39028 cytochrome P450 4F
128 36 50.7 522 2 JC4532 hypothetical prote
129 36 50.7 605 2 T35047 hypothetical prote
130 36 50.7 643 2 E69234 acetyl-CoA synthet
131 36 50.7 656 2 T01573 conserved hypothet
132 36 50.7 670 2 A75542 toxin secretion AT
133 36 50.7 704 2 H82381 probable cytoplasm
134 36 50.7 720 2 C85547 NADH dehydrogenase
135 36 50.7 774 2 A70010 probable Na+/H+-ex
136 36 50.7 804 2 S61395 Na+/H+ antiporter
137 36 50.7 804 2 G83814 pled protein - Syn
138 36 50.7 829 2 S75776 hypothetical prote
139 36 50.7 861 2 S77086 hypothetical prote
140 36 50.7 959 2 T14761 hypothetical prote
141 36 50.7 1038 2 T25033 hypothetical prote
142 36 50.7 1039 2 T22982 hypothetical prote
143 36 50.7 1377 2 T19214 UDP-glucose-glyco
144 36 50.7 1493 2 T16404 hypothetical prote
145 36 50.7 1674 2 G96736 kakapo gene protei
146 36 50.7 2396 2 T13714 giant protein p619
147 35.5 50.0 4861 2 S71752

ALIGNMENTS

RESULT 1
SPHO substance P - horse
C:Species: Equus caballus (domestic horse)
C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996
C:Accession: A01558
R:Studer, R.O.; Trzeciak, A.; Lergier, W.
Helv. Chim. Acta 56, 860-866, 1973
A:Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.
A:Reference number: A01558
A:Accession: A01558
A:Molecule type: protein
A:Residues: 1-11 <STU>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end; hormone
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.096;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11

Db 1 RPKPQQFFGLM 11
|||||:|
RESULT 2
A60654 substance P - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995
C:Accession: A60654
R:Murphy, R.
Neuropeptides 14, 105-110, 1989
A:Title: Primary amino acid sequence of guinea-pig substance P.
A:Reference number: A60654; MUID:90044685
A:Accession: A60654
A:Molecule type: protein
A:Residues: 1-11 <MUR>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.096;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
|||||:|
Db 1 RPKPQQFFGLM 11
|||||:|
RESULT 3
JC2412 tachykinin gamma chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Feb-1995 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: JC2412
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in
A:Reference number: JC2411; MUID:94324969
A:Accession: JC2412
A:Molecule type: mRNA
A:Residues: 1-63 <KHA>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:12-21/Product: substance P #status predicted <SUP>
F:21/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match 67.6%; Score 48; DB 2; Length 63;
Best Local Similarity 81.8%; Pred. No. 0.54;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
|||||:|
Db 11 RPKPQQFFGLM 21
|||||:|
RESULT 4
I62742 tachykinin A gamma chain precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C:Accession: I62742; JC5453
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mo
A:Reference number: JC5450; MUID:91209287
A:Accession: I62742
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-72 <RES>

A:Cross-references: GB:M68909; NID:g200469; PIDN:AAA39970.1; PID:g554261
C:Comment: This protein contains two tachykinin peptide hormone substance-P which is involved in nociception.
C:Genetics:
A:Gene: gamma-PPT-A
C:Superfamily: substance P precursor
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-33/Product: substance-P #status predicted <STP>
F:48-57/Product: neurokinin-A #status predicted <NKA>

Query Match 67.6%; Score 48; DB 2; Length 72;
Best Local Similarity 81.8%; Pred. No. 0.61;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQQFWFLM 11
|||||:||
DB 23 RPKPQQQFFGLM 33

RESULT 5
JC5455
substance P alpha precursor - bovine
N:Alternates: Bos primigenius taurus (cattle)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 16-Jul-1999
C:Accession: JC5455; I45967
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse testis.
A:Reference number: JC5450; MUID:91209287
A:Accession: JC5455
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-72 <CHI>
A:Cross-references: GB:M68912; NID:g163593; PIDN:AAA30725.1; PID:g552336
C:Comment: This protein contains two tachykinin peptide hormone substance-P which is involved in nociception.
C:Genetics:
A:Gene: PPT-A
C:Superfamily: substance P precursor
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-33/Product: substance-P #status predicted <STP>
F:48-57/Product: neurokinin-A #status predicted <NKA>

Query Match 67.6%; Score 48; DB 2; Length 72;
Best Local Similarity 81.8%; Pred. No. 0.61;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQQFWFLM 11
|||||:||
DB 23 RPKPQQQFFGLM 33

RESULT 6
SI2958
tachykinin delta precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: SI2958; JC2413
R:Harmat, A.J.; Hyde, V.; Chapman, K.
FEBS Lett. 275, 22-24, 1990
A:Title: Identification and cDNA sequence of delta-preprotachykinin, a fourth splicing variant of the rat tachykinin gene.
A:Reference number: SI2958; MUID:91085565
A:Accession: SI2958
A:Molecule type: mRNA
A:Residues: 1-97 <CHAR>
A:Cross-references: GB:X56306; NID:g56067; PIDN:CAA39752.1; PID:g56068
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in the rat brain.
A:Reference number: JC2411; MUID:94324969
A:Accession: JC2413
A:Molecule type: mRNA
A:Residues: 48-92 <KHA>

A:Cross-references: GB:S72369; NID:g632805; PIDN:AAB31499.1; PID:g632806
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:59-68/Product: substance P #status predicted <SUP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match 67.6%; Score 48; DB 2; Length 97;
Best Local Similarity 81.8%; Pred. No. 0.82;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQQFWFLM 11
|||||:||
DB 58 RPKPQQQFFGLM 68

RESULT 7
SPRTA
substance P alpha precursor - rat
N:Alternates: preprotachykinin alpha
N:Contains: substance P
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: B26590
R:Krause, J.E.; Chirgwin, J.M.; Carter, M.S.; Xu, Z.S.; Hershey, A.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 881-885, 1987
A:Title: Three rat preprotachykinin mRNAs encode the neuropeptides substance P and neuropeptide Y.
A:Reference number: A94187; MUID:87118268
A:Accession: B26590
A:Molecule type: mRNA
A:Residues: 1-112 <KRA>
A:Cross-references: GB:M34184; NID:g206329; PIDN:AAA41975.1; PID:g206330
C:Comment: Alternative splicing of the mRNA for substance P precursor yields the alpha and beta forms.
C:Superfamily: substance P precursor
F:1-112/Product: substance P alpha precursor #status predicted <SIG>
F:1-15/Domain: signal sequence #status predicted <SIG>
F:58-68/Product: substance P #status predicted <SBP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match 67.6%; Score 48; DB 1; Length 112;
Best Local Similarity 81.8%; Pred. No. 0.95;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQQFWFLM 11
|||||:||
DB 58 RPKPQQQFFGLM 68

RESULT 8
SPRBG
substance P gamma precursor - rabbit
N:Alternates: gamma-neuropeptide K; gamma-preprotachykinin I precursor; tachykinin N; Contains: neurokinin A; neuropeptide K; substance P
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Nov-1992 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: JN0709; A60302; A60200; S18922
R:Maegert, H.J.; Heitland, A.; Rose, M.; Forssmann, W.G.
Biochem. Biophys. Res. Commun. 195, 128-131, 1993
A:Title: Nucleotide sequence of the rabbit gamma-preprotachykinin I cDNA.
A:Reference number: JN0709; MUID:93371392
A:Accession: JN0709
A:Molecule type: mRNA
A:Residues: 1-115 <MA>
A:Cross-references: EMBL:X62994; NID:g1565; PIDN:CAA44728.1; PID:g1566
R:Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.
Regul. Pept. 18, 346, 1987
A:Title: gamma-Neuropeptide K: a peptide isolated from rabbit gut that is derived from the same gene as neuropeptide Y.
A:Reference number: A60302
A:Accession: A60302
A:Molecule type: protein

A;Residues: 72-92 <KAG>
 J. Neurochem. 50, 1412-1417, 1988
 A;Title: Neuropeptide-gamma: a peptide isolated from rabbit intestine that is derived from
 A;Reference number: A60200; MUID:88199570
 A;Accession: A60200
 A;Molecule type: protein
 A;Residues: 72-92 <KA2>
 C;Comment: The gamma alternatively spliced form is processed to yield substance P and neuropeptide K precursor
 C;Superfamily: substance P precursor
 C;Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin
 F;1-15/Domain: signal sequence #status predicted <SIG>
 F;58-68/Product: substance P #status predicted <SBP>
 F;72-92/Product: gamma-neuropeptide K #status experimental <NPK>
 F;83-92/Product: neurokinin A #status predicted <NKA>
 F;68/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycosylation)
 F;92/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycosylation)

Query Match 67.6% Score 48; DB 1; Length 115;
 Best Local Similarity 81.8%; Pred. No. 0.97;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQWFWM 11
 |||||:|
 Db 58 RPKPQWFWM 68

RESULT 9
 S47039
 tachykinin 1 precursor - golden hamster
 C;Species: Mesocricetus auratus (golden hamster)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
 C;Accession: S47039
 R;Heitland, A.; Kruhoffer, M.; Juergen Maegert, H.J.; Forssmann, W.G.
 submitted to the EMBL Data Library, July 1994
 A;Reference number: S47038
 A;Accession: S47039
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-115 <HEI>
 A;Cross-references: EMBL:X80663; NID:g520938; PIDN:CAA56692.1; PID:g520939
 C;Superfamily: substance P precursor

Query Match 67.6% Score 48; DB 2; Length 115;
 Best Local Similarity 81.8%; Pred. No. 0.97;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQWFWM 11
 |||||:|
 Db 58 RPKPQWFWM 68

RESULT 10
 SPHUB
 neurokinin 1 precursor, beta splice form [validated] - human
 N;Alternate names: neurokinin A; neurokinin alpha; neuromedin L; neuropeptide K; preprotachykinin
 N;Contains: neurokinin 1; neurokinin 1 precursor, alpha splice form; neurokinin 1 precursor
 C;Species: Homo sapiens (man)
 C;Date: 12-Feb-1988 #sequence_revision 26-May-1995 #text_change 19-May-2000
 R;Harmar, A.J.; Armstrong, A.; Pascall, J.C.; Chapman, K.; Rosle, R.; Curtis, A.; Goings, F.E.B. Lett. 208, 67-72, 1986
 A;Title: cDNA sequence of human beta-preprotachykinin, the common precursor to substance P and neuropeptide K
 A;Accession: A24805
 A;Molecule type: mRNA
 A;Residues: 1-129 <HAR>
 A;Cross-references: EMBL:X54469; EMBL:X28109; NID:g29482; PIDN:CAA38351.1; PID:g29483
 R;McGregor, G.P.; Conlon, J.M.
 Peptides 11, 907-910, 1990
 A;Title: Characterization of the C-terminal flanking peptide of human beta-preprotachykinin

A;Reference number: A60425; MUID:91133994
 A;Accession: A60425
 A;Molecule type: protein
 A;Residues: 111-126 <MCG>
 A;Experimental source: neuroendocrine tumor of adrenal medulla
 R;Theodorsson-Norheim, E.; Joernvall, H.; Andersson, M.; Norheim, I.; Oberg, K.; Jac Eur. J. Biochem. 166, 693-697, 1987
 A;Title: Isolation and characterization of neurokinin A, neurokinin A(3-10) and neurokinin B
 A;Reference number: S00069; MUID:87275962
 A;Accession: S00069
 A;Molecule type: protein
 A;Residues: 98-107 <THE>
 R;Kage, R.; Thim, L.; Creutzfeldt, W.; Conlon, J.M.
 Biochem. J. 253, 203-207, 1988
 A;Title: Post-translational processing of preprotachykinins. Isolation of protachykinin
 A;Reference number: S03033; MUID:88339887
 A;Accession: S03033
 A;Molecule type: protein
 A;Residues: 20-30 <KAG>
 R;Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
 Endocrinology 128, 2441-2448, 1991
 A;Title: tachykinin (substance-P) gene expression in Leydig cells of the human and mouse
 A;Reference number: JC5450; MUID:91209287
 A;Accession: JC5451
 A;Status: translation not shown; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 36-73, 89-122 <CHII>
 A;Cross-references: GB:M68907; NID:g190292; PIDN:AAA60160.1; PID:g553619
 A;Accession: JC5450
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 36-86, 'P', 88-122 <CHII>
 A;Cross-references: GB:M68906; NID:g190290; PIDN:AAA60159.1; PID:g553618
 R;Tan, A.; Too, H.P.
 submitted to GenBank, October 1995
 A;Reference number: A59269
 A;Accession: A59269
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-129 <TAN>
 A;Cross-references: GB:U037529; NID:g1017792; PIDN:AAA79195.1; PID:g1017793
 A;Experimental source: tissue brain cortex
 R;Lai, J.P.; Douglas, S.D.; Rappaport, E.; Wu, J.M.; Ho, W.Z.
 submitted to GenBank, February 1998
 A;Description: Identification of a delta isoform of preprotachykinin mRNA in human
 A;Reference number: A59270
 A;Accession: A59270
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 36-96, 'M', 116-118 <LAI1>
 A;Cross-references: GB:AF050656; NID:g3098594; PIDN:AAC15702.1; PID:g3098595
 A;Experimental source: alpha splice form; tissue blood; tissue brain; cell type monoclonal K)
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 36-73, 89-96, 'M', 116-122 <LAI2>
 A;Cross-references: GB:AF050658; NID:g3098598; PIDN:AAC15704.1; PID:g3098599
 A;Experimental source: delta splice form; tissue blood; tissue brain; cell type monoclonal K)
 C;Comment: This protein is processed to produce the tachykinin peptide hormones neurokinin K).

C;Genetics:
 A;Gene: GDB:TAC1; TAC2; NKNA; PPT-A
 A;Cross-references: GDB:119452; OMIM:162320
 A;Map position: 7q21-q22
 C;Superfamily: substance P precursor
 C;Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin
 F;1-129/Product: neurokinin 1 precursor, beta splice form #status predicted <SPB>
 F;1-96, 'M', 116-118/Product: neurokinin 1 precursor, alpha splice form #status predicted <S>
 F;1-73, 89-129/Product: neurokinin 1 precursor, gamma splice form #status predicted <S>
 F;1-73, 89-96, 'M', 116-122/Product: neurokinin 1 precursor, alpha splice form #status predicted <S>
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-57/Domain: amino-terminal propeptide #status predicted <PRO>
 F;58-68/Product: neurokinin 1 #status experimental <NK1>

F:72-107/Product: neuropeptide K #status predicted <NEK>
F:98-107/Product: neurokinin 2 #status experimental <NK2>
F:100-107/Product: neurokinin 2(3-10) #status experimental <NK23>
F:101-107/Product: neurokinin 2(4-10) #status experimental <NK24>
F:111-126/Domain: carboxyl-terminal propeptide #status experimental <CTP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 67.6%; Score 48; DB 1; Length 129;
Best Local Similarity 81.8%; Pred. No. 1.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQWFWM 11
|||||:|
DB 58 RPKPOQFFGLM 68

RESULT 11
SPRTB
Substance P beta precursor - rat
N:Alternate names: preprotachykinin beta; preprotachykinin gamma; substance K
N:Contains: neurokinin A; substance P; substance P gamma precursor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: A37163; A26590; C26590; A25067; JC2411
R:Carter, M.S.; Krause, J.E.
J. Neurosci. 10, 2203-2214, 1990
A:Title: Structure, expression, and some regulatory mechanisms of the rat preprotachykinin
A:Reference number: A37163; MUID:90331040
A:Accession: A37163
A:Molecule type: DNA
A:Residues: 1-130 <CA>
A:Cross-references: GB:M34159; GB:M34160; GB:M34162; NID:g206334; PIDN:AAA41926.1; PID:g206344
R:Krause, J.E.; Chirgwin, J.M.; Carter, M.S.; Xu, Z.S.; Hershey, A.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 881-885, 1987
A:Title: Three rat preprotachykinin mRNAs encode the neuropeptides substance P and neurokinin B
A:Reference number: A94187; MUID:87118268
A:Accession: A26590
A:Molecule type: mRNA
A:Residues: 1-130 <KRA>
A:Cross-references: GB:M15191; NID:g206341; PIDN:AAA41928.1; PID:g206342; GB:M35277
A:Accession: C26590
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <KR2>
A:Cross-references: GB:M34183; NID:g206343; PIDN:AAA41929.1; PID:g206344
R:Kawaguchi, Y.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 139, 1040-1046, 1986
A:Title: Sequence analysis of cloned cDNA for rat substance P precursor: existence of a
A:Reference number: A25067; MUID:87025808
A:Accession: A25067
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <KAW>
A:Cross-references: GB:M14312; NID:g206339; PIDN:AAA41927.1; PID:g206340
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in the
A:Reference number: JC2411; MUID:94324969
A:Accession: JC2411
A:Molecule type: mRNA
A:Residues: 48-110 <KHA>
A:Experimental source: intestine
C:Comment: Alternative splicing of the mRNA for substance P precursor yields the beta and gamma forms
C:Comment: The beta and gamma forms are processed to yield substance P and neurokinin A
C:Genetics:
A:Introns: 41/3; 74/1; 89/1; 97/1; 115/1
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin
F:1-130/Product: substance P beta precursor #status predicted <PREB>
F:1-73, 89-130/Product: substance P gamma precursor #status predicted <SIG>
F:1-15/Domain: signal sequence #status predicted <SIG>
F:58-68/Product: neurokinin A #status predicted <SBP>
F:98-107/Product: neurokinin A #status predicted <NKA>

F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match 67.6%; Score 48; DB 1; Length 130;
Best Local Similarity 81.8%; Pred. No. 1.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQWFWM 11
|||||:|
DB 58 RPKPOQFFGLM 68

RESULT 12
SPROB
neurokinin 1 precursor, beta splice form [validated] - bovine
N:Alternate names: neurokinin A; preprotachykinin; substance K; substance P
N:Contains: neurokinin 1; neurokinin 1 precursor, alpha splice form; neurokinin 1 pre
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 16-Jun-2000
C:Accession: A05093; A01559; A01557; B25067; A61460; JC5454; I45966
R:Nawa, H.; Kotani, H.; Nakanishi, S.
Nature 312, 729-734, 1984
A:Title: Tissue-specific generation of two preprotachykinin mRNAs from one gene by al
A:Reference number: A05093; MUID:85086245
A:Accession: A05093
A:Molecule type: DNA
A:Residues: 1-130 <NAW1>
A:Cross-references: GB:X02351; GB:M14786; NID:g655; PIDN:CAA24942.1; PID:g1197197
R:Nawa, H.; Hirose, T.; Takashima, H.; Inayama, S.; Nakanishi, S.
Nature 306, 32-36, 1983
A:Title: Nucleotide sequences of cloned cDNAs for two types of bovine brain substance
A:Reference number: A93318; MUID:84039802
A:Accession: A01559
A:Molecule type: mRNA
A:Residues: 1-130 <NAW2>
A:Cross-references: GB:X00075; NID:g758; PIDN:CAA24939.1; PID:g759
A:Accession: A01557
A:Molecule type: mRNA
A:Residues: 1-96, 'M', 116-130 <NAW3>
A:Cross-references: GB:X00076; NID:g762; PIDN:CAA24942.1; PID:g763
R:Kawaguchi, Y.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 139, 1040-1046, 1986
A:Title: Sequence analysis of cloned cDNA for rat substance P precursor: existence of
A:Reference number: A25067; MUID:87025808
A:Accession: B25067
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <KAW>
R:McGregor, G.P.; Kage, R.; Thim, L.; Conlon, J.M.
J. Neurochem. 53, 1871-1877, 1989
A:Title: Quantitation and characterization of peptides from the C-terminal flanking r
A:Reference number: A61460; MUID:90039314
A:Accession: A61460
A:Molecule type: protein
A:Residues: 111-126 <MCG>
A:Experimental source: corpus striatum
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mo
A:Reference number: JC5450; MUID:91209287
A:Accession: JC5454
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 36-120, 'A', 122 <CHI>
A:Cross-references: GB:M68911; NID:q163591; PIDN:AAA30724.1; PID:g552335
C:Comment: The protein is processed to produce neurokinin 1 (substance P) and neuroki
C:Genetics:
A:Introns: 41/3; 74/1; 89/1; 97/1; 115/1
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachy
F:1-130/Product: neurokinin 1 precursor, beta splice form #status predicted <SPB>
F:1-96, 'M', 116-130/Product: neurokinin 1 precursor, alpha splice form #status predict

F;1-73,89-130/Product: neurokinin 1 precursor, gamma splice form #status predicted <SPG>
F;1-19/Domains: signal sequence #status predicted <SIG>
F;20-57/Domains: amino-terminal propeptide #status predicted <PRO>
F;58-68/Product: neurokinin 1 #status experimental <SBP>
F;98-107/Product: neurokinin 2 #status predicted <NEK>
F;111-126/Domains: carboxyl-terminal propeptide #status experimental <CTP>
F;68/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly
F;107/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 67.6%; Score 48; DB 1; Length 130;
Best Local Similarity 81.8%; Pred. No. 1.1;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|
Db 58 RPKPQQFFGLM 68

RESULT 13
S47038
tachykinin 1 precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S47038
R;Heitland, A.; Kruhoffer, M.; Juergen Maegert, H.J.; Forssmann, W.G.
submitted to the EMBL Data Library, July 1994
A;Reference number: S47038
A;Accession: S47038
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <HEI>
A;Cross-references: EMBL:X80662; NID:g520917; PIDN:CAA56691.1; PID:g520918
C;Superfamily: substance P precursor

Query Match 67.6%; Score 48; DB 2; Length 130;
Best Local Similarity 81.8%; Pred. No. 1.1;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|
Db 58 RPKPQQFFGLM 68

RESULT 14
I52526
neurokinin 1 precursor - mouse
N;Alternate names: neurokinin A; preprotachykinin; substance K; substance P
N;Contains: neurokinin 1; neurokinin 2
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-2000
C;Accession: I52526; JC5452; I62741
R;Kako, K.; Muneakata, E.; Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 14, 253-259, 1993
A;Title: Cloning and sequence analysis of mouse cDNAs encoding preprotachykinin A and B.
A;Reference number: I52526
A;Accession: I52526
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-130 <KAK>
R;Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A;Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse
A;Reference number: JC5452; MUID:91209287
A;Accession: JC5452
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 36-122 <CHI>
A;Cross-references: GB:M68908; NID:g200467; PIDN:AAA39969.1; PID:g554260
C;Genetics:
A;Gene: PPT-A

C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end
F;1-19/Domains: signal sequence #status predicted <SIG>
F;20-57/Domains: amino-terminal propeptide #status predicted <PRO>
F;58-68/Product: neurokinin 1 #status predicted <NK1>
F;98-107/Product: neurokinin 2 #status predicted <NK2>
F;111-126/Domains: carboxyl-terminal propeptide #status predicted <CTP>
F;68/Modified site: amidated carboxyl end (Met) (amide in mature form from following
F;107/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match 67.6%; Score 48; DB 2; Length 130;
Best Local Similarity 81.8%; Pred. No. 1.1;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|
Db 58 RPKPQQFFGLM 68

RESULT 15
JN0023
substance P - chicken
C;Species: Gallus gallus (chicken)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997
C;Accession: JN0023
R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
Regul. Pept. 20, 171-180, 1988
A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.
A;Reference number: JN0023; MUID:86204263
A;Accession: JN0023
A;Molecule type: protein
A;Residues: 1-11 <CON>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 63.4%; Score 45; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.28;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||:|:|
Db 1 RRPQPQFFGLM 11

RESULT 16
F81720
lipid A biosynthesis lauroyl acyltransferase, probable TC0278 [imported] - Chlamydia
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C;Accession: F81720
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A;Reference number: A81500; MUID:20150255
A;Accession: F81720
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-453 <TET>
A;Cross-references: GB:AE002295; GB:AE002160; NID:g7190314; FIDN:AAF39146.1; PID:g719
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0278

Query Match 63.4%; Score 45; DB 2; Length 453;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPPQWFWM 10

Db 303 KPEQWLWL 310
||:||||

RESULT 17

E71569
probable acyltransferase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C:Accession: E71569
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
A:Reference number: A71570; MUID:99000809
A:Accession: E71569
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-455 <ARN>
A:Cross-references: GB:AE001275; GB:AE001273; NID:g3328386; PIDN:AAC67600.1; PID:g332839
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: htrB

Query Match 63.4%; Score 45; DB 2; Length 455;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 KPQQWFWL 10
||:||||

Db 303 KPEQWLWL 310

RESULT 18

B29336
ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Rhodobacter capsulatus
C:Species: Rhodobacter capsulatus
C:Date: 31-Dec-1988 #sequence_revision 22-Jul-1994 #text_change 03-Mar-2000
C:Accession: B29336; B25405; S09373
R:Davidson, E.; Daidal, F.
J. Mol. Biol. 195, 13-24, 1987
A:Title: Primary structure of the bc-1 complex of Rhodospseudomonas capsulata. Nucleotide sequence and transcription of the fbc operon from Rhodospseudomonas sphaeroides
A:Reference number: A92938; MUID:88011223
A:Accession: B29336
A:Molecule type: DNA
A:Residues: 1-437 <DAV>
A:Cross-references: EMBL:X05630; NID:g46093; PIDN:CAA29117.1; PID:g46095
R:Gabellini, N.; Sebal, W.
Eur. J. Biochem. 154, 569-579, 1986
A:Title: Nucleotide sequence and transcription of the fbc operon from Rhodospseudomonas sphaeroides

A:Reference number: A91162; MUID:86136096

A:Note: source is designated as Rhodospseudomonas sphaeroides

A:Accession: B25405

A:Molecule type: DNA

A:Residues: 1-66, 'ID', 69-280, 'I', 282-437 <GAB>

A:Cross-references: EMBL:X03476; NID:g46007; PIDN:CAA27195.1; PID:g46009

C:Genetics:

A:Gene: fbcB; petB

C:Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; cytochrome b6 homology; cytochrome b6 homology; electron transfer; heme; iron; metalloprotein; oxidoreductase
C:Keywords: cytochrome b homology <CBH>
F:26-381/Domain: cytochrome b homology <CBH>
F:26-225/Domain: cytochrome b6 homology <CB6>

F:51-67/Domain: transmembrane #status predicted <TM1>

F:96-114/Domain: transmembrane #status predicted <TM2>

F:134-150/Domain: transmembrane #status predicted <TM3>

F:146-193/Domain: periplasmic #status predicted <PER1>

F:195-217/Domain: transmembrane #status predicted <TM4>

F:245-381/Domain: plastoquinol--plastocyanin reductase 17K protein homology <17K>

F:253-269/Domain: transmembrane #status predicted <TM5>

F:270-329/Domain: periplasmic #status predicted <PER2>

F:330-346/Domain: transmembrane #status predicted <TM6>

F:365-383/Domain: transmembrane #status predicted <TM7>

F:395-411/Domain: transmembrane #status predicted <TM8>
F:97,198/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted <F97,198>
F:111,212/Binding site: heme iron (His) (axial ligands) (high potential) #status predicted <F111,212>

Query Match 62.0%; Score 44; DB 1; Length 437;

Best Local Similarity 54.5%; Pred. No. 15;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKQWFWL 11

||:||||

Db 360 RPKRWFNFWL 370

RESULT 19

C81050
cytochrome c oxidase, chain III NMB1723 [imported] - Neisseria meningitidis (strain M)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: C81050
R:Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. et al.; Qi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; et al.
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755
A:Accession: C81050
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-365 <TET>
A:Cross-references: GB:AE002522; GB:AE002098; NID:g7226972; PIDN:AAF42068.1; PID:g722
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1723

Query Match 60.6%; Score 43; DB 2; Length 365;

Best Local Similarity 56.7%; Pred. No. 18;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PKPQWFWL 10

||:||||

Db 62 PLPRWFWL 70

RESULT 20

F81826
probable cytochrome c NMA1977 [imported] - Neisseria meningitidis (strain Z2491 serog)
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: F81826
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; MO et al.; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491

A:Reference number: A81775; MUID:20222556

A:Accession: F81826

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-365 <PAR>

A:Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85197.1; PID:g738

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: NMA1976; NMA1977

Query Match 60.6%; Score 43; DB 2; Length 365;

Best Local Similarity 56.7%; Pred. No. 18;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PKPQWFWL 10

||:||||

Db 62 PLPRWFWL 70

RESULT 21

A40004

histidine decarboxylase (EC 4.1.1.22) - Enterobacter aerogenes

C:Species: Enterobacter aerogenes

C>Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 18-Jun-1999

C:Accession: A40004

R:Kamath, A.V.; Vaaler, G.L.; Snell, E.E.

J. Biol. Chem. 266, 9432-9437, 1991

A:Title: Pyridoxal phosphate-dependent histidine decarboxylases. Cloning, sequencing, and enzymes.

A:Reference number: A40004; MUID:91236707

A:Accession: A40004

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-378 <RAM>

A:Cross-references: GB:M62745; NID:g435593; PIDN:AAA24802.1; PID:g435594

C:Superfamily: Klebsiella histidine decarboxylase

C:Keywords: carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

F:233/Binding site: pyridoxal phosphate (Lys) (covalent) #status Predicted

Query Match 59.2%; Score 42; DB 1; Length 378;

Best Local Similarity 62.5%; Pred. No. 26;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPQOWFW 9

||| :|

Db 329 PKPSEWVW 336

RESULT 22

T11538

H+-transporting ATP synthase (EC 3.6.1.34) protein 8 - spiny dogfish mitochondrion

C:Species: mitochondrion Squalus acanthias (spiny dogfish)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T11538

R:Rasmussen, A.S.; Arnason, U.

J. Mol. Evol. 48, 118-123, 1999

A:Title: Phylogenetic studies of complete mitochondrial DNA molecules place cartilaginous

A:Reference number: Z17281; MUID:99091711

A:Accession: T11538

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-55 <RAS>

A:Cross-references: EMBL:Y18134; NID:g4186095; PIDN:CAA77053.1; PID:g4186100

C:Genetics:

A:Genome: mitochondrion

A:Genetic code: SGC1

C:Superfamily: H+-transporting ATP synthase protein 8

C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; ox

Query Match 57.7%; Score 41; DB 2; Length 55;

Best Local Similarity 55.6%; Pred. No. 5.6;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQOWFW 9

:||| :|

Db 44 KKPPEPWNW 52

RESULT 23

H70028

conserved hypothetical protein yvaw - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999

C:Accession: H70028

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berta

C.; Bron, S.; Brouillet, S.; Bruchli, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosa, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Zanchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis

A:Reference number: A69580; MUID:98044033

A:Accession: H70028

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-158 <KUN>

A:Cross-references: GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CAB15380.1; PID:ell860

A:Experimental source: strain 168

C:Genetics:

A:Gene: yvaw

Query Match 57.7%; Score 41; DB 2; Length 158;

Best Local Similarity 50.0%; Pred. No. 16;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQOWFWL 10

||| :|

Db 131 RQKPLSYWI 140

RESULT 24

D71500

hypothetical protein CT556 - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C:Species: Chlamydia trachomatis

C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 18-Aug-2000

C:Accession: D71500

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, F.; Aravind, L.; Mitche

Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t

A:Reference number: A71570; MUID:99000809

A:Accession: D71500

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-159 <ARN>

A:Cross-references: GB:AE001326; GB:AE001273; NID:g3328990; PILEN:AA68158.1; PID:g332

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: CT556

C:Superfamily: conserved hypothetical protein TC0844

Query Match 57.7%; Score 41; DB 2; Length 159;

Best Local Similarity 66.7%; Pred. No. 16;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQOWFWL 10

||| :|

Db 89 PAFSQWDWL 97

RESULT 25

C83157

hypothetical protein PA3907 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: C83157

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337
A:Accession: C83157
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-261 <STO>
A:Cross-references: GB:AE004808; GB:AE004091; NID:g9950086; PIDN:AAG07294.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3907

Query Match 57.7%; Score 41; DB 2; Length 261;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPQQWF 9
| | : |||
Db 126 PPHFW 133

RESULT 26
B82564
acetylglucan esterase XF2395 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: B82564
R:anonymous. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: B82564

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-286 <SIM>

A:Cross-references: GB:AE004048; GB:AE003849; NID:g9107566; PIDN:AAF85194.1; GSPDB:GN001
A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

B:Riones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tshukako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Contents: annotation

C:Genetics:

A:Gene: XF2395

Query Match 57.7%; Score 41; DB 2; Length 286;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQQWF 11
| | | | |
Db 165 PQHFW 172

RESULT 27

S76015

hypothetical protein - Synecocystis sp. (strain PCC 6803)

C:Species: Synecocystis sp.

A:Variety: PCC 6803

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

C:Accession: S76015

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocys
s.

A:Reference number: S74322; MUID:97061201

A:Accession: S76015

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-291 <KAN>

A:Cross-references: EMBL:D64006; GB:AB001339; NID:g1001291; PID:g1001372

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Superfamily: Aquifex aeolicus cyso protein

Query Match 57.7%; Score 41; DB 1; Length 291;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQQWF 11
| | | | |
Db 88 PLPQDWVII 97

RESULT 28

A84353

acetyltransferase homolog [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: A84353

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky

; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja

ung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483

A:Accession: A84353

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-304 <STO>

A:Cross-references: GB:AE004437; NID:g10581454; PIDN:AAG20189.1; GSPDB:GN00138

C:Genetics:

A:Gene: Yyai

Query Match 57.7%; Score 41; DB 2; Length 304;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
| | | | |
Db 96 RSKPLQWLW 104

RESULT 29

S76167

hypothetical protein - Synecocystis sp. (strain PCC 6803)

C:Species: Synecocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C:Accession: S76167

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocys

s.

A:Reference number: S74322; MUID:97061201

A:Accession: S76167

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-529 <KAN>

A:Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAAL8426.1; PID:d101

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

```
Query Match          57.7%; Score 41; DB 2; Length 529;
Best Local Similarity 70.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQFWL 10
   |||||
Db 368 RPLPQDWFLL 377

RESULT 30
C82182
hypothetical protein VC1577 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: C82182
R:Heidelbergl, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
  Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
  L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833
A:Accession: C82182
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-273 <HEI>
A:Cross-references: GB:AE004235; GB:AE003852; NID:g9656082; PIDN:AAF94731.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1577
A:Map position: 1

Query Match          56.3%; Score 40; DB 2; Length 273;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQFWL 10
   ||||
Db 262 PEQIWL 268

RESULT 31
D81085
HtrB/MsbB family protein NMB1418 [imported] - Neisseria meningitidis (strain MC58 serog
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: D81085
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
  Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
  ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandl, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755
A:Accession: D81085
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <PFT>
A:Cross-references: GB:AE002491; GB:AE002098; NID:g7226655; PIDN:AAF41779.1; PID:g722665
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1418

Query Match          56.3%; Score 40; DB 2; Length 289;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQFWL 10
   |||||
Db 265 REHPEQYFWL 274
```

```
RESULT 32
B81857
probable acetyltransferase NMA1630 [imported] - Neisseria meningitidis (strain 22491
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: B81857
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
  Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
  Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491
A:Reference number: A81775; MUID:20222556
A:Accession: B81857
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <PAR>
A:Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CA884858.1; PID:g738
A:Experimental source: serogroup A, strain 22491
C:Genetics:
A:Gene: NMA1630

Query Match          56.3%; Score 40; DB 2; Length 289;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQFWL 10
   |||||
Db 265 REHPEQYFWL 274

RESULT 33
E71631
Lipid A biosynthesis lauroyl acyltransferase (htrB) RP718 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C:Accession: E71631
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
  Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499
A:Accession: E71631
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-290 <AND>
A:Cross-references: GB:AJ235273; GB:AJ235269; NID:g3861237; PIDN:CAA15149.1; PID:e134
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: htrB; RP718

Query Match          56.3%; Score 40; DB 2; Length 290;
Best Local Similarity 55.6%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQFW 9
   : ||||
Db 275 KQNPQQFW 283

RESULT 34
G82350
Lipid A biosynthesis lauroyl acyltransferase VC0213 [imported] - Vibrio cholerae (str
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: G82350
R:Heidelbergl, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
  Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers
  L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833
A:Accession: G82350
```


A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-318 <HEI>
A:Cross-references: GB:AE004111; GB:AE003852; NID:g9654614; PIDN:AAF93389.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype E1 Tor
C:Genetics:
A:Gene: VC0213
A:Map position: 1

Query Match 56.3%; Score 40; DB 2; Length 318;
Best Local Similarity 71.4%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQWFWL 10
|:|:| |
DB 294 PQQWFWL 300

RESULT 35
T42129
Probable acyltransferase (EC 2.3.1.-) - Escherichia coli plasmid pO157
C:Species: Escherichia coli
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Nov-2000
C:Accession: T42129; T00321
R:Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
Nucleic Acids Res. 26, 4196-4204, 1998
A:Title: The complete DNA sequence and analysis of the large virulence plasmid of Escherichia coli O157:H7
A:Reference number: Z22068; MUID:98391744
A:Accession: T42129
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-343 <BUR>
A:Cross-references: EMBL:AF074613; PIDN:AAC70097.1
A:Experimental source: strain EDL933; serotype O157:H7
R:Makino, K.; Ishii, K.; Yasunaga, T.; Hattori, M.; Yokoyama, K.; Yatsudo, H.C.; Kubota, S.; Shinagawa, H.
DNA Res. 5, 1-9, 1998
A:Title: Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an enterohemorrhagic E. coli O157:H7 strain
A:Reference number: Z14127; MUID:98290540
A:Accession: T00321
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 12-343 <MAK>
A:Cross-references: EMBL:AB011549; NID:g4589740; PIDN:BAA31840.1; PID:g3337081
A:Experimental source: strain EHEC O157:H7, substrain RMD 050952
C:Genetics:
A:Genome: plasmid pO157
A:Note: L7029
C:Keywords: acyltransferase

Query Match 56.3%; Score 40; DB 2; Length 343;
Best Local Similarity 45.5%; Pred. No. 49;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQWFWL 11
|:|:| |
DB 319 RPKPQWFWL 329

RESULT 36
S74814
Hypothetical protein slr1737 - Synecocystis sp. (strain PCC 6803)
C:Species: Synecocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S74814
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis sp.

A:Reference number: S74322; MUID:97061201
A:Accession: S74814
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-363 <KAN>
A:Cross-references: EMBL:D90909; GB:AB001339; NID:g1652844; PIDN:BAAL7775.1; PID:dl01
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 56.3%; Score 40; DB 2; Length 363;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQWFWL 10
|:|:| |
DB 211 PSRWFWL 217

RESULT 37
S52072
DMCNC protein - fruit fly (Drosophila sp.)
C:Species: Drosophila sp.
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 16-Jul-1999
C:Accession: S52072
R:Baumann, A.; Frings, S.; Godde, M.; Seifert, R.; Kaupp, U.B.
EMBO J. 13, 5040-5050, 1994
A:Title: Primary structure and functional expression of a Drosophila cyclic nucleotidic guanylate cyclase
A:Reference number: S52072; MUID:95045396
A:Accession: S52072
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-665 <BAU>
C:Genetics:
A:Gene: FlyBase:Cng
A:Cross-references: FlyBase:FBgn0014462
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotidic guanylate cyclase
F:429-553/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CA

Query Match 56.3%; Score 40; DB 2; Length 665;
Best Local Similarity 75.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQWFWL 8
|:|:| |
DB 52 RPKPQWFWL 59

RESULT 38
B75427
Hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: B75427
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1
A:Reference number: A75250; MUID:20036896
A:Accession: B75427
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-548 <WHI>
A:Cross-references: GB:AE001967; GB:AE005513; NID:g6458915; PIDN:AAF10758.1; PID:g645
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1179
A:Map position: 1

Query Match 55.6%; Score 39.5; DB 2; Length 548;
Best Local Similarity 70.0%; Pred. No. 93;

Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 RPKPQOWFWL 10
||| ||| ||
Db 521 RPVPQEW-WL 529
RESULT 39
T11768
H+-transporting ATP synthase (EC 3.6.1.34) protein 8 - Mustelus manazo mitochondrion
C:Species: mitochondrion Mustelus manazo
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C:Accession: T11768
R:Cao, Y.; Wadell, P.J.; Okada, N.; Hasegawa, M.
Mol. Biol. Evol. 15, 1637-1646, 1998
A:Title: The complete mitochondrial DNA sequence of the shark (Mustelus manazo): Evaluation of the complete mitochondrial DNA sequence
A:Reference number: Z17338; MUID:99083431
A:Accession: T11768
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-55 <CAO>
A:Cross-references: EMBL:AB015962; PIDN:BAA33040.1
A:Experimental source: liver
C:Genetics:
A:Genome: mitochondrion
A:Note: Atp8
C:Superfamily: H+-transporting ATP synthase protein 8
C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxid

Query Match 54.9%; Score 39; DB 2; Length 55;
Best Local Similarity 55.6%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 RPKPQOWFW 9
:|:|:| | |
Db 44 KPKPNPNW 52
RESULT 40
JQ1632
HCLF1 protein - human herpesvirus 6 (strain U1102)
C:Species: human herpesvirus 6
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 08-Oct-1999
C:Accession: JQ1632
R:Thomson, B.J.; Honess, R.W.
J. Gen. Virol. 73, 1649-1660, 1992
A:Title: The right end of the unique region of the genome of human herpesvirus 6 U1102 c

A:Reference number: PQ0406; MUID:92333248
A:Accession: JQ1632
A:Molecule-type: DNA
A:Residues: 1-99 <THO>
A:Cross-references: DBJ:D11134; NID:9221448; PIDN:BAA01908.1; PID:d1002385; PID:g221454

Query Match 54.9%; Score 39; DB 2; Length 99;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 4 PQOWFWLM 11
|:|:|:|
Db 86 PSRWYLL 93
RESULT 41
S76097
hypothetical protein - Synecocystis sp. (strain PCC 6803)
C:Species: Synecocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S76097
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocys
S.
A:Reference number: S74322; MUID:97061201
A:Accession: S76097
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-208 <KAN>
A:Cross-references: EMBL:D63999; GB:AB001339; NID:q1001396; PIDN:BAA10075.1; PID:g100
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Start codon: GTG

Query Match 54.9%; Score 39; DB 2; Length 208;
Best Local Similarity 55.6%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 PKPQOWFWL 10
|:|:|:|
Db 34 PSPQPQWMI 42
RESULT 42
B86503
acyltransferase [imported] - Chlamydomophila pneumoniae (strain J138)
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: B86503
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138:
A:Reference number: A86491; MUID:20330349
A:Accession: B86503
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-341 <STO>
A:Cross-references: GB:BA000008; NID:g8978471; PIDN:BAA98308.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: htrB_2

Query Match 54.9%; Score 39; DB 2; Length 341;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 KPQOWFWL 10
:|:|:| |
Db 180 QPEQWMI 187
RESULT 43
A36669
galactoside 3(4)-L-fucosyltransferase (EC 2.4.1.65) - human
N:Alternate names: alpha (1,3/1,4) fucosyltransferase; blood group Lewis alpha-4-fuco
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 29-Sep-1999
C:Accession: A36669; I39043; I39044; I39045; S12123
R:Kukowska-Latallo, J.F.; Larsen, R.D.; Nair, R.P.; Lowe, J.B.
Genes Dev. 4, 1288-1303, 1990
A:Title: A cloned human cDNA determines expression of a mouse stage-specific embryoni
A:Reference number: A36669; MUID:91032981
A:Accession: A36669
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-361 <KUK>
A:Cross-references: GB:X53578; NID:g28529; PIDN:CAA37641.1; PID:g28530
R:Cameron, H.S.; Szczepaniak, D.; Weston, B.W.
J. Biol. Chem. 270, 20112-20122, 1995
A:Title: Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in no
A:Reference number: I39043; MUID:95378269

A:Accession: I39043
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-361 <RES>
A:Cross-references: EMBL:U27326; NID:967188; PIDN:AAC50185.1; PID:967189
A:Accession: I39044
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-361 <RE2>
A:Cross-references: EMBL:U27327; NID:967190; PIDN:AAC50186.1; PID:967191
A:Accession: I39045
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-361 <RE3>
A:Cross-references: EMBL:U27328; NID:967192; PIDN:AAC50187.1; PID:967193
C:Genetics:
A:Gene: GDB:FUT3; LE
A:Cross-references: GDB:135717; OMIM:111100
A:Map position: 19p13.3-19p13.3
A:Note: alternative splicing 5' to the coding region
C:Superfamily: galactoside 3(4)-L-fucosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 54.9%; Score 39; DB 2; Length 361;
Best Local Similarity 55.6%; Pred. No. 73;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
||:|:|
Db 126 RPQQRWIW 134

RESULT 44
A42270
alpha (1,3) fucosyltransferase FUT5 - human
N:Alternate names: fucosyltransferase 5
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 29-Sep-1999
C:Accession: A42270; I39046; I39047
R:Weston, B.W.; Nair, R.P.; Larsen, R.D.; Lowe, J.B.
J. Biol. Chem. 267, 4152-4160, 1992
A:Title: Isolation of a novel human alpha (1,3)fucosyltransferase gene and molecular cloning of the complementary DNA
A:Keywords: fucosyltransferase; alpha (1,3)-fucosyltransferase; fucose; glycosylation
A:Reference number: A42270; MUID:92156161
A:Accession: A42270
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-374 <WES>
A:Cross-references: GB:M81485; NID:q128490; PIDN:AAA98117.1; PID:q1280209
A:Note: sequence extracted from NCBI backbone (NCBIN:82825, NCBIIP:82826)
R:Cameron, H.S.; Szczepaniak, D.; Weston, B.W.
J. Biol. Chem. 270, 20112-20122; 1995
A:Title: Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in normal cells
A:Reference number: I39043; MUID:95378269
A:Accession: I39046
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RES>
A:Cross-references: EMBL:U27329; NID:967194; PIDN:AAC50188.1; PID:967195
A:Accession: I39047
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RE2>
A:Cross-references: EMBL:U27330; NID:967196; PIDN:AAC50189.1; PID:967197
C:Genetics:
A:Gene: GDB:FUT5
A:Cross-references: GDB:131644; OMIM:136835
A:Map position: 19p13.3-19p13.3
C:Superfamily: galactoside 3(4)-L-fucosyltransferase

Query Match 54.9%; Score 39; DB 2; Length 374;
Best Local Similarity 55.6%; Pred. No. 73;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Best Local Similarity 55.6%; Pred. No. 76;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
||:|:|
Db 139 RPQQRWIW 147

RESULT 45
D71803
ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Helicobacter pylori (s)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Apr-2000
C:Accession: D71803
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p
A:Reference number: A71800; MUID:99120557
A:Accession: D71803
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-412 <ARN>
A:Cross-references: GB:AE001568; GB:AE001439; NID:g4156083; PIDN:AAD07046.1; PID:g415
A:Experimental source: strain J99
C:Genetics:
A:Gene: petB
C:Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastocou
C:Keywords: electron transfer; heme; iron; metalloprotein; oxidoreductase
F:21-370/Domain: cytochrome b homology <CYB>
F:21-223/Domain: cytochrome b6 homology <CB6>
F:250-370/Domain: plastocoulin--plastocyanin reductase 17K protein homology <17K>
F:94,195/Binding site: heme iron (His) (axial ligands) (low potential) #status predic
F:108,210/Binding site: heme iron (His) (axial ligands) (high potential) #status predic

Query Match 54.9%; Score 39; DB 2; Length 412;
Best Local Similarity 54.5%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPKPQQWF 11
||:|:|
Db 349 RPAFWFWLL 359

RESULT 46
F83010
probable oxidoreductase PA5084 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83010
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337
A:Accession: F83010
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-416 <STO>
A:Cross-references: GB:AE004921; GB:AE004091; NID:g9951372; PIDN:AAG08469.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA5084

Query Match 54.9%; Score 39; DB 2; Length 416;
Best Local Similarity 53.8%; Pred. No. 84;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 RPK--PQQWF 11

Db 80 RPLDPAQWFWLL 92
||: | || ||:

RESULT 47

B29413
ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Paracoccus denitrificans
N:Alternate names: bcl complex; complex III
C:Species: Paracoccus denitrificans
C:Date: 31-Mar-1989 #sequence_revision 20-Aug-1994 #text_change 03-Mar-2000
C:Accession: B29413
R:Kuroski, B.; Ludwig, B.
J. Biol. Chem. 262, 13805-13811, 1987
A:Title: The genes of the Paracoccus denitrificans bc-1 complex. Nucleotide sequence and
A:Reference number: A92613; MUID:88007612
A:Accession: B29413
A:Molecule type: DNA
A:Residues: 1-440 <KUR>
A:Cross-references: GB:M17522; NID:g150569; PIDN:AAA25572.1; PID:g150571
C:Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastocyanin
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; oxidoreductase
F:26-381/Domain: cytochrome b homology <CBH>
F:26-225/Domain: cytochrome b6 homology <CB6>
F:51-67/Domain: transmembrane #status predicted <TM1>
F:96-114/Domain: transmembrane #status predicted <TM2>
F:134-150/Domain: transmembrane #status predicted <TM3>
F:195-217/Domain: transmembrane #status predicted <TM4>
F:245-361/Domain: plastocyanin--plastocyanin reductase 17K protein homology <L7K>
F:253-269/Domain: transmembrane #status predicted <TM5>
F:330-346/Domain: transmembrane #status predicted <TM6>
F:365-383/Domain: transmembrane #status predicted <TM7>
F:395-411/Domain: transmembrane #status predicted <TM8>
F:97,198/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted
F:111,212/Binding site: heme iron (His) (axial ligands) (high potential) #status predicted

Query Match 54.9%; Score 39; DB 1; Length 440;
Best Local Similarity 54.5%; Pred. No. 89;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKQOQWFWLM 11
||: ||||:
Db 360 RPLKFWFWLL 370

RESULT 48

F81436
probable integral membrane protein with hemeolysin domain Cj0183 [imported] - Campylobacter
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 21-Jul-2000
C:Accession: F81436
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912
A:Accession: F81436
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-452 <PAR>
A:Cross-references: GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB72666.1; PID:g696767
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj0183
C:Superfamily: hypothetical protein HI0107

Query Match 54.9%; Score 39; DB 2; Length 452;
Best Local Similarity 44.4%; Pred. No. 92;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPOQWFWLM 11
||: ||||:

Db 160 RPLHFWFWML 168

RESULT 49

E81551
lipid A biosynthesis lauroyl acyltransferase, probable CP0676 [imported] - Chlamydia
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C:Accession: E81551
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A:Reference number: A81500; MUID:20150255
A:Accession: E81551
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-462 <REA>
A:Cross-references: GB:AE002225; GB:AE002161; NID:g7189583; PIDN:AAF38487.1; PID:g718
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0676

Query Match 54.9%; Score 39; DB 2; Length 462;
Best Local Similarity 50.0%; Pred. No. 94;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 KPOQWFWL 10
||: ||||:
Db 301 QPEQWMI 308

RESULT 50

B72119
acyltransferase - Chlamydia pneumoniae (strain CWL029)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C:Accession: B72119
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Pan, J.; Olinger, L.; Grimwood,
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606
A:Accession: B72119
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-467 <ARN>
A:Cross-references: GB:AE001596; GB:AE001363; NID:g4376357; PIDN:AAD18251.1; PID:g437
A:Experimental source: strain CWL029
C:Genetics:
A:Gene: htrB

Query Match 54.9%; Score 39; DB 2; Length 467;
Best Local Similarity 50.0%; Pred. No. 95;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 KPOQWFWL 10
||: ||||:
Db 301 QPEQWMI 308

RESULT 51

E72682
hypothetical protein APE0879 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: E72682
R:Kavarabavasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
A:Reference number: A72450; MUID:99310339

A:Accession: E72682
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-480 <RAW>
A:Cross-references: DDBJ:AF000060; NID:g5104188; PIDN:BAA79861.1; PID:g5104546
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0879
C:Superfamily: Aeropyrum pernix hypothetical protein APE0879

Query Match 54.9%; Score 39; DB 2; Length 480;
Best Local Similarity 55.6%; Pred. No. 97;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQQWFWM 11
| | | | |
Db 283 KPQEWFI 291

RESULT 52

H71365

Probable linc protein (linc) - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999

C:Accession: H71365

R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: A71250; MUID:98332770

A:Accession: H71365

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-525 <COL>

A:Cross-references: GB:AF001195; GB:AF000520; NID:g322366; PIDN:AAC26555.1; PID:g332237

A:Experimental source: strain Nichols

C:Genetics:

A:Gene: TP0107

Query Match 54.9%; Score 39; DB 2; Length 525;

Best Local Similarity 55.6%; Pred. No. 1.1e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPQQWFW 9

| | | | |

Db 173 RPNRANFW 181

RESULT 53

TL3062

CLOCK protein - fruit fly (Drosophila melanogaster)

N:Alternate names: circadian rhythm protein

C:Species: Drosophila melanogaster

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C:Accession: TL3062

R:Allada, R.; White, N.E.; So, W.V.; Hall, J.C.; Rosbash, M.

Cell 93, 791-804, 1998

A:Title: A mutant Drosophila homolog of mammalian CLOCK disrupts circadian rhythms and t

A:Reference number: 217596; MUID:98292177

A:Accession: TL3062

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1015 <ALL>

A:Cross-references: EMBL:AF065133; NID:g3213257; PID:g3213258; PIDN:AAC39101.1

A:Gene: Clk

A:Cross-references: FlyBase:FBgn0023076

A:Map position: 3

Query Match 54.9%; Score 39; DB 2; Length 1015;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQQWFWM 10

| | | | |

Db 331 KGQQWIWL 338

RESULT 54

TL3068

CLOCK protein - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C:Accession: TL3068

R:Darlington, T.K.; Wager-Smith, K.; Ceriani, M.F.; Staknis, D.; Gekakis, N.; Steeves
Science 280, 1599-1603, 1998

A:Title: Closing the circadian loop: CLOCK-induced transcription of its own inhibitor

A:Reference number: 217599; MUID:98279147

A:Accession: TL3068

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1023 <DAR>

A:Cross-references: EMBL:AF067207; NID:g3192866; PID:g3192867; PIDN:AAD10630.1

C:Genetics:

A:Cross-references: FlyBase:FBgn0023076

C:Function:

A:Description: required for circadian behavioral rhythms

Query Match 54.9%; Score 39; DB 2; Length 1023;

Best Local Similarity 75.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQQWFWM 10

| | | | |

Db 331 KGQQWIWL 338

RESULT 55

TL3071

CLOCK protein - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C:Accession: TL3071

R:Bae, K.; Lee, C.; Sidote, D.; Chuang, K.Y.; Edery, I.

Mol. Cell. Biol. 18, 6142-6151, 1998

A:Title: Circadian regulation of a drosophila homolog of the mammalian clock gene: PE

A:Reference number: 217601; MUID:98414630

A:Accession: TL3071

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1027 <BAE>

A:Cross-references: EMBL:AF069997; NID:g3219725; PID:g3219726; PIDN:AAC62234.1

C:Genetics:

A:Cross-references: FlyBase:FBgn0023076

C:Function:

A:Description: required for circadian behavioral rhythms

Query Match 54.9%; Score 39; DB 2; Length 1027;

Best Local Similarity 75.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KPQQWFWM 10

| | | | |

Db 335 KGQQWIWL 342

RESULT 56

DB3242

hypothetical protein PA3216 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

A30533

Lymphocyte-specific protein LSP1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 07-May-1999
C:Accession: A30533; PC1325
R:Jongstra, J.; Tidmarsh, G.F.; Jongstra-Bilen, J.; Davis, M.M.
J. Immunol. 141, 3999-4004, 1988
A:Title: A new lymphocyte-specific gene which encodes a putative Ca(2+)-binding protein
A:Reference number: A30533; MUID:89035543
A:Accession: A30533
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-330 <JON>
R:Matsumoto, N.; Toyoshima, S.; Osawa, T.
J. Biochem. 113, 630-636, 1993
A:Title: Characterization of the 50 kDa protein phosphorylated in concanavalin A-stimulated lymphocytes
A:Reference number: PC1325; MUID:93340113
A:Accession: PC1325
A:Molecule type: protein
A:Residues: 55-77, 'X', 79-81, 131-144, 'XX', 211-218, 'X', 220-229, 238-242, 'X', 244-252, 'S', 254-255
C:Genetics:
A:Gene: LSP1
C:Keywords: calcium binding; phosphoprotein

Query Match 53.5%; Score 38; DB 2; Length 330;
Best Local Similarity 55.6%; Pred. No. 96;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9

:|:|:|

Db 92 KPEPQQWF 100

RESULT 61

Lymphocyte-specific protein - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999
C:Accession: I57835
R:Jongstra, J.; Ittel, M.E.; Iscove, N.N.; Brady, G.
Mol. Immunol. 31, 1125-1131, 1994
A:Title: The LSP1 gene is expressed in cultured normal and transformed mouse macrophages
A:Reference number: I57835; MUID:95021322
A:Accession: I57835
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-330 <RES>
A:Cross-references: GB:S74179; NID:G709978; PIDN:AAB32257.1; PID:G709979
C:Genetics:
A:Gene: LSP1

Query Match 53.5%; Score 38; DB 2; Length 330;
Best Local Similarity 55.6%; Pred. No. 96;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9

:|:|:|

Db 92 KPEPQQWF 100

RESULT 62

JE0111
Lectin-like oxidized LDL receptor - mouse
N:Alternate names: LDX-1
C:Species: Mus musculus (house mouse)
C:Date: 22-May-1998 #sequence_revision 29-May-1998 #text_change 07-May-1999
C:Accession: JE0111
R:Hoshikawa, H.; Sawamura, T.; Kakutani, M.; Aoyama, T.; Nakamura, T.; Masaki, T.
Biochem. Biophys. Res. Commun. 245, 841-846, 1998
A:Title: High affinity binding of oxidized LDL to mouse lectin-like oxidized LDL receptor
A:Reference number: JE0111; MUID:98249801

A:Accession: JE0111
A:Molecule type: mRNA
A:Residues: 1-363 <HOS>
F:34-59/Domain: transmembrane #status predicted <TM>

Query Match 53.5%; Score 38; DB 2; Length 363;
Best Local Similarity 62.5%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RPKQQWF 9

|:|:|

Db 234 PCPQDWI 241

RESULT 63

B82697
rod shape-determining protein Xfl1313 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
C:Accession: B82697
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: B82697
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-373 <SIM>
A:Cross-references: GB:AE003964; GB:AE003849; NID:G9106300; PIDN:AAF84122.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, D.M.; Carraro, D.M.; Carrier
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Miyaki, C.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: Xfl1313
C:Superfamily: rod shape-determining protein

Query Match 53.5%; Score 38; DB 2; Length 373;
Best Local Similarity 62.5%; Pred. No. 11e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQQWF 11

|:|:|

Db 201 PFSFWLL 208

RESULT 64

JE04591
alpha-1,3 fucosyltransferase (EC 2.4.1.-) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 16-Apr-1996 #sequence_revision 24-May-1996 #text_change 24-Nov-1999
C:Accession: JC4591
R:Ozawa, M.; Muramatsu, T.
J. Biochem. 119, 302-308, 1996
A:Title: Molecular cloning and expression of a mouse alpha-1,3 fucosyltransferase gen
A:Reference number: JC4591; MUID:97037075
A:Accession: JC4591
A:Molecule type: mRNA
A:Residues: 1-400 <OZA>

A:Cross-references: DBJ:D63379
A:Experimental source: Embryonal carcinoma F9 cells
C:Superfamily: galactoside 3(4)-L-fucosyltransferase
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane protein
F:1-23/Domain: Intracellular #status predicted <INT>
F:24-49/Domain: transmembrane #status predicted <TRM>
F:84,185/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 53.5%; Score 38; DB 2; Length 400;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWFNL 10
||| | | | | |
DB 156 RPPGQRWVWM 165

RESULT 65
B36340
N:Alternate names: CD15; ELAM-1 ligand fucosyltransferase (ELFT); FCT3A; FUC-TIV; myeloid
C:Species: Homo sapiens (man)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: B36340; A36340; A40976; A41202
R:Goelz, S.E.; Hession, C.; Goff, D.; Griffiths, B.; Tizard, R.; Newman, B.; Chi-Rosso, C.
Cell 63, 1349-1356, 1990
A:Title: ELFT: a gene that directs the expression of an ELAM-1 ligand.
A:Reference number: A36340; MUID:91084863
A:Accession: B36340
A:Molecule type: mRNA
A:Residues: 1-405 <GOE1>
A:Cross-references: GB:M58596; NID:g182068; PIDN:AAA63172.1; PID:g182069
A:Accession: A36340
A:Molecule type: mRNA
A:Residues: 'MRLWGARKPSGAGWEKEAEQAEAGNSRLGPGR','SGRKRAVPGWASWPAHLALARPRLHGGACQ
A:Cross-references: GB:M58597; NID:g182070; PIDN:AAA63173.1; PID:g182071
A:Note: the codon used as an initiator for this translation is not in a good context for
R:Low, J.B.; Kukowska-Latallo, J.F.; Nair, R.P.; Larsen, R.D.; Marks, R.M.; Macher, B.A.
J. Biol. Chem. 266, 17467-17477, 1991
A:Title: Molecular cloning of a human fucosyltransferase gene that determines expression
A:Reference number: A40976; MUID:91373370
A:Accession: A40976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86,'p',88-405 <LOW>
A:Cross-references: GB:M65030; NID:g182791; PIDN:AAA92977.1; PID:g1236720
B:Kumar, R.; Potvin, B.; Muller, W.A.; Stanley, P.
J. Biol. Chem. 266, 21777-21783, 1991
A:Title: Cloning of a human alpha(1,3)-fucosyltransferase gene that encodes ELFT but doe
A:Reference number: A41202; MUID:92042084
A:Accession: A41202
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-240,'D',242-400 <KUM>
A:Cross-references: GB:S65161; NID:g239005; PIDN:AAB20349.1; PID:g239006
C:Genetics:
A:Gene: GDB:FUT4; CD15; FCT3A; FUC-TIV
A:Cross-references: GDB:131563; OMIM:104230
A:Map position: llq21-llq21
C:Superfamily: galactoside 3(4)-L-fucosyltransferase
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F:1-48/Domain: signal sequence #status predicted <SIG>
F:49-405/Product: alpha(1,3)-fucosyltransferase 4 #status predicted <MAT>
F:91,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 53.5%; Score 38; DB 2; Length 405;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWFNL 10
||| | | | | |

DB 161 RPPGQRWVWM 170

RESULT 66
C64712
ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Helicobacter pylori (s
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 20-Apr-2000
C:Accession: C64712
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; Mcke
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467
A:Accession: C64712
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-412 <TOM>
A:Cross-references: GB:AE000652; GB:AE000511; NID:g2314720; PIDN:AAD08579.1; PID:g231
C:Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoqui
C:Keywords: electron transfer; heme; iron; metalloprotein; oxidoreductase
F:21-370/Domain: cytochrome b6 homology <CBH>
F:21-223/Domain: cytochrome b6 homology <CBH>
F:250-370/Domain: plastocyanin reductase 17K protein homology <17K>
F:94,195/Binding site: heme iron (His) (axial ligands) (low potential) #status predic
F:108,210/Binding site: heme iron (His) (axial ligands) (high potential) #status pred

Query Match 53.5%; Score 38; DB 2; Length 412;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPKPQQWFNL 11
||| | | | | |
DB 349 RPAFMVFWLV 359

RESULT 67
C96806
unknown protein T5M16.25 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: C96806
R:Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: C96806
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-421 <STO>
A:Cross-references: GB:AE005173; NID:g6382510; PIDN:AAF07796.1; GSPDB:GN00141
C:Genetics:
A:Gene: T5M16.25
A:Map position: 1

Query Match 53.5%; Score 38; DB 2; Length 421;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWF 8
||| | | | | |
DB 145 KRPVQWY 152


```
RESULT 68
A57396
N:Alternate names: ELAM-1 ligand fucosyltransferase homolog
C:Species: Mus musculus (house mouse)
C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 11-Jan-2000
C:Accession: A57596
R:Gersten, K.M.; Natsuka, S.; Trinchera, M.; Petryniak, B.; Kelly, R.J.; Hiraiwa, N.; Je
J. Biol. Chem. 270, 25047-25056, 1995
A:Title: Molecular cloning, expression, chromosomal assignment, and tissue-specific exp
erase.
A:Reference number: A57596; MUID:96027607
A:Accession: A57596
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-433 <GER>
A:Cross-references: GB:U33457; NID:g1039426; PIDN:AAC52269.1; PID:g1039427
C:Superfamily: galactoside 3(4)-L-fucosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 53.5%; Score 38; DB 2; Length 433;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQWFWL 10
|| | | |
DB 189 RPPGQRVWM 198

RESULT 69
T04448
Hypothetical protein F4D11.30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C:Accession: T04448
R:Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoerge, W.; Hohelsel, J.; Mewes, H.W
submitted to the Protein Sequence Database, April 1998
A:Reference number: T04448
A:Accession: T04448
A:Molecule type: DNA
A:Residues: 1-455 <BEV>
A:Cross-references: EMBL:AL022537
A:Experimental source: cultivar Columbia; BAC clone F4D11
C:Genetics:
A:Map position: 4
A:Introns: 106/1; 132/3; 158/2; 215/1; 247/3; 283/3; 322/3; 372/3
A:Note: F4D11.30

Query Match 53.5%; Score 38; DB 2; Length 455;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQQWFWL 10
|::|||
DB 242 PRKWFV 248

RESULT 70
S02489
Hypothetical protein SPAC4G8.l2c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 31-Jan-2000
C:Accession: T38857; S62489
R:Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A:Reference number: T38857
A:Accession: T38857
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA

A:Residues: 1-533 <BA2>
A:Cross-references: EMBL:Z56276; NID:g1022345; PIDN:CAA91213.1; PID:g10223357; GSPDB:G
A:Experimental source: strain 972h-; cosmid c4G8
C:Genetics:
A:Gene: SPAC4G8.l2c
A:Map position: 1L
A:Introns: 42/1; 84/1; 107/1; 162/3; 215/2

Query Match 53.5%; Score 38; DB 2; Length 533;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 KPQQWFWL 11
|| | | |
DB 296 KPATWLL 304

RESULT 71
I59550
aryl hydrocarbon receptor nuclear translocator Arnt [imported] - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C:Accession: I59550
R:Hoffman, E.C.; Reyes, H.; Chu, F.F.; Sander, F.; Conley, L.H.; Brooks, B.A.; Hankin
Science 252, 954-958, 1991
A:Title: Cloning of a factor required for activity of the Ah (dioxin) receptor.
A:Reference number: I59550; MUID:91240280
A:Accession: I59550
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-789 <RES>
A:Cross-references: GB:M69238; NID:g179003; PIDN:AAA51777.1; PID:g179004
C:Genetics:
A:Gene: GDB:ARNT
A:Cross-references: GDB:119701; OMIM:126110
A:Map position: 1q21-1q21

Query Match 53.5%; Score 38; DB 2; Length 789;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQWFWL 10
| | | | |
DB 430 RSKNQEWLWM 439

RESULT 72
WNNVTN
104K glycoprotein - Trichoplusia ni granulosis virus
C:Species: Trichoplusia ni granulosis virus, TnGV.
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Jun-2000
C:Accession: J01328
R:Hashimoto, Y.; Corsaro, B.G.; Granados, R.R.
J. Gen. Virol. 72, 2645-2651, 1991
A:Title: Location and nucleotide sequence of the gene encoding the viral enhancing fa
A:Reference number: J01328; MUID:92044434
A:Accession: J01328
A:Molecule type: DNA
A:Residues: 1-901 <HAS>
A:Cross-references: GB:D12617; NID:g221443; PIDN:BAA02141.1; PID:g221444
A:Note: the authors translated the codon CTA for residue 12 as Val
C:Comment: This protein is involved in disruption of the peritrophic membrane and fus
C:Superfamily: Trichoplusia ni granulosis virus 104K glycoprotein
C:Keywords: glycoprotein
F:65,265,306,339,349,540,594,595,621,642,683,698/Binding site: carbohydrate (Asn) (CO

Query Match 53.5%; Score 38; DB 1; Length 901;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 2 PKPQOWFWL 10
||| |||
Db 353 PYPQIWSWL 361

RESULT 73

S76899
hypothetical protein - Synecocystis sp. (strain PCC 6803)
C:Species: Synecocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S76899
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis s.
A:Reference number: S74322; MUID:97061201
A:Accession: S76899
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-909 <KAN>
A:Cross-references: EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAA18811.1; PID:dl01954
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Start codon: GTG

Query Match 53.5%; Score 38; DB 2; Length 909;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPQOWF 8
||| |||
Db 445 PRPQSWF 451

RESULT 74

T09484
cartilage intermediate layer protein precursor - human
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T09484
R:Lorenz, P.; Neame, P.; Sommarin, Y.; Heinegard, D.
J. Biol. Chem. 273, 23469-23475, 1998
A:Title: Cloning and deduced amino acid sequence of a novel cartilage protein (CILP) id
A:Reference number: Z16689; MUID:98389785
A:Accession: T09484
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1184 <LOR>
A:Cross-references: EMBL:AF035408; NID:g3513502; PIDN:AAC33838.1; PID:g3513503
A:Experimental source: tissue type articular cartilage
C:Genetics:
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-1184/Product: cartilage intermediate layer protein #status predicted <MAT>

Query Match 53.5%; Score 38; DB 2; Length 1184;
Best Local Similarity 44.4%; Pred. No. 3.4e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOWFW 9
||| :|||
Db 335 KPRPKYFW 343

RESULT 75

T31113
mucin-like glycoprotein 900 - Cryptosporidium parvum
C:Species: Cryptosporidium parvum
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C:Accession: T31113
R:Barnes, D.A.; Bonnin, A.; Huang, J.X.; Gousset, L.; Wu, J.; Gut, J.; Doyle, P.; Dub Mol. Biochem. Parasitol. 96, 93-110, 1998
A:Title: A novel multi-domain mucin-like glycoprotein of Cryptosporidium parvum media
A:Reference number: Z20989; MUID:99066935

A:Accession: T31113
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1832 <BAR>
A:Cross-references: EMBL:AF068065; NID:g4063041; PID:g4063042; FIDN:AAC98153.1

Query Match 53.5%; Score 38; DB 2; Length 1832;
Best Local Similarity 62.5%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPQOWFWL 10
||: |||
Db 527 KPDEWCWL 534

RESULT 76

D69351
hypothetical protein AF0812 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000
C:Accession: D69351
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343
A:Accession: D69351
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-298 <KLE>
A:Cross-references: GB:AE001048; GB:AE000782; NID:g2689371; PIDN:AAB90432.1; PID:g264
C:Superfamily: Archaeoglobus fulgidus hypothetical protein AF0812

Query Match 52.8%; Score 37.5; DB 2; Length 293;
Best Local Similarity 66.7%; Pred. No. 1e+02; 1; Indels 1; Gaps 1;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 2 PKPQOWF-W 9
|||: |||
Db 62 PKPEYWFRW 70

RESULT 77

JQ0846
DNA-binding protein - equine herpesvirus 1 (fragment)
C:Species: equine herpesvirus 1
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Feb-1997
C:Accession: JQ0846
R:Bell, C.W.; Whalley, J.M.
submitted to JIPID, January 1991
A:Reference number: JQ0846
A:Accession: JQ0846
A:Molecule type: DNA
A:Residues: 1-375 <BEL>
C:Superfamily: herpesvirus DNA-binding protein
C:Keywords: DNA binding; nucleus

Query Match 52.8%; Score 37.5; DB 2; Length 375;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 2 PKPQOWFWLM 11

Db 10 PNP-QWFWTL 18
| | | | |

RESULT 78
DNBEV1
major DNA-binding protein UL29 - human herpesvirus 1 (strain 17)
C:Species: human herpesvirus 1
A:Note: host Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 16-Jun-2000
C:Accession: A03790; B30085
R:Quinn, J.P.; McGeoch, D.J.
Nucleic Acids Res. 13, 8143-8163, 1985
A:Title: DNA sequence of the region in the genome of herpes simplex virus type 1 containing
A:Reference number: A93601; MUID:86067223
A:Accession: A03790
A:Molecule type: DNA
A:Residues: 1-1196 <QUI>
A:Cross-references: GB:M12356; PIDN:CAA26940.1; PID:g59863
A:Experimental source: strain 17
R:McGeoch, D.J.; Balrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; Perz
J. Gen. Virol. 69, 1531-1574, 1988
A:Title: The complete DNA sequence of the long unique region in the genome of herpes sim
A:Reference number: A30083; MUID:88274327
A:Accession: B30085
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1196 <MCG>
A:Cross-references: GB:D10879; PIDN:BAA01675.1; PID:g221750; GB:D00317
C:Genetics:
A:Gene: UL29
A:Map position: 0.38-0.409
C:Superfamily: herpesvirus DNA-binding protein
C:Keywords: DNA binding

Query Match 52.8%; Score 37.5; DB 1; Length 1196;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 RPKPOQWFW 9
: | | | | |
Db 837 QPNP-QWFW 844

RESULT 79
DNBEKS
DNA-binding protein - human herpesvirus 1 (strain KOS1.1)
C:Species: human herpesvirus 1
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 16-Jul-1999
C:Accession: A28601
R:Gao, M.; Bouchev, J.; Curtin, K.; Knipe, D.M.
Virology 163, 319-329, 1988
A:Title: Genetic identification of a portion of the herpes simplex virus ICP8 protein re
A:Reference number: A28601; MUID:88179536
A:Accession: A28601
A:Molecule type: DNA
A:Residues: 1-1196 <GAO>
A:Cross-references: GB:M20165; PIDN:AAA45793.1; PID:g330121
C:Genetics:
A:Map position: 0.38-0.409
C:Superfamily: herpesvirus DNA-binding protein
C:Keywords: DNA binding

Query Match 52.8%; Score 37.5; DB 1; Length 1196;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 RPKPOQWFW 9
: | | | | |
Db 837 QPNP-QWFW 844

RESULT 80
DNBEHF
DNA-binding protein - human herpesvirus 1 (strain F)
C:Species: human herpesvirus 1
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 07-Jun-1996
C:Accession: D29242
R:Hammerschmidt, W.; Conraths, F.; Mankertz, J.; Pauli, G.; Ludwig, H.; Buhk, H.J.
Virology 165, 388-405, 1988
A:Title: Conservation of a gene cluster including glycoprotein B in bovine herpesviro
A:Reference number: A94381; MUID:88306231
A:Accession: D29242
A:Molecule type: DNA
A:Residues: 1-1196 <HAM>
A:Cross-references: GB:M21629
C:Superfamily: herpesvirus DNA-binding protein
C:Keywords: DNA binding

Query Match 52.8%; Score 37.5; DB 1; Length 1196;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 RPKPOQWFW 9
: | | | | |
Db 837 QPNP-QWFW 844

RESULT 81
A48350
DNA-binding protein - human herpesvirus 2
C:Species: human herpesvirus 2
A:Note: host Homo sapiens (man)
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 31-May-1996
C:Accession: A48350
R:Toh, Y.; Liu, Y.; Tanaka, S.; Mori, R.
Arch. Virol. 129, 183-196, 1993
A:Title: Nucleotide sequence of the major DNA-binding protein gene of herpes simplex
A:Reference number: A48350; MUID:93228441
A:Accession: A48350
A:Molecule type: DNA
A:Residues: 1-1197 <TOH>
A:Note: sequence extracted from NCBI backbone (NCBIN:129069, NCBIIP:129070)
C:Genetics:
A:Map position: 0.375-0.405
C:Superfamily: herpesvirus DNA-binding protein
C:Keywords: DNA binding; zinc finger
F:499-512/Region: zinc finger

Query Match 52.8%; Score 37.5; DB 1; Length 1197;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 RPKPOQWFW 9
: | | | | |
Db 837 QPNP-QWFW 844

RESULT 82
DNBE29
DNA-binding protein - human herpesvirus 3
C:Species: human herpesvirus 3, varicella-zoster virus
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
C:Accession: C27214
R:Davidson, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
A:Title: The complete DNA sequence of varicella-zoster virus.
A:Reference number: A27345; MUID:86306657
A:Accession: C27214
A:Molecule type: DNA

A;Residues: 1-1204 <DAV>
A;Cross-references: EMBL:X04370; NID:g59989; PIDN:CAA27912.1; PID:g60018
C;Genetics:
A;Gene: 29
C;Superfamily: herpesvirus DNA-binding protein
C;Keywords: DNA binding

Query Match 52.8%; Score 37.5; DB 1; Length 1204;
Best Local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 2 PKPOQWFWM 11
| | | | |
DB 836 PNP-QWFWTL 844

RESULT 83
T42574
DNA-binding protein - equine herpesvirus 4 (strain NS80567)
C;Species: equine herpesvirus 4
A;Variety: strain NS80567
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T42574
R;Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
J. Gen. Virol. 79, 1197-1203, 1998
A;Title: The DNA sequence of equine herpesvirus-4.
A;Reference number: 222173; MUID:98264497
A;Accession: T42574
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1208 <TEL>
A;Cross-references: EMBL:AF030027; NID:g2605950; PIDN:AAC59547.1; PID:g2605975
A;Experimental source: strain NS80567
C;Genetics:
A;Gene: 31
C;Superfamily: herpesvirus DNA-binding protein
C;Keywords: DNA binding

Query Match 52.8%; Score 37.5; DB 2; Length 1208;
Best Local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 2 PKPOQWFWM 11
| | | | |
DB 844 PNP-QWFWTL 852

RESULT 84
DNBEC4
DNA-binding protein - equine herpesvirus 1 (strain AB4p)
C;Species: equine herpesvirus 1
A;Note: host Equus caballus (domestic horse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Jul-1999
C;Accession: E36798
R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
submitted to GenBank, March 1992
A;Description: The DNA sequence of equine herpesvirus-1.
A;Reference number: A36805
A;Accession: E36798
A;Molecule type: DNA
A;Residues: 1-1209 <TEL>
A;Cross-references: GB:M86664; NID:g330791; PIDN:AB02466.1; PID:g330823
R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
Virology 189, 304-316, 1992
A;Title: The DNA sequence of equine herpesvirus-1.
A;Reference number: A41831; MUID:92295566
A;Contents: annotation; possible protein-coding frames
A;Note: neither amino acid nor nucleotide sequence is given
C;Genetics:
A;Gene: 31
C;Superfamily: herpesvirus DNA-binding protein

C;Keywords: DNA binding

Query Match 52.8%; Score 37.5; DB 1; Length 1209;
Best Local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 2 PKPOQWFWM 11
| | | | |
DB 844 PNP-QWFWTL 852

RESULT 85
S23308
substance P - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C;Accession: S23308
R;Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the
A;Reference number: S23186; MUID:92298992
A;Accession: S23308
A;Molecule type: protein
A;Residues: 1-11 <JEN>
A;Experimental source: brain
C;Function:
A;Description: may play a physiological role in the regulation of cardiovascular and
A;Note: substance P is derived by post-translational processing of preprotachykinin A
C;Superfamily: unassigned animal peptides
C;Keywords: neuropeptide; amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 52.1%; Score 37; DB 2; Length 11;
Best Local Similarity 54.5%; Pred. No. 4.7;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
: | : | : | : |
DB 1 KPRPHQFFGLM 11

RESULT 86
S50061
DNA binding protein, replication-origin specific - Escherichia coli
C;Species: Escherichia coli
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 08-Oct-1999
C;Accession: S50061; S37475
R;Herrick, J.; Kern, R.; Guha, S.; Landoulsi, A.; Fayet, O.; Malki, A.; Kohiyama, M.
EMBO J. 13, 4695-4703, 1994
A;Title: Parental strand recognition of the DNA replication origin by the outer membr
A;Reference number: S50061; MUID:95009972
A;Accession: S50061
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-175 <HER>
A;Cross-references: EMBL:Z26592
R;Herrick, J.; Kern, R.; Fayet, O.; Guha, S.; Kohiyama, M.
submitted to the EMBL data Library, September 1993
A;Description: Cloning and characterization of a novel DNA binding protein specific o
A;Reference number: S37475
A;Accession: S37475
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 85-97, 'A', 99-149, 'ACEAIFNCLDRNPMNGLFSKPGNVSPPVVR' <HE2>
A;Cross-references: EMBL:Z26592; NID:g404853; PIDN:CAA81346.1; PID:g404854

Query Match 52.1%; Score 37; DB 2; Length 175;
Best Local Similarity 71.4%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOW 7
||||:|
Db 160 RPKPNEW 166

RESULT 87

hypothetical protein SPAC7D4.09c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T39087
R:Gentles, S.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1997
A:Reference number: 221826
A:Accession: T39087
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-274 <GEN>
A:Cross-references: EMBL:Z99532; PIDN:CAB16726.2; GSPDB:GNO0066; SPDB:SPAC7D4.09c
A:Experimental source: strain 972h-; cosmid c7D4
C:Genetics:
A:Gene: SPDB:SPAC7D4.09c
A:Map position: 1

Query Match 52.1%; Score 37; DB 2; Length 274;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 PQOWFW 9
|::|||
Db 61 PKRWF 66

RESULT 88

alpha(1,3)-fucosyltransferase (EC 2.4.1.-) 7 precursor - human
N:Alternate names: leukocyte fucosyltransferase FucVII
C:Species: Homo sapiens (man)
C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 20-Apr-2000
C:Accession: A54057; PIDN:94237894
R:Sasaki, K.; Kurata, K.; Funayama, K.; Nagata, M.; Watanabe, E.; Ohta, S.; Hanai, N.; N
J. Biol. Chem. 269, 14730-14737, 1994
A:Title: Expression cloning of a novel alpha1,3-fucosyltransferase that is involved in b
A:Reference number: A54057; MUID:94237894
A:Accession: A54057
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-342 <SAS>
A:Cross-references: GB:X78031; NID:g516292; PIDN:CAA54962.1; PID:g516293
R:Natsuka, S.; Gersten, K.M.; Zenita, K.; Kannagi, R.; Lowe, J.B.
J. Biol. Chem. 269, 16789-16794, 1994
A:Title: Molecular cloning of a cDNA encoding a novel human leukocyte alpha-1,3-fucosylt
A:Reference number: A53713; MUID:94266898
A:Accession: A53713
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-160, 'A', 163-303, 'SV', 306-342 <NAT>
A:Cross-references: GB:U08112; NID:g520463; PIDN:AAA56869.1; PID:g520464
C:Genetics:
A:Gene: GDB:FUT7
A:Cross-references: GDB:373982
A:Map position: 9pter-9qter
C:Superfamily: galactoside 3(4)-L-fucosyltransferase
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-342/Product: alpha(1,3)-fucosyltransferase 7 #status predicted <MAT>
F:81,291/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.1%; Score 37; DB 2; Length 342;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOOWFW 9
||:| | |
Db 110 RPRGPWVW 118

RESULT 89

alpha(1,3/4)-fucosyltransferase - bovine
S55498
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 13-Sep-1998
C:Accession: S55498
R:Oulmouden, A.; Wierinckx, A.; Petit, J.M.; Julien, R.
submitted to the EMBL Data Library, June 1995
A:Description: Molecular cloning and expression of bovine alpha (1,3/4)-fucosyltransf
A:Reference number: S55498
A:Accession: S55498
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-365 <OUL>
A:Cross-references: EMBL:X87810; NID:g860807; PID:g860808
C:Superfamily: galactoside 3(4)-L-fucosyltransferase

Query Match 52.1%; Score 37; DB 2; Length 365;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOOWFW 9
|| | | |
Db 130 RPDQRWVW 138

RESULT 90

H64861
hypothetical protein bll163 - Escherichia coli
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C:Accession: H64861
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: H64861
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-403 <BLAT>
A:Cross-references: GB:AE000215; GB:U00096; NID:gl787405; PIDN:AAC74247.1; PID:gl7874
A:Experimental source: strain K-12, substrain MG1655

Query Match 52.1%; Score 37; DB 2; Length 403;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PQOWFWL 10
|::| | |
Db 367 PEEWVWL 373

RESULT 91

S25953
ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b - liverwort (Marchantia
C:Species: Marchantia polymorpha
C:Date: 07-May-1993 #sequence_revision 02-Aug-1994 #text_change 03-Mar-2000
C:Accession: S25953
R:Oda, K.; Yamato, K.; Ohta, E.; Nakamura, Y.; Takemura, M.; Nozato, N.; Akashi, K.;
J. Mol. Biol. 223, 1-7, 1992
A:Title: Gene organization deduced from the complete sequence of liverwort Marchantia
A:Reference number: S25941; MUID:92114051
A:Accession: S25953
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-404 <ODA>
A:Cross-references: EMBL:M68929; NID:g786182; PIDN:AA09441.1; PID:g786227
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
C:Genetics:
A:Gene: cob
A:Genome: 124/3; 261/3; 275/2
C:Function:
A:Description: the net reaction catalyzed by the ubiquinol--cytochrome-c reductase complex with two hydrogen ions taken up from the mitochondrial matrix and four hydrogen ions released
A:Pathway: oxidative phosphorylation; respiratory chain
C:Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastocytin
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; mitochondrion;
F:13-343/Domain: cytochrome b homology <CBH>
F:13-213/Domain: cytochrome b6 homology <CB6>
F:38-54/Domain: transmembrane #status predicted <TM1>
F:83-101/Domain: transmembrane #status predicted <TM2>
F:121-137/Domain: transmembrane #status predicted <TM3>
F:182-204/Domain: transmembrane #status predicted <TM4>
F:225-343/Domain: plastocytin-plastocyanin reductase 17K protein homology <17K>
F:233-249/Domain: transmembrane #status predicted <TM5>
F:232-308/Domain: transmembrane #status predicted <TM6>
F:327-347/Domain: transmembrane #status predicted <TM7>
F:357-372/Domain: transmembrane #status predicted <TM8>
F:85,186/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted
F:99,200/Binding site: heme iron (His) (axial ligands) (high potential) #status predicted

Query Match 52.1%; Score 37; DB 1; Length 404;
Best Local Similarity 54.5%; Pred. No. 1.7e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
II I::III
Db 322 RPIHQKFWLL 332

RESULT 92
B82147
conserved hypothetical protein VC1884 [imported] - Vibrio cholerae (strain N16961 serotype O1)

C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: B82147
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-406 <HEI>
A:Cross-references: GB:AE004263; GB:AE003852; NID:g9656399; PIDN:AAF95032.1; GSPDB:GN00118886
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1884
A:Map position: 1
C:Superfamily: hypothetical protein HI1555

Query Match 52.1%; Score 37; DB 2; Length 406;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 9
II I::II
Db 243 QPLPQDWOW 251

RESULT 93
C82433
methyl-accepting chemotaxis protein VCA0658 [imported] - Vibrio cholerae (strain N16961 serotype O1)

C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: C82433
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-406 <HEI>
A:Cross-references: GB:AE004263; GB:AE003852; NID:g9656399; PIDN:AAF95032.1; GSPDB:GN00118886
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1884
A:Map position: 1
C:Superfamily: hypothetical protein HI1555

Query Match 52.1%; Score 37; DB 2; Length 536;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQWFWL 10
I::II I
Db 188 PEQWQL 194

RESULT 94
A54306
proteinkinase 4 (EC 3.4.21.-) precursor - mouse

C:Species: Mus musculus (house mouse)
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
C:Accession: A54306; A42151; D45357
R:McKibbin, M.; Raffin-Sanson, M.L.; Tadros, H.; Sirols, F.; Seidah, N.G.; Chretien, M.
Genomics 20, 231-237, 1994
A:Title: Structure of the gene for the testis-specific proprotein convertase 4 and of its precursor - mouse

A:Reference number: A54306; MUID:94292203
A:Accession: A54306
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-655 <MBI>
A:Cross-references: GB:I21210
A:Note: authors translated the codon AAC for residue 65 as Asp, and CCG for residue 8 as Arg.
R:Nakayama, K.; Kim, W.S.; Torii, S.; Hosaka, M.; Nakagawa, T.; Ikemizu, J.; Baba, T.
J. Biol. Chem. 267, 5897-5900, 1992
A:Title: Identification of the fourth member of the mammalian endoprotease family homology 100

A:Reference number: A42151; MUID:92210552
A:Accession: A42151
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-64, D', 66-86, 'R', 88-655 <NAK>
A:Cross-references: GB:D01093; NID:g220363; PIDN:BAA00877.1; PID:g220564
R:Seidah, N.G.; Day, R.; Hamelin, J.; Gaspar, A.; Collard, M.W.; Chretien, M.
Mol. Endocrinol. 6, 1559-1570, 1992
A:Title: Testicular expression of PC4 in the rat: molecular diversity of a novel germ protein

A:Reference number: A45357; MUID:93078790
A:Accession: D45357
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 586-639 <SEI>
A:Note: sequence extracted from NCBI backbone (NCBI:P118886)
C:Genetics:
A:Gene: PC4
C:Superfamily: kexin; subtilisin homology
C:Keywords: hydrolase; serine proteinase; testis; zymogen
F:1-26/Domain: signal sequence #status predicted <SIG>
F:146-384/Domain: subtilisin homology <SBT>
F:155,196,370/Active site: Asp, His, Ser #status predicted

Query Match 52.1%; Score 37; DB 1; Length 655;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QQWFWL 10
| | | | |
Db 625 QQWWWL 630

RESULT 95
TOBPU
transposase - phage Mu
C:Species: phage Mu
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 23-Jul-1999
C:Accession: A24746; S09550; S06975; S57318
R:Harshey, R.M.; Getroff, E.D.; Baldwin, D.L.; Miller, J.L.; Chaconas, G.
Proc. Natl. Acad. Sci. U.S.A. 82, 7676-7680, 1985
A:Title: Primary structure of phage mu transposase: homology to mu repressor.
A:Reference number: A24746; MUID:86067968
A:Accession: A24746
A:Molecule type: DNA
A:Residues: 1-662 <HAR>
A:Cross-references: GB:M11195
R:Wu, Z.; Chaconas, G.
EMBO J. 14, 3835-3843, 1995
A:Title: A novel DNA binding and nuclease activity in domain III of Mu transposase: evidence
A:Reference number: S57318; MUID:95369255
A:Contents: annotation
R:Priess, H.; Kamp, D.; Kahmann, R.; Braeuer, B.; Delius, H.
Mol. Gen. Genet. 186, 315-321, 1982
A:Title: Nucleotide sequence of the immunity region of bacteriophage Mu.
A:Reference number: S07291; MUID:83012203
A:Accession: S09550
A:Molecule type: DNA
A:Residues: 1-88 <PRI>
A:Cross-references: EMBL:V01464; NID:g15807; PIDN:CAA24713.1; PID:g15810
C:Genetics:
A:Gene: A
C:Function:
A:Description: it is essential for integration, replication-transposition, and excision
C:Superfamily: phage Mu transposase
C:Keywords: DNA binding; DNA replication

Query Match 52.1%; Score 37; DB 1; Length 662;
Best Local Similarity 57.1%; Pred. No. 2.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 KPQOWFW 9
| | | | |
Db 285 RPKTWF 291

RESULT 96
I78558
hypothetical Brachyury (T)-related transcription factor - mouse
C:Species: Mus sp. (mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C:Accession: I78558
R:Bulfone, A.; Smiga, S.M.; Shimamura, K.; Peterson, A.; Puelles, L.; Rubenstein, J.L.
Neuron 15, 63-78, 1995
A:Title: T-brain-1: a homolog of Brachyury whose expression defines molecularly distinct
A:Reference number: I58171; MUID:95344783
A:Accession: I78558
A:Status: preliminary;
A:Molecule type: mRNA
A:Residues: 1-681 <RES>
A:Cross-references: GB:S78858; NID:g1222544; PIDN:AAA92011.1; PID:g1222545
C:Genetics:
A:Gene: Tbr-1/Tes-56
C:Superfamily: T-box homology
F:213-401/Domain: T-box homology <TBX>

Query Match 52.1%; Score 37; DB 2; Length 747;
Best Local Similarity 83.3%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KPQOW 7
| | | | |
Db 528 KPQOW 533

RESULT 98
S54252
deep orange protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 24-Sep-1998
C:Accession: S54252
R:Shetopal, S.A.
submitted to the EMBL Data Library, April 1995
A:Reference number: S54252
A:Accession: S54252
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1002 <SHE>
A:Cross-references: EMBL:X86683; NID:g798831; PID:g798832
C:Genetics:
A:Gene: FlyBase:dor
A:Cross-references: FlyBase:FBgn0000482

Query Match 52.1%; Score 37; DB 2; Length 1002;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PQOWFWL 10
| | | | |
Db 301 PKQAWL 307

RESULT 99
G02750

Query Match 52.1%; Score 37; DB 2; Length 681;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PKPQOWF 8
| | | | |
Db 479 PSPQOWF 485

RESULT 97
I39444
AMP deaminase (EC 3.5.4.6) - human
N:Alternate names: myoadenylate deaminase
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 22-Jun-1999
C:Accession: I39444
R:Sabina, R.L.; Fishbein, W.N.; Pezeshkpour, G.; Clarke, P.R.; Holmes, E.W.
Neurology 42, 170-179, 1992
A:Title: Molecular analysis of the myoadenylate deaminase deficiencies.
A:Reference number: I39444; MUID:92131279
A:Accession: I39444
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-747 <RES>
A:Cross-references: GB:M60092; NID:g178543; PIDN:AAA57281.1; PID:g178544
C:Genetics:
A:Gene: GDB:AMPDL
A:Cross-references: GDB:I19677; OMIM:102770
A:Map position: lp13-lp13
C:Superfamily: AMP deaminase
C:Keywords: hydrolase

DNA-directed DNA polymerase (EC 2.7.7.7) gamma - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Sep-1999
C;Accession: G02750
R;Ropp, P.A.; Copeland, W.C.
submitted to the EMBL Data Library, June 1996
A;Reference number: H01679
A;Accession: G02750
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1239 <ROP>
A;Cross-references: EMBL:U60325; NID:gl399955; PID:gl399956
C;Superfamily: DNA-directed DNA polymerase, mitochondrial
C;Keywords: nucleotidyltransferase

Query Match 52.1%; Score 37; DB 2; Length 1239;
Best Local Similarity 62.5%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQQWF 9
||| |

Db 164 PKPPAW 171

RESULT 100
T26656
hypothetical protein Y38E10A.f - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26656
R;Wallis, J.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z20252
A;Accession: T26656
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1384 <WIL>
A;Cross-references: EMBL:AL110484; NID:el542205; PIDN:CAB54397.1; CESP:Y38E10A.f
A;Experimental source: clone Y38E10A
C;Genetics:
A;Gene: CESP:Y38E10A.f
A;Introns: 84/3; 115/3; 154/1; 187/3; 245/3; 325/3; 365/3; 422/3; 480/3; 525/3; 565/3; 6

Query Match 52.1%; Score 37; DB 2; Length 1384;
Best Local Similarity 54.5%; Pred. No. 5.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 RPKP--QQWF 9
||| :|||

Db 361 RPRPFVLKWF 371

RESULT 101
T32452
hypothetical protein F48A11.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32452
R;Bradshaw, H.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F48A11.
A;Reference number: Z21171
A;Accession: T32452
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1635 <BRA>
A;Cross-references: EMBL:AF026210; PIDN:AAB71283.1; GSPDB:GN00020; CESP:F48A11.1
A;Experimental source: strain Bristol N2, clone F48A11
C;Genetics:
A;Gene: CESP:F48A11.1
A;Map position: 2

Query Match 52.1%; Score 37; DB 2; Length 1635;
Best Local Similarity 71.4%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQQWF 10
||| |

Db 580 PQTWL 586

RESULT 102
T17420
probable polyketide synthase type I - Pseudomonas fluorescens
C;Species: Pseudomonas fluorescens
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Nov-2000
C;Accession: T17420
R;Nowak-Thompson, B.; Chaney, N.; Wing, J.S.; Gould, S.J.; Lopez, J.E.
J. Bacteriol. 181, 2166-2174, 1999
A;Title: Characterization of the pyoluteorin biosynthetic gene cluster of Pseudomonas
A;Reference number: Z18776; MUID:99194726
A;Accession: T17420
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2458 <NOW>
A;Cross-references: EMBL:AF081920; NID:g4582974; PID:g2781416; PIDN:AAC38075.1
C;Genetics:
A;Gene: plbB
C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology; acyl carrier pro
C;Keywords: carrier protein
F;31-429/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS1>
F;535-815/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F;939-1009/Domain: acyl carrier protein homology <ACP1>
F;1053-1446/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS2>
F;2337-2408/Domain: acyl carrier protein homology <ACP2>

Query Match 52.1%; Score 37; DB 2; Length 2458;
Best Local Similarity 55.6%; Pred. No. 9.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRPQQWF 9
||| |

Db 1613 RPAGQLWY 1621

RESULT 103
JC4534
cytochrome P450 4F6 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 28-Jul-2000
C;Accession: JC4534
R;Kawashima, H.; Strobel, H.W.
Biochem. Biophys. Res. Commun. 217, 1137-1144, 1995
A;Title: cDNA cloning of three new forms of rat brain cytochrome P450 belonging to th
A;Reference number: JC4532; MUID:96125358
A;Accession: JC4534
A;Molecule type: mRNA
A;Residues: 1-537 <KAW>
A;Cross-references: NID:gl146439; PIDN:AAC52360.1; PID:gl146440
A;Experimental source: brain
C;Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology
C;Keywords: brain; chromoprotein; heme; iron; metalloprotein
F;325-490/Domain: cytochrome P450 homology <P45>
F;468/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 51.4%; Score 36.5; DB 2; Length 537;
Best Local Similarity 75.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 PKPQQWF 9

DB 55 PKP-SWFW 61
||| |||
A;Description: may play a physiological role in the regulation of cardiovascular and
A;Note: substance P is derived by post-translational processing of preprotachykinin A
C;Superfamily: unassigned animal peptides
C;Keywords: neuropeptide; amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

RESULT 104
S77658
hypothetical protein o659 - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 11-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 22-Oct-1999
C;Accession: S77658; S49520
R;Fsihi, H.; Cole, S.T.
Mol. Microbiol. 16, 909-919, 1995
A;Title: The Mycobacterium leprae genome: systematic sequence analysis identifies key ca
A;Reference number: S77658; MUID:96059637
A;Accession: S77658
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-659 <PSI>
A;Cross-references: EMBL:246257; NID:g559905; PIDN:CAA86362.1; PID:g559911
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994

Query Match 51.4%; Score 36.5; DB 2; Length 659;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 RPKPQQWF-WLM 11
:|:|:| |||
DB 464 OPGPREWLTWLM 475

RESULT 105
DNBBEG
DNA-binding protein - bovine herpesvirus 2 (strain BMV)
C;Species: bovine herpesvirus 2
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 07-Jun-1996
C;Accession: A29242
R;Hammerschmidt, W.; Conraths, F.; Mankertz, J.; Pauli, G.; Ludwig, H.; Buhk, H.J.
Virology 165, 388-405, 1988
A;Title: Conservation of a gene cluster including glycoprotein B in bovine herpesvirus t
A;Reference number: A94381; MUID:88306231
A;Accession: A29242
A;Molecule type: DNA
A;Residues: 1-1186 <HAM>
A;Cross-references: GB:M21628
A;Superfamily: herpesvirus DNA-binding protein
C;Keywords: DNA binding

Query Match 51.4%; Score 36.5; DB 1; Length 1186;
Best Local Similarity 75.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 PKPQQWF 9
:|:|:| |||
DB 834 PNP-QWFW 840

RESULT 106
S23306
substance P - Atlantic cod
C;Species: Gadus morhua (Atlantic cod)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C;Accession: S23306
R;Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod
A;Reference number: S23186; MUID:92298992
A;Accession: S23306
A;Molecule type: protein
A;Residues: 1-11 <JEN>
A;Experimental source: brain
C;Function:

Query Match 50.7%; Score 36; DB 2; Length 11;
Best Local Similarity 54.5%; Pred. No. 6.7;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
:|:|:| |||
DB 1 KRPQQQTGLM 11

RESULT 107
S45489
H+-transporting ATP synthase (EC 3.6.1.34) protein 8 - European seabass mitochondrion
C;Species: mitochondrion Dicentrarchus labrax (European seabass)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-Dec-1999
C;Accession: S45489
R;Venanzetti, F.; Cecconi, F.; Giorgi, M.; Cesaroni, D.; Sbordoni, V.; Mariottini, P.
Curr. Genet. 26, 139-145, 1994
A;Title: Cloning and characterization of the European seabass, Dicentrarchus labrax,
A;Reference number: S45489; MUID:95094310
A;Accession: S45489
A;Molecule type: DNA
A;Residues: 1-55 <VEN>
A;Cross-references: EMBL:X74147; NID:g521076; PIDN:CAA52244.1; PID:g521077
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SSCI
C;Superfamily: H+-transporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;

Query Match 50.7%; Score 36; DB 2; Length 55;
Best Local Similarity 44.4%; Pred. No. 33;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPKPQQWF 9
:|:|:| |||
DB 44 KPSEHSWF 52

RESULT 108
S77270
hypothetical protein slr0881 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S77270
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
S.
A;Reference number: S74322; MUID:97061201
A;Accession: S77270
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-103 <KAN>
A;Cross-references: EMBL:D90907; GB:AB001339; NID:gl652618; PIDN:BAAL7604.1; PID:gl65
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein slr0881

Query Match 50.7%; Score 36; DB 2; Length 103;
Best Local Similarity 42.9%; Pred. No. 61;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPQQWF 9

Db 84 RPEHWY 90
:|:|:|
RESULT 109
C75435
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C:Accession: C75435
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: C75435
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-154 <WHI>
A:Cross-references: GB:AE001961; GB:AE000513; NID:g6458843; PIDN:AAF10689.1; PID:g645885
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1108
A:Map position: 1
C:Superfamily: Deinococcus radiodurans hypothetical protein DR1108
Query Match 50.7%; Score 36; DB 2; Length 154;
Best Local Similarity 54.5%; Pred. No. 91;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RPKPOQWFWM 11
|:|:|:|
Db 46 RQOPQAFWLL 56
:|:|:|
RESULT 110
E83140
phosphatidylglycerophosphatase A PA4050 [imported] - Pseudomonas aeruginosa (strain PA01
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: E83140
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337
A:Accession: E83140
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-171 <STO>
A:Cross-references: GB:AE004821; GB:AE004091; NID:g9950236; PIDN:AAG07437.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: pg; PA4050
C:Superfamily: conserved hypothetical protein H11306
Query Match 50.7%; Score 36; DB 2; Length 171;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 4 PQQWFWM 11
|:|:|:|
Db 107 PEGWFWLL 114
:|:|:|
RESULT 111
S43177
p18 protein - Leishmania tarentolae
C:Species: Leishmania tarentolae
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Nov-1999
C:Accession: S43177
R:Bringaud, F.; Freedland, S.; Liu, X.; Peris, M.; Turck, C.; Simpson, L.
submitted to the EMBL Data Library, March 1994
A:Description: Identification of several proteins in mitochondrial nucleoprotein T-co
A:Reference number: S43177
A:Accession: S43177
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-187 <BR1>
A:Cross-references: EMBL:Z31697; NID:g469151; PID:g469152
C:Superfamily: Leishmania tarentolae p18 protein
Query Match 50.7%; Score 36; DB 2; Length 187;
Best Local Similarity 36.4%; Pred. No. 1.1e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 RPKPOQWFWM 11
:|:|:|:|
Db 113 KPNEESWTWVM 123
:|:|:|:|
RESULT 112
T16544
hypothetical protein K03C7.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
C:Accession: T16544
R:Leimbach, D.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid K03C7.
A:Reference number: Z18532
A:Accession: T16544
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-268 <LEI>
A:Cross-references: EMBL:U40059; NID:g1055170; PID:g1055172; PIDN:AAA81139.1; CESP:K0
C:Genetics:
A:Gene: CESP:K03C7.2
A:Introns: 32/3; 106/3; 153/1
C:Superfamily: unassigned fork head proteins; fork head DNA-binding domain homology
Query Match 50.7%; Score 36; DB 2; Length 268;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 RPKPOQWFWM 9
|:|:|:|
Db 116 RHRPDQWGW 124
:|:|:|:|
RESULT 113
A82185
glycerol-3-phosphate ABC transporter, permease protein VC1551 [imported] - Vibrio cho
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: A82185
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers
L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82095; MUID:20406833
A:Accession: A82185
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-280 <HEI>
A:Cross-references: GB:AE004233; GB:AE003852; NID:g9656055; PIDN:AAF94705.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1551

A;Map position: 1

Query Match 50.7% Score 36; DB 2; Length 280;
Best Local Similarity 50.0% Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PKPQQWFWM 11
| | | | |
Db 105 PYASAWFWLI 114

RESULT 114

A75511
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: A75511
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: A75511
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-287 <WHI>
A:Cross-references: GB:AE001909; GB:AE000513; NID:96458188; PIDN:AAF10080.1; PID:9645818
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0500
A:Map position: 1
C:Superfamily: Mycoplasma hypothetical protein MG326

Query Match 50.7% Score 36; DB 2; Length 287;
Best Local Similarity 71.4% Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQW 7
| | | | |
Db 64 QPSPQQW 70

RESULT 115

I64053
membrane-bound lytic transglycosylase homolog - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C:Accession: I64053
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: I64053
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-318 <TIIGR>
A:Cross-references: GB:U32705; GB:I42023; NID:gi573156; PIDN:AAC21868.1; PID:gi573159; T

Query Match 50.7% Score 36; DB 2; Length 318;
Best Local Similarity 40.0% Pred. No. 1.9e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PKPQQWFWM 11
| | | | |
Db 295 PAPEQYVWIL 304

RESULT 116

S76408
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.

A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S76408
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima,
O.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
s.

A:Reference number: S74322; MUID:97061201
A:Accession: S76408
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-330 <KAN>
A:Cross-references: EMBL:D90915; GB:AB001339; NID:gi1653604; PIDN:BAAL8537.1; PID:dl01
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 50.7% Score 36; DB 2; Length 330;
Best Local Similarity 71.4% Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQW 7
| | | | |
Db 64 RPQPNW 70

RESULT 117

S44995
pectate lyase - Erwinia carotovora
C:Species: Erwinia carotovora
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C:Accession: S44995
R;Heikinheimo, R.; Flego, D.; Pirhonen, M.; Karlsson, M.B.; Eriksson, A.; Mae, A.; KO
submitted to the EMBL Data Library, May 1994
A:Description: Characterization of a novel pectate lyase from Erwinia carotovora subs
A:Reference number: S44995
A:Accession: S44995
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <HEI>
A:Cross-references: EMBL:X79232; NID:9488382; PIDN:CAA55814.1; PID:9488383

Query Match 50.7% Score 36; DB 2; Length 347;
Best Local Similarity 44.4% Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PKPQQWFWM 10
| | | | |
Db 82 PKSDYVYVW 90

RESULT 118

I59347
hypothetical glutathione transporter, sinusoidal - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Mar-1999 #sequence_revision 12-Mar-1999 #text_change 31-Dec-2000
C:Accession: I59347
R;Yi, J.R.; Lu, S.; Fernandez-Checa, J.; Kaplowitz, N.
Proc. Natl. Acad. Sci. U.S.A. 92, 1495-1499, 1995
A:Title: Expression cloning of the cDNA for a polypeptide associated with rat hepatic
A:Reference number: I59347; MUID:95183492
A:Accession: I59347
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-353 <YIJ>
A:Cross-references: EMBL:U16358; NID:9687585; PIDN:AAA62498.1; PID:9687586
C:Comment: This sequence is very similar to two adjoining hypothetical sequences from

C;Genetics:
A;Gene: Ragshrt

Query Match 50.7%; Score 36; DB 4; Length 353;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOQWFWLM 11
| | | | | | | | | |
DB 124 PVPMTWFFMM 133

RESULT 119
S34173
Wnt-5c protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C;Accession: S34173; S45242
R;Koster, J.G.; Kuiken, G.A.; Stegeman, B.; Peterson, J.; Eizema, K.; Stabel, L.; Dekker
submitted to the EMBL Data Library, June 1993
A;Description: Differential Xwt-5c expression during early development of Xenopus laevis
A;Reference number: S34173
A;Accession: S34173
A;Molecule type: mRNA
A;Residues: 1-360 <ROS>
A;Cross-references: EMBL:X73510; NID:g313267; PIDN:CAA51916.1; PID:g313268
R;Kuiken, G.A.; Bertens, P.J.A.; Peterson-Maduro, J.; Veenstra, G.J.C.; Koster, J.G.; De
Nucleic Acids Res. 22, 1675-1680, 1994
A;Title: The promoter of the Xwt-5c gene contains octamer and AP-2 motifs functional in
A;Reference number: S45242; MUID:94261437
A;Accession: S45242
A;Molecule type: DNA
A;Residues: 1-28 <KUI>
C;Superfamily: Int-1 transforming protein

Query Match 50.7%; Score 36; DB 2; Length 360;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 RPK--PQOWFW 9
| | | | | | | | | |
DB 149 RPKDLPRDWLW 159

RESULT 120
A48914
proto-oncogene Wnt-5A precursor - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999
C;Accession: A48914
R;Clark, C.C.; Cohen, I.; Eichstetter, I.; Cannizzaro, L.A.; McPherson, J.D.; Wasmuth, J.
Genomics 18, 249-260, 1993
A;Title: Molecular cloning of the human proto-oncogene Wnt-5A and mapping of the gene (W
A;Reference number: A48914; MUID:94116991
A;Accession: A48914
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-365 <CLA>
A;Cross-references: GB:L20861; NID:g348917; PIDN:AAA16842.1; PID:g348918
C;Genetics:
A;Gene: GDB:WNT5A
A;Cross-references: GDB:141726; OMIM:164975
A;Map position: 3p21-3p14
C;Superfamily: Int-1 transforming protein

Query Match 50.7%; Score 36; DB 2; Length 365;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 RPK--PQOWFW 9

DB 154 RPKDLPRDWLW 164

RESULT 121
S75038
hypothetical protein sll1611 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S75038
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
S.
A;Reference number: S74322; MUID:97061201
A;Accession: S75038
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-369 <KAN>
A;Cross-references: EMBL:D90910; GB:AB001339; NID:g1652956; PIDN:BAAL7900.1; PID:d101
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Start codon: GTG

Query Match 50.7%; Score 36; DB 2; Length 369;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOWFWL 10
| | | | | | | | | |
DB 52 PQQWLWL 58

RESULT 122
E36470
Wnt-5b protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 16-Jul-1999
C;Accession: E36470
R;Gavin, B.J.; McMahon, J.A.; McMahon, A.P.
Genes Dev. 4, 2319-2332, 1990
A;Title: Expression of multiple novel Wnt-1/int-1-related genes during fetal and adul
A;Reference number: A36470; MUID:91122634
A;Accession: E36470
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-372 <GAV>
A;Cross-references: GB:W89799; NID:g202405; PIDN:AAA40568.1; PID:g202406
C;Superfamily: int-1 transforming protein

Query Match 50.7%; Score 36; DB 2; Length 372;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 RPK--PQOWFW 9
| | | | | | | | | |
DB 161 RPKDLPRDWLW 171

RESULT 123
D36470
Wnt-5a protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 16-Jul-1999
C;Accession: D36470
R;Gavin, B.J.; McMahon, J.A.; McMahon, A.P.
Genes Dev. 4, 2319-2332, 1990
A;Title: Expression of multiple novel Wnt-1/int-1-related genes during fetal and adul
A;Reference number: A36470; MUID:91122634

A:Accession: D36470
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-379 <GAV>
A:Cross-references: GB:M89798; NID:g202403; PIDN:AAA04567.1; PID:g202404
C:Superfamily: int-1 transforming protein

Query Match 50.7%; Score 36; DB 2; Length 379;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 RPK--PQQWF 9
||| | : |
Db 168 RPKDLPDQLW 178

RESULT 124

ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b - common lancelet mitochondrion
A:Accession: A71390
C:Species: Branchiostoma lanceolatum (common lancelet)
C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000
C:Accession: A71390
R:Spruyt, N.; Delarbre, C.; Gachelin, G.; Laudet, V.
Nucleic Acids Res. 26, 3279-3285, 1998
A:Title: Complete sequence of the amphioxus (Branchiostoma lanceolatum) mitochondrial gene
A:Reference number: A71390; MUID:98292550

A:Accession: A71390
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-380 <SPR>

A:Cross-references: GB:Y16474; NID:g3292989; PIDN:CAA76246.1; PID:g3292990

C:Genetics:

A:Gene: cytb

A:Genome: mitochondrion

A:Genetic code: SGC4

C:Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; mitochondrion;
F:12-210/Domain: cytochrome b6 homology <CB6>

F:37-53/Domain: transmembrane #status predicted <TM1>

F:82-100/Domain: transmembrane #status predicted <TM2>

F:118-134/Domain: transmembrane #status predicted <TM3>

F:179-201/Domain: transmembrane #status predicted <TM4>

F:222-340/Domain: plastoquinol--plastocyanin reductase 17K protein homology <17K>

F:230-246/Domain: transmembrane #status predicted <TM5>

F:289-305/Domain: transmembrane #status predicted <TM6>

F:324-344/Domain: transmembrane #status predicted <TM7>

F:354-371/Domain: transmembrane #status predicted <TM8>

F:84,183/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted
F:98,197/Binding site: heme iron (His) (axial ligands) (high potential) #status predicted

Query Match 50.7%; Score 36; DB 2; Length 380;
Best Local Similarity 63.6%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RPKPQQWF 11
||| | : ||||
Db 319 RPLAQVLF 329

RESULT 125

ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b - starfish (Asterina pectinifera)
A:Accession: S70594
C:Species: Asterina pectinifera
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 04-Mar-2000
C:Accession: S70594

R:Asakawa, S.; Hmeno, H.; Miura, K.; Watanabe, K.

Genetics 140, 1047-1060, 1995

A:Title: Nucleotide sequence and gene organization of the starfish Asterina pectinifera

A:Reference number: S70589; MUID:95402698

A:Accession: S70594

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-380 <ASA>

A:Cross-references: EMBL:D16387

A:Experimental source: ovary

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993

C:Genetics:

A:Gene: cytb

A:Genome: mitochondrion

A:Genetic code: SGC8

A:Start codon: ATT

C:Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol

C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; mitochondrion

F:13-341/Domain: cytochrome b homology <CBH>

F:13-211/Domain: cytochrome b6 homology <CB6>

F:38-54/Domain: transmembrane #status predicted <TM1>

F:83-101/Domain: transmembrane #status predicted <TM2>

F:119-135/Domain: transmembrane #status predicted <TM3>

F:180-202/Domain: transmembrane #status predicted <TM4>

F:223-341/Domain: plastoquinol--plastocyanin reductase 17K protein homology <17K>

F:231-247/Domain: transmembrane #status predicted <TM5>

F:290-306/Domain: transmembrane #status predicted <TM6>

F:325-345/Domain: transmembrane #status predicted <TM7>

F:355-371/Domain: transmembrane #status predicted <TM8>

F:85,184/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted

F:99,198/Binding site: heme iron (His) (axial ligands) (high potential) #status predicted

Query Match 50.7%; Score 36; DB 2; Length 380;

Best Local Similarity 54.5%; Pred. No. 2.2e+02;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RPKPQQWF 11

||| | : |||

Db 320 RPLAQVLF 330

RESULT 126

ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b - red alga (Chondrus cri

S59093

N:Alternate names: apocytochrome b

C:Species: Chondrus crispus (carrageen)

C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 20-Jun-2000

C:Accession: S59093

R:Leblanc, C.; Boyen, C.; Richard, O.; Bonnard, G.; Grienberger, J.M.; Kloareg, B.

J. Mol. Biol. 250, 484-495, 1995

A:Title: Complete sequence of the mitochondrial DNA of the rhodophyte Chondrus crispus

A:Reference number: S59078; MUID:95341681

A:Accession: S59093

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-381 <LEB>

A:Cross-references: EMBL:Z47547; NID:g1019057; PIDN:CAA87609.1; PID:g1334487

A:Experimental source: female gametophytes

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995

C:Genetics:

A:Gene: cob

A:Genome: mitochondrion

A:Genetic code: SGC3

C:Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol

C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; mitochondrion

F:9-339/Domain: cytochrome b homology <CBH>

F:9-209/Domain: cytochrome b6 homology <CB6>

F:34-50/Domain: transmembrane #status predicted <TM1>

F:79-97/Domain: transmembrane #status predicted <TM2>

F:117-133/Domain: transmembrane #status predicted <TM3>

F:178-200/Domain: transmembrane #status predicted <TM4>

F:221-339/Domain: plastoquinol--plastocyanin reductase 17K protein homology <17K>

F:229-245/Domain: transmembrane #status predicted <TM5>

F:288-304/Domain: transmembrane #status predicted <TM6>

F:323-343/Domain: transmembrane #status predicted <TM7>

F:353-369/Domain: transmembrane #status predicted <TM8>

F:81,182/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted

F:95.196/Binding site: heme iron (His) (axial ligands) (high potential) #status,predicted

Query Match 50.7%; Score 36; DB 2; Length 381;
Best Local Similarity 44.4%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPQOWFWLM 11

||:|:|:

Db 107 KPRHWVVI 115

RESULT 127

T39028

C:Title: citrate synthase precursor, mitochondrial - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000

C:Accession: T39028

R:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, February 1996

A:Reference number: Z21750

A:Accession: T39028

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-473 <DEV>

A:Cross-references: EMBL:Z69731; PIDN:CAA93617.2; GSPDB:GN00066; SPDB:SPAC6C3.04

A:Experimental source: strain 972h-; cosmid c6C3

C:Genetics:

A:Gene: SPDB:SPAC6C3.04

A:Map position: 1

A:Genome: nuclear

C:Superfamily: citrate (sl)-synthase

C:Keywords: mitochondrion

Query Match 50.7%; Score 36; DB 2; Length 473;

Best Local Similarity 45.5%; Pred. No. 2.8e+02;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQWFWM 11

||:|:|:

Db 122 QPLPESLFWLL 132

RESULT 128

JC4532

C:Title: cytochrome P450 4F4 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 15-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 28-Jul-2000

C:Accession: JC4532

R:Kawashima, H.; Strobel, H.W.

Biochem. Biophys. Res. Commun. 217, 1137-1144, 1995

A:Title: cDNA cloning of three new forms of rat brain cytochrome P450 belonging to the C

A:Reference number: JC4532; MUID:96125358

A:Accession: JC4532

A:Molecule type: mRNA

A:Residues: 1-522 <KAW>

A:Cross-references: GB:U39206; NID:g1146435; PIDN:AA52358.1; PID:g1146436

A:Experimental source: brain

C:Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology

C:Keywords: brain; chromoprotein; heme; iron; metalloprotein

F:325-490/Domain: cytochrome P450 homology <P45>

F:468/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 50.7%; Score 36; DB 2; Length 522;

Best Local Similarity 40.0%; Pred. No. 3.1e+02;

Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOQWFWM 11

||:|:|:

Db 52 PQPKWNWL 61

RESULT 129

T35047

C:Title: hypothetical protein SC4G2.12c SC4G2.12c - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 01-Dec-2000

C:Accession: T35047; T30206

R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1998

A:Reference number: Z21566

A:Accession: T35047

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-605 <SEE>

A:Cross-references: EMBL:AL031371; PIDN:CAA20549.1; GSPDB:GN00070; SCODB:SC4G2.12c

A:Experimental source: strain A3(2)

R:Bedford, D.J.; Laity, C.; Buttner, M.J.

J. Bacteriol. 177, 4681-4689, 1995

A:Title: Two genes involved in the phase-variable phi C31 resistance mechanism of Str

A:Reference number: Z20777; MUID:95370146

A:Accession: T30206

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 304-605 <BED>

A:Cross-references: EMBL:L37531; NID:g576537; PID:g576541; PIDN:AAB00368.1

C:Genetics:

A:Gene: SCODB:SC4G2.12c

Query Match 50.7%; Score 36; DB 2; Length 605;

Best Local Similarity 57.1%; Pred. No. 3.5e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQWFW 9

||:|:|:

Db 396 KTEQWY 402

RESULT 130

E69334

C:Title: acetyl-CoA synthetase (acs-3) homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C:Accession: E69334

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod

.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes,

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch

A:Reference number: A69250; MUID:98049343

A:Accession: E69334

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-643 <KLE>

A:Cross-references: GB:AE001058; GB:AE000782; NID:g2689381; PIDN:AAB90564.1; PID:g264

C:Superfamily: acetate--CoA ligase; acetate--CoA ligase homology

F:108-609/Domain: acetate--CoA ligase homology <ACL>

Query Match 50.7%; Score 36; DB 2; Length 643;

Best Local Similarity 57.1%; Pred. No. 3.8e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQWFWL 10

||:|:|:

Db 377 PEVWYWL 383

RESULT 131

T01573

earl protein - maize

C:Species: Zea mays (maize)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 29-Oct-1999
C:Accession: T01573
R:Veit, B.E.; Briggs, S.P.; Schmidt, R.J.; Yanofsky, M.F.; Hake, S.
Nature 393, 166-169, 1998
A:Title: Regulation of leaf initiation by the terminal earl gene of maize.
A:Reference number: Z14351; MUID:98264681
A:Accession: T01573
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-656 <VEI>
A:Cross-references: EMBL:AF047852; NID:g3153236; PIDN:AAC39463.1; PID:g3153237
A:Experimental source: cultivar B73
C:Genetics:
A:Map position: 3

Query Match 50.7%; Score 36; DB 2; Length 656;
Best Local Similarity 62.5%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PKPQQWF 9
| | | | |
Db 172 PTPQAWDM 179

RESULT 132
A73542
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: A75542
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: A75542
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-670 <WHI>
A:Cross-references: GB:AE001886; GB:AE000513; NID:g6457921; PIDN:AAF09837.1; PID:g645792
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0250
A:Map position: 1

Query Match 50.7%; Score 36; DB 2; Length 670;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QQFWL 10
| | | | |
Db 95 QRWFVI 100

RESULT 133
H82381
toxin secretion ATP-binding protein VCA1084 [imported] - Vibrio cholerae (strain N16961)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: H82381
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H
L. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833
A:Accession: H82381
A>Status: preliminary
A:Molecule type: DNA

A:Residues: 1-704 <HEI>
A:Cross-references: GB:AE004433; GB:AE003853; NID:g9658519; PIDN:AAF96977.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA1084
A:Map position: 2

Query Match 50.7%; Score 36; DB 2; Length 704;
Best Local Similarity 44.4%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKPQQWF 9
| | | | |
Db 136 KPRDGHWF 144

RESULT 134
C85547
probable cytoplasmic membrane export protein Z0634 [imported] - Escherichia coli (str
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: C85547
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: C85547
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-720 <SPO>
A:Cross-references: GB:AE005174; NID:gl2513369; PIDN:AAG54839.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z0634

Query Match 50.7%; Score 36; DB 2; Length 720;
Best Local Similarity 55.6%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RPKPQQWF 9
| | | | |
Db 141 RPYQANWF 149

RESULT 135
A70010
NADH dehydrogenase homolog yufT - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: A70010
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivoita, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A:Reference number: A69580; MUID:98044033
A:Accession: A70010
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-774 <KUN>

A:Cross-references: GB:299120; GB:AL009126; NID:g2635613; PIDN:CAB15149.1; PID:g2635656
A:Experimental source: strain 168
C:Genetics:
A:Gene: yufT
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5

Query Match 50.7%; Score 36; DB 2; Length 774;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 QWFWLM 11
:||||:
DB 245 QWFWIV 250

RESULT 136
S61395
probable Na⁺/H⁺-exchanging protein system component - Bacillus sp. (strain C-125)
N:Alternate names: NADH dehydrogenase (ubiquinone) chain 5 homolog; probable Na⁺/H⁺ antiporter
C:Species: Bacillus sp.
A:Variety: strain C-125
C:Date: 01-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: S61395; S61392
R:Hamamoto, T.; Hashimoto, M.; Hino, M.; Kitada, M.; Seto, Y.; Kudo, T.; Horikoshi, K.
submitted to the EMBL Data Library, June 1994
A:Description: Characterization of a gene responsible for Na⁺/H⁺ antiporter system of al
A:Reference number: S61395
A:Accession: S61395
A:Molecule type: DNA
A:Residues: 1-804 <HAW>
A:Cross-references: EMBL:D31823; NID:g854654; PIDN:BAA06609.1; PID:g854655
A:Experimental source: Bacillus sp. strain C-125
R:Hamamoto, T.; Hashimoto, M.; Hino, M.; Kitada, M.; Seto, Y.; Kudo, T.; Horikoshi, K.
Mol. Microbiol. 14, 939-946, 1994
A:Title: Characterization of a gene responsible for the Na⁺/H⁺ antiporter system of
A:Reference number: S61392; MUID:95231300
A:Accession: S61392
A:Molecule type: DNA
A:Residues: 123-166; 214-267; 282-314; 355-474 <HAW>
A:Cross-references: EMBL:D31823
A:Experimental source: Bacillus sp. strain C-125
A:Note: only a part of the coding sequence is given
C:Genetics:
A:Start codon: TTG
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5

Query Match 50.7%; Score 36; DB 2; Length 804;
Best Local Similarity 66.7%; Pred. No. 4.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 QWFWLM 11
:||||:
DB 272 EWFLL 277

RESULT 137
G83814
Na⁺/H⁺ antiporter BH1319 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C:Accession: G83814
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: AB3650; MUID:20263314
A:Accession: G83814
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-804 <STO>
A:Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BA805038.1; GSPDB:GN00
A:Experimental source: strain C-125

A:Cross-references: GB:299120; GB:AL009126; NID:g2635613; PIDN:CAB15149.1; PID:g2635656
A:Experimental source: strain 168
C:Genetics:
A:Gene: BH1319
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5

Query Match 50.7%; Score 36; DB 2; Length 804;
Best Local Similarity 66.7%; Pred. No. 4.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 QWFWLM 11
:||||:
DB 272 EWFLL 277

RESULT 138
S75776
pled protein - Synechocystis sp. (strain PCC 6803)
N:Alternate names: protein slr0829
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S75776
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
s.
A:Reference number: S74322; MUID:97061201
A:Accession: S75776
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-829 <KAN>
A:Cross-references: EMBL:D64003; GB:AB001339; NID:g1001200; PIDN:BAA10511.1; PID:d101
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Gene: pld
A:Start codon: GTG

Query Match 50.7%; Score 36; DB 2; Length 829;
Best Local Similarity 54.5%; Pred. No. 4.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPKPQQWFWLM 11
:||||:
DB 325 RDARQQWRLL 335

RESULT 139
S77086
hypothetical protein sl10737 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S77086
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
s.
A:Reference number: S74322; MUID:97061201
A:Accession: S77086
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-861 <KAN>
A:Cross-references: EMBL:D64005; GB:AB001339; NID:g1001779; PIDN:BAA10778.1; PID:g100
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: Synechocystis hypothetical protein sl10737

Query Match 50.7%; Score 36; DB 2; Length 861;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 QOWFWL 10
| | | | |
Db 57 QTWFWL 62

RESULT 140

T14761

hypothetical protein DKFzP434K233.1 - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14761
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, August 1999
A:Reference number: Z18181
A:Accession: nt14761
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-959 <WAM>
A:Cross-references: EMBL:AL110222
A:Experimental source: adult testis; clone DKFzP434K233
C:Genetics:
A:Note: DKFzP434K233.1

Query Match 50.7%; Score 36; DB 2; Length 959;
Best Local Similarity 62.5%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQWFW 8
| | | | |
Db 682 KPKPPAWF 689

RESULT 141

T25033

hypothetical protein T20D3.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25033
R:Lloyd, C.
submitted to the EMBL Data Library, December 1995
A:Reference number: Z19971
A:Accession: T25033
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1038 <WIL>
A:Cross-references: EMBL:Z68220; PIDN:CAA92492.2; GSPDB:GN000022; CESP:T20D3.9
A:Experimental source: clone T20D3
C:Genetics:
A:Gene: CESP:T20D3.9
A:Map position: 4
A:Introns: 36/3; 341/3; 380/1; 574/2; 771/2; 966/1; 1010/3
C:Superfamily: Caenorhabditis elegans hypothetical protein T20D3.9

Query Match 50.7%; Score 36; DB 2; Length 1038;
Best Local Similarity 44.4%; Pred. No. 6e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 RPKPOQWFWL 10
| : | : | : |
Db 246 PRPSKFFWV 254

RESULT 142

T22982

hypothetical protein F59B10.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Sep-2000
C:Accession: T22982; T27953
R:Lloyd, C.
submitted to the EMBL Data Library, March 1995
A:Reference number: Z19646

A:Accession: T22982
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1039 <WIL>
A:Cross-references: EMBL:Z48716; PIDN:CAA88602.2; GSPDB:GN000020; CESP:F59B10.1
A:Experimental source: clone F59B10
R:Wilkinson, J.
submitted to the EMBL Data Library, April 1995
A:Reference number: Z20445
A:Accession: T27953
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1039 <WIL>
A:Cross-references: EMBL:Z49132; PIDN:CAA88990.2; GSPDB:GN000020; CESP:F59B10.1
A:Experimental source: clone ZK666
C:Genetics:
A:Gene: CESP:F59B10.1
A:Map position: 2
A:Introns: 9/1; 73/3; 293/3; 711/1; 754/3; 837/2; 877/3; 927/2
C:Superfamily: Caenorhabditis elegans hypothetical protein F59B10.1

Query Match 50.7%; Score 36; DB 2; Length 1039;
Best Local Similarity 54.5%; Pred. No. 6e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQWFWL 11
| | | | | : | : | : |
Db 387 RNPQKFFEL 397

RESULT 143

T19214

UDP-glucose--glycoprotein glucosyltransferase (EC 2.4.1.-) precursor F26H9.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T19214; T21444
R:Barlow, K.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19091
A:Accession: T19214
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1377 <WIL>
A:Cross-references: EMBL:Z81467; PIDN:CAB03874.1; GSPDB:GN000019; CESP:F26H9.8
A:Experimental source: clone C12C8
R:Baynes, C.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19422
A:Accession: T21444
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1377 <WIL>
A:Cross-references: EMBL:Z81516; PIDN:CAB04207.1; GSPDB:GN000019; CESP:F26H9.8
A:Experimental source: clone F26H9

C:Genetics:
A:Gene: CESP:F26H9.8
A:Map position: 1
A:Introns: 40/2; 70/1; 152/2; 318/2; 429/3; 494/2; 538/3; 564/3; 625/3; 654/3; 782/3;
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase

Query Match 50.7%; Score 36; DB 2; Length 1377;
Best Local Similarity 66.7%; Pred. No. 8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RPKPOQWFW 9
| | | | |
Db 1305 POEWLW 1310

RESULT 144

T16404

hypothetical protein F48E3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16404
R;Pauley, A.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid F48E3.
A;Reference number: Z18508
A;Accession: T16404
A;Molecule type: DNA
A;Residues: 1-1493 <PAU>
A;Cross-references: EMBL:U28735; NID:g860712; PIDN:AAA68266.1; CESP:F48E3.3
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:F48E3.3
A;Introns: 42/2; 72/1; 115/3; 203/3; 391/3; 421/3; 634/1; 712/3; 1017/2; 1190/2; 1438/3

Query Match 50.7%; Score 36; DB 2; Length 1493;
Best Local Similarity 66.7%; Pred. No. 8.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQFW 9
||| |
Db 1415 PQEWLW 1420

RESULT 145

G96736
hypothetical protein F3117.13 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: G96736
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: G96736
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1674 <STO>
A;Cross-references: GB:AE0051173; NID:g6714344; PIDN:AAF26036.1; GSPDB:GN00141
C;Genetics:
A;Gene: F3117.13
A;Map position: 1

Query Match 50.7%; Score 36; DB 2; Length 1674;
Best Local Similarity 66.7%; Pred. No. 9.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQFW 9
||| |
Db 1575 PQEWLW 1580

RESULT 146

T13714
kakapo gene protein - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13714; T13715
R;Gregory, S.L.; Brown, N.H.
J. Cell Biol. 143, 1271-1282, 1998
A;Title: Kakapo, a gene required for adhesion between and within cell layers in Drosophila

A;Reference number: Z17707; MUID:99054753
A;Accession: T13714
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-2396 <GRE>
A;Cross-references: EMBL:AJ011924; NID:g3758908; PIDN:CAA09869.1; PID:g3758909
A;Accession: T13715
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 'NM', 77-79, 'SL', 82, 'E', 'WAKDK', 108-109, 'SILOLD', 116-117, 'DR', 138, 'VLRIA',
A;Cross-references: EMBL:AJ011925; NID:g3758910; PIDN:CAA09870.1; PID:g3758911
C;Genetics:
A;Gene: kak
A;Cross-references: FlyBase:FBgn0013733
A;Note: kak

Query Match 50.7%; Score 36; DB 2; Length 2396;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QQWFELM 11
||| |
Db 815 QQAWALL 821

RESULT 147

S71752
giant protein p619 - human
N;Alternate names: chromosome condensation regulator RCC1 homolog p619
C;Species: Homo sapiens (man)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 21-Jul-2000
C;Accession: S71752
R;Rosa, J.L.; Casaroli-Marano, R.P.; Buckler, A.J.; Villaro, S.; Barbacid, M.
EMBO J. 15, 4262-4273, 1996
A;Title: p619, a giant protein related to the chromosome condensation regulator RCC1.
A;Reference number: S71752; MUID:97015127
A;Accession: S71752
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-4861 <ROS>
A;Cross-references: EMBL:U50078; NID:g4220427; PIDN:AAD12586.1; PID:g1477565
C;Genetics:
A;Gene: p619
C;Function:
A;Description: may play an important role in the regulation of membrane trafficking;
C;Superfamily: human giant protein p619; ubiquitin-protein ligase homology; WD repeat
C;Keywords: leucine zipper
F;1771-1805/Region: leucine zipper motif
F;3424-3457/Domain: WD repeat homology <WD1>
F;3743-3776/Domain: WD repeat homology <WD2>
F;4484-4838/Domain: ubiquitin-protein ligase homology <UBI>

Query Match 50.0%; Score 35.5; DB 2; Length 4861;
Best Local Similarity 54.5%; Pred. No. 3.3e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 2 PKP-QQWFELM 11
||| |
Db 1129 PQAQSWVLV 1139

Search completed: April 1, 2002, 16:19:21
Job time: 112 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 1, 2002, 16:20:17 ; Search time 13.22 seconds
(without alignments)
30.508 Million cell updates/sec

Title: US-09-988-792-2
Perfect score: 71
Sequence: 1 RPKPQQWFWM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 92

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 50%
Maximum Match 100%
Listing first 1000 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	67.6	11	1	TKNA_HORSE
2	48	67.6	115	1	TKN1_RABIT
3	48	67.6	129	1	TKN1_HUMAN
4	48	67.6	130	1	TKN1_BOVIN
5	48	67.6	130	1	TKN1_MESAU
6	48	67.6	130	1	TKN1_MOUSE
7	48	67.6	130	1	TKN1_RAT
8	45	63.4	11	1	TKNA_CHICK
9	44	62.0	436	1	CYB_RHOCA
10	43	60.6	902	1	VEF_GVHA
11	42	59.2	377	1	DCHS_ENTAE
12	41	57.7	55	1	ATP8_SQUAC
13	40	56.3	411	1	CIW2_MOUSE
14	40	56.3	426	1	CIW2_HUMAN
15	40	56.3	538	1	CIWA_HUMAN
16	40	56.3	538	1	CIWA_RAT
17	40	56.3	665	1	CNG_DRONE
18	39	54.9	361	1	FUT3_HUMAN
19	39	54.9	372	1	FUT3_PANTR
20	39	54.9	374	1	FUT5_HUMAN
21	39	54.9	374	1	FUT5_PANTR
22	39	54.9	440	1	CYB_PARDE
23	39	54.9	816	1	NPA2_MOUSE
24	39	54.9	824	1	NPA2_HUMAN
25	39	54.9	846	1	CLOC_HUMAN
26	39	54.9	855	1	CLOC_MOUSE
27	39	54.9	1023	1	CLOC_DRONE
28	38	53.5	323	1	MSBB_ECOLI
29	38	53.5	330	1	LSPI_MOUSE
30	38	53.5	405	1	FUT4_HUMAN
31	38	53.5	433	1	FUT4_MOUSE
32	38	53.5	433	1	FUT4_RAT
33	38	53.5	533	1	YADC_SCHPO

34	38	53.5	789	1	ARNT_HUMAN
35	38	53.5	901	1	VEF_GVPU
36	38	53.5	901	1	VEF_GVTN
37	37.5	52.8	298	1	Y812_ARCFU
38	37.5	52.8	375	1	DNBI_HSV1
39	37.5	52.8	1196	1	DNBI_HSV11
40	37.5	52.8	1196	1	DNBI_HSV1F
41	37.5	52.8	1196	1	DNBI_HSV1K
42	37.5	52.8	1196	1	DNBI_HSV2H
43	37.5	52.8	1197	1	DNBI_HSV2
44	37.5	52.8	1204	1	DNBI_VZVD
45	37.5	52.8	1209	1	DNBI_HSV2B
46	37	52.1	11	1	TKNA_ONCMY
47	37	52.1	175	1	HOBB_ECOLI
48	37	52.1	253	1	HRB3_XANCV
49	37	52.1	342	1	FUT7_HUMAN
50	37	52.1	403	1	YCGF_ECOLI
51	37	52.1	404	1	CYB_MARPO
52	37	52.1	655	1	NEC3_MOUSE
53	37	52.1	663	1	TRA_BPMU
54	37	52.1	681	1	TBR1_MOUSE
55	37	52.1	682	1	TBR1_HUMAN
56	37	52.1	747	1	AMDI_HUMAN
57	37	52.1	764	1	METE_SOLSC
58	37	52.1	956	1	NUTI_MAGGR
59	37	52.1	971	1	AREA_GIBFU
60	37	52.1	1002	1	DOR_DRONE
61	37	52.1	1239	1	DPOG_HUMAN
62	37	52.1	1629	1	ATS9_HUMAN
63	36.5	51.4	537	1	CPF6_RAT
64	36.5	51.4	564	1	NOX1_HUMAN
65	36.5	51.4	659	1	Y102_MYCLE
66	36.5	51.4	1186	1	DNBI_HSVB2
67	36	50.7	11	1	TKNA_GADMO
68	36	50.7	55	1	ATP8_DICLA
69	36	50.7	187	1	P18_LEITA
70	36	50.7	257	1	IOD1_MOUSE
71	36	50.7	318	1	MSBB_HAETN
72	36	50.7	330	1	Y355_SYNY3
73	36	50.7	359	1	WN5B_HUMAN
74	36	50.7	359	1	WN5B_MOUSE
75	36	50.7	360	1	WN5C_XENLA
76	36	50.7	365	1	FUT3_BOVIN
77	36	50.7	365	1	WN5A_HUMAN
78	36	50.7	379	1	CYB_ASTPE
79	36	50.7	379	1	WN5A_MOUSE
80	36	50.7	379	1	WN5A_RAT
81	36	50.7	380	1	CYB_BRAFL
82	36	50.7	380	1	CYB_BRALA
83	36	50.7	380	1	WN5A_XENLA
84	36	50.7	381	1	CYB_CARPL
85	36	50.7	381	1	CYB_CHOCR
86	36	50.7	381	1	CYB_PRIGL
87	36	50.7	393	1	CIW4_HUMAN
88	36	50.7	398	1	CIW4_MOUSE
89	36	50.7	473	1	CISY_SCHPO
90	36	50.7	522	1	CPF4_RAT
91	36	50.7	1238	1	DPOG_MOUSE
92	36	50.7	1507	1	Y056_HUMAN

ALIGNMENTS

RESULT	TKNA_HORSE	STANDARD	PRT	11 AA
AC	PO1290			
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DT	30-MAY-2000	(Rel. 39, Last annotation update)		
DE	SUBSTANCE P			
GN	TAC1 OR NKNA OR TAC2 OR NKA			

OS Equus caballus (Horse), and Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796, 10141;
RN SEQUENCE.
RP SPECIES=Horse;
RC Studer R.O., Trzeciak A., Lergier W.;
RA "Isolation and amino-acid sequence of substance P from horse
RT intestine";
RL Helv. Chim. Acta 56:860-866(1973).
RN [2]
RP SEQUENCE.
RX SPECIES=C.porcellus;
RC MEDLINE=90044685; PubMed=2478925;
RA Murphy R.;
RT "Primary amino acid sequence of guinea-pig substance P";
RL Neuropeptides 14:105-110(1989).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC
DR PIR; A01558; SPHO.
DR PIR; A60654; A60654.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11
FT AMIDATION.
SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.17;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFGLM 11
|||||:|:|

DB 1 RPKPQQFFGLM 11

RESULT 2
TKNL_RABBIT
ID TKNL_RABBIT STANDARD; PRT; 115 AA.
AC P41540;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
(NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE GAMMA; C-TERMINAL
DE FLANKING PEPTIDE].
DE TAC1 OR NKNA OR TAC2 OR NKA.
GN Oryctolagus cuniculus (Rabbit).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93371392; PubMed=8363593;
RA Maegert H.J., Heitland A., Rose M., Forssmann W.G.;
RT "Nucleotide sequence of the rabbit gamma-preprotachykinin I cDNA";
RL Biochem. Biophys. Res. Commun. 193:128-131(1993).
RN [2]
RP SEQUENCE OF 72-92.
RA Kage R., McGregor G.P., Thim L., Conlon J.M.;
RT "Gamma-neuropeptide K: a peptide isolated from rabbit gut that is
RT derived from gamma-preprotachykinin";
Regul. Pept. 18:346-346(1987).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,

CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X62994; CAA44728.1; -
DR PIR; S18922; S18922.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR ProDom; PD005598; Protachykinin; 1.
DR SMART; SM00203; TK; 2.
DR PROSITE; PS00267; TACHYKININ; 2.
KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
KW Amidation; Alternative splicing; Signal; Neurotransmitter.
FT SIGNAL 1 19 POTENTIAL.
FT PEPTIDE 20 56 SUBSTANCE P.
FT PEPTIDE 58 68 SUBSTANCE P.
FT PEPTIDE 72 92 NEUROPEPTIDE GAMMA.
FT PEPTIDE 83 92 NEUROKININ A.
FT PEPTIDE 96 111 C-TERMINAL FLANKING PEPTIDE.
FT MOD_RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
FT MOD_RES 92 92 AMIDATION (G-93 PROVIDE AMIDE GROUP).
SQ SEQUENCE 115 AA; 13370 MW; 5EC76F7C9B10E1C6 CRC64;

Query Match 67.6%; Score 48; DB 1; Length 115;
Best Local Similarity 81.8%; Pred. No. 1.4;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFGLM 11
|||||:|:|

DB 58 RPKPQQFFGLM 68

RESULT 3
TKNL_HUMAN
ID TKNL_HUMAN STANDARD; PRT; 129 AA.
AC P20366; Q00072; O60600; O60601;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
(NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
DE TAC1 OR NKNA OR TAC2 OR NKA.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RX MEDLINE=87030957; PubMed=3770210;
RA Harnar A.J., Armstrong A., Pascall J.C., Chapman K., Rosie F.,
RT Curtis A., Goring J., Edwards C.R.W., Fink G.;
RT "cDNA sequence of human beta-preprotachykinin, the common precursor
RT to substance P and neurokinin A";
FEBS Lett. 208:67-72(1986).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC TISSUE=Brain;
RA Tan A., Too H.P.;
Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.

[3]
RP SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
RC TISSUE-Testis;
RX MEDLINE=91209287; PubMed=1708336;
RA Chiwakata C., Brackmann B., Hunt N., Davidoff M., Schulze W.,
RA Iveli R.;
RT "Tachykinin (substance-P) gene expression in Leydig cells of the
RT human and mouse testis.";
RL Endocrinology 128:2441-2448(1991).
RN [4];
RP SEQUENCE OF 98-107.
RX MEDLINE=87275962; PubMed=3038549;
RA Theodorsson-Norheim E., Joernvall H., Andersson M., Norheim I.,
RA Oeberg K., Jacobsson G.;
RT "Isolation and characterization of neurokinin A, neurokinin A(3-10)
RT and neurokinin A(4-10) from a neutral water extract of a metastatic
RT ileal carcinoid tumour.";
RL Eur. J. Biochem. 166:693-697(1987).
RN [5];
RP SEQUENCE OF 36-118 FROM N.A. (ISOFORM ALPHA).
RC TISSUE-Blood, and Brain;
RA Lai J.P., Douglas S.D., Rappaport E., Wu J.M., Ho W.Z.;
RT "Identification of a delta isoform of preprotachykinin mRNA in human
RT mononuclear phagocytes and lymphocytes.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [6];
RP SEQUENCE OF 111-126.
RC TISSUE-Adrenal medulla;
RX MEDLINE=91133994; PubMed=2284201;
RA McGregor G.P., Conlon J.M.;
RT "Characterization of the C-terminal flanking peptide of human
RT beta-preprotachykinin.";
RL Peptides 11:907-910(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
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CC -----
DR EMBL; X54469; CAA38351.1; -;
DR EMBL; U37529; AAA79195.1; -;
DR EMBL; M68906; AAA60159.1; -;
DR EMBL; M68907; AAA60160.1; -;
DR EMBL; AF050636; AAC15702.1; -;
DR EMBL; AF050638; AAC15704.1; -;
DR PIR; A24805; A24805.
DR PIR; S00069; S00069.
DR MIM; 162320; -;
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR ProDom; PD005598; Protachykinin; 1.
DR SMART; SM00203; TK; 2.
DR PROSITE; PS00267; TACHYKININ; 2.
KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
KW Amidation; Alternative splicing; Signal; Neurotransmitter.
FT SIGNAL 1 19
FT PEPTIDE 20 56
FT PEPTIDE 58 68
FT PEPTIDE 72 107
FT PEPTIDE 72 73
FT PEPTIDE 89 107
FT PEPTIDE 98 107
FT NEUROPEPTIDE K.
FT NEUROPEPTIDE GAMMA 1ST PART.
FT NEUROPEPTIDE GAMMA 2ND PART.
FT NEUROKININ A.

FT PEPTIDE 111 126
FT MOD_RES 68
FT MOD_RES 107 107
FT VARSPLIC 74 88
FT VARSPLIC 97 114
FT VARSPLIC 115 115
FT CONFLICT 87 87
SQ SEQUENCE 129 AA; 15003 MW; 51412C1692368DE4 CRC64;
L -> P (IN REF. 4).
Query Match 67.6%; Score 48; DB 1; Length 129;
Best Local Similarity 81.8%; Pred No. 1.6;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKQQQFWLM 11
DB 58 RPKQQQFFGLM 68
IIIIII:II
RESULT 4
TKNL_BOVIN
ID ID TKNL_BOVIN STANDARD; PRT; 130 AA.
AC P01289; P01291; P04091; P20773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
GN TACI OR NKNA OR TAC2 OR NKA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RX MEDLINE=85086245; PubMed=6083453;
RA Nawa H., Kotani H., Nakanishi S.;
RT "Tissue-specific generation of two preprotachykinin mRNAs from one
RT gene by alternative RNA splicing.";
RL Nature 312:729-734(1984).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RX MEDLINE=84039802; PubMed=6195531;
RA Nawa H., Hirose T., Takashima H., Inayama S., Nakanishi S.;
RT "Nucleotide sequences of cloned cDNAs for two types of bovine brain
RT substance P precursor.";
RL Nature 306:32-36(1983).
RN [3]
RP SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
RC TISSUE-Hypothalamus;
RX MEDLINE=91209287; PubMed=1708336;
RA Chiwakata C., Brackmann B., Hunt N., Davidoff M., Schulze W.,
RA Iveli R.;
RT "Tachykinin (substance-P) gene expression in Leydig cells of the
RT human and mouse testis.";
RL Endocrinology 128:2441-2448(1991).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
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CC EMBL; X00075; CAA24939.1; -;
 CC EMBL; X00075; CAA24940.1; -;
 CC EMBL; X00075; CAA24941.1; -;
 CC EMBL; X00076; CAA24942.1; -;
 CC EMBL; X00076; CAA24943.1; ALT_SEQ.
 CC EMBL; X02351; CAA26206.1; -;
 CC EMBL; X01396; CAA26206.1; JOINED.
 CC EMBL; X01397; CAA26206.1; JOINED.
 CC EMBL; X01398; CAA26206.1; JOINED.
 CC EMBL; X01399; CAA26206.1; JOINED.
 CC EMBL; X01400; CAA26206.1; JOINED.
 CC EMBL; M68911; AAA30724.1; -;
 CC EMBL; M68912; AAA30725.1; -;
 CC PIR; A01557; SPBOA.
 CC PIR; A05093; SPBOB.
 CC PIR; A05093; SPBOB.
 CC PIR; B25067; B25067.
 CC InterPro; IPR003580; Protachykinin.
 CC InterPro; IPR002040; Tachykinin.
 CC Pfam; PF02202; Tachykinin; 1.
 CC ProDom; PD005598; Protachykinin; 1.
 CC SMART; SM00203; TK; 2.
 CC PROSITE; PS00267; TACHYKININ; 2.
 CC Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 CC Amidation; Alternative splicing; Signal; Neurotransmitter.
 CC SIGNAL 1 19 POTENTIAL.
 CC PROPEP 20 56 SUBSTANCE P.
 CC PEPTIDE 58 68 NEUROPEPTIDE K.
 CC PEPTIDE 72 107 NEUROPEPTIDE GAMMA 1ST PART.
 CC PEPTIDE 72 73 NEUROPEPTIDE GAMMA 2ND PART.
 CC PEPTIDE 89 107 NEUROKININ A.
 CC PEPTIDE 98 107 NEUROKININ A.
 CC PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
 CC PEPTIDE 111 126 AMIDATION (G-69 PROVIDE AMIDE GROUP).
 CC MOD_RES 68 68 AMIDATION (G-108 PROVIDE AMIDE GROUP).
 CC MOD_RES 107 107 MISSING (IN ISOFORM GAMMA AND ISOFORM DELTA).
 CC VARSPLIC 74 88 MISSING (IN ISOFORM ALPHA AND ISOFORM DELTA).
 CC VARSPLIC 97 114 MISSING (IN ISOFORM ALPHA AND ISOFORM DELTA).
 CC VARSPLIC 115 115 V -> M (IN ISOFORM ALPHA AND ISOFORM DELTA).
 CC CONFLICT 121 121 V -> A (IN REF. 3).
 CC SEQUENCE 130 AA; 15076 MW; CE2A28572305DEB7 CRC64;

Query Match 67.6%; Score 48; DB 1; Length 130;
 Best Local Similarity 81.8%; Pred. No. 1.6;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
 Db 58 RPKPQQWFGLM 68
 |||||:|

RESULT 5

TKNL_MESAU
 ID TKNL_MESAU STANDARD; PRT; 130 AA.
 AC Q60541; P49110;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTACHYKININ 1 PRECURSOR (PTP) [CONTAINS: SUBSTANCE P; NEUROKININ A
 DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
 DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.

OX NCBI_TaxID=10036;
 RN [1]
 RC SEQUENCE FROM N.A. (ISOFORMS BETA AND GAMMA).
 RA STRAIN=AURA; TISSUE=Brain;
 RA Heitland A., Kruhofer M., Juergen Maegert H.J., Forssmann W.G.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
 CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
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 CC or send an email to license@isb-sib.ch).

CC EMBL; X80662; CAA56691.1; -;
 CC EMBL; X80663; CAA56692.1; -;
 CC InterPro; IPR003580; Protachykinin.
 CC InterPro; IPR002040; Tachykinin.
 CC Pfam; PF02202; Tachykinin; 1.
 CC ProDom; PD005598; Protachykinin; 1.
 CC SMART; SM00203; TK; 2.
 CC PROSITE; PS00267; TACHYKININ; 2.
 CC Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 CC Amidation; Alternative splicing; Signal; Neurotransmitter.
 CC SIGNAL 1 19 POTENTIAL.
 CC PROPEP 20 56 SUBSTANCE P.
 CC PEPTIDE 58 68 NEUROPEPTIDE K.
 CC PEPTIDE 72 107 NEUROPEPTIDE GAMMA 1ST PART.
 CC PEPTIDE 72 73 NEUROPEPTIDE GAMMA 2ND PART.
 CC PEPTIDE 89 107 NEUROKININ A.
 CC PEPTIDE 98 107 NEUROKININ A.
 CC PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
 CC PEPTIDE 111 126 AMIDATION (G-69 PROVIDE AMIDE GROUP).
 CC MOD_RES 68 68 AMIDATION (G-108 PROVIDE AMIDE GROUP).
 CC MOD_RES 107 107 MISSING (IN ISOFORM GAMMA).
 CC VARSPLIC 74 88 MISSING (IN ISOFORM GAMMA).
 CC SEQUENCE 130 AA; 14907 MW; CC92E9371A646F2E CRC64;

Query Match 67.6%; Score 48; DB 1; Length 130;
 Best Local Similarity 81.8%; Pred. No. 1.6;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
 Db 58 RPKPQQWFGLM 68
 |||||:|

RESULT 6

TKNL_MOUSE
 ID TKNL_MOUSE STANDARD; PRT; 130 AA.
 AC P41539; Q00073;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTACHYKININ 1 PRECURSOR (PTP) [CONTAINS: SUBSTANCE P; NEUROKININ A
 DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
 DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A. (ISOFORM BETA).
 RC STRAIN=ICR; TISSUE=Brain;

RA KAKO K., MUNEKATA E., HOSAKA M., MURAKAMI K., NAKAYAMA K.;
RT "Cloning and sequence analysis of mouse cDNAs encoding
RT preprotachykinin A and B";
RL Biomed. Res. 14:253-259(1993).
RN [2]
RP SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
RC TISSUE=Brain;
RX MEDLINE=91209287; PubMed=1708336;
RA Chikakata C., Brackmann B., Hunt N., Davidoff M., Schulze W.,
RA Iwells R.;
RT "Tachykinin (substance-P) gene expression in Leydig cells of the
RT human and mouse testis";
RL Endocrinology 128:2441-2448(1991).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
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CC -----
DR EMBL; D17584; BAA04508.1; -;
DR EMBL; M68908; AAA39969.1; -;
DR EMBL; M68909; AAA39970.1; -;
DR MGD; MGI:98474; Tactl.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR ProDom; PD005598; Protachykinin; 1.
DR SMART; SM00203; TK; 2.
DR PROSITE; PS00267; TACHYKININ; 2.
KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
KW Amidation; Alternative splicing; Signal; Neurotransmitter.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 56 SUBSTANCE P.
FT PEPTIDE 58 68 NEUROPEPTIDE K.
FT PEPTIDE 72 107 NEUROPEPTIDE GAMMA 1ST PART.
FT PEPTIDE 72 73 NEUROPEPTIDE GAMMA 2ND PART.
FT PEPTIDE 89 107 NEUROKININ A.
FT PEPTIDE 98 107 NEUROKININ A.
FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
FT MOD_RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
FT MOD_RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
FT VARSPIC 74 88 MISSING (IN ISOFORM GAMMA).
SQ SEQUENCE 130 AA; 15045 MW; 7BE8DA15FDE72FF8 CRC64;

Query Match 67.6%; Score 48; DB 1; Length 130;
Best Local Similarity 81.8%; Pred. No. 1.6;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQFWLM 11
|||||:|:|
Db 58 RPKPQQFFGLM 68

RESULT 7
TKN1_RAT STANDARD; PRT; 130 AA.
AC P06767; P08856; P22356;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE

DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
GN TAC1 OR NKNA OR TAC2 OR NKA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).
RX MEDLINE=90331040; PubMed=1695945;
RA Carter M.S., Krause J.E.;
RT "Structure, expression, and some regulatory mechanisms of the rat
RT preprotachykinin gene encoding substance P, neurokinin A,
RT neuropeptide K, and neuropeptide gamma";
RL J. Neurosci. 10:2203-2214(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).
RX MEDLINE=87118268; PubMed=2433692;
RA Krause J.E., Chirgwin J.M., Carter M.S., Xu Z.S., Hershey A.D.;
RT "Three rat preprotachykinin mRNAs encode the neuropeptides substance
RT P and neurokinin A";
RL Proc. Natl. Acad. Sci. U.S.A. 84:881-885(1987).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
RX MEDLINE=87025808; PubMed=2429656;
RA Kawaguchi Y., Hoshimaru M., Nawa H., Nakanishi S.;
RT "Sequence analysis of cloned cDNA for rat substance P precursor:
RT existence of a third substance P precursor";
RL Biochem. Biophys. Res. Commun. 139:1040-1046(1986).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RC TISSUE=Dorsal root ganglion;
RX MEDLINE=91085565; PubMed=1702066;
RA Harmar A.J., Hyde V., Chapman K.E.;
RT "Identification and cDNA sequence of delta-preprotachykinin, a fourth
RT splicing variant of the rat substance P precursor";
RL FEBS Lett. 275:22-24(1990).
RN [5]
RP SEQUENCE OF 1-41 FROM N.A.
RX MEDLINE=93192337; PubMed=8448217;
RA Chapman K.E., Lyons V., Harmar A.J.;
RT "The sequence of 5' flanking DNA from the rat preprotachykinin gene;
RT analysis of putative transcription factor binding sites";
RL Biochim. Biophys. Acta 1172:361-363(1993).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M34162; AAA41926.1; -;
DR EMBL; M34159; AAA41926.1; JOINED.
DR EMBL; M34160; AAA41926.1; JOINED.
DR EMBL; M34161; AAA41926.1; JOINED.
DR EMBL; M34184; AAA41925.1; -;
DR EMBL; M34183; AAA41929.1; -;
DR EMBL; M15191; AAA41928.1; -;
DR EMBL; M14312; AAA41927.1; -;
DR EMBL; L07328; AAA41924.1; -;
DR EMBL; X56306; CAA39752.1; -;
DR PIR; A26590; A26590.
DR PIR; B26590; B26590.
DR PIR; C26590; C26590.
DR PIR; A37163; A37163.

DR PIR; S12958; S12958.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR ProDom; PD005598; Protachykinin; 1.
DR SMART; SM00203; TK; 2.
DR PROSITE; PS00267; TACHYKININ; 2.
KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
KW Amidation; Alternative splicing; Signal; Neurotransmitter.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 56 POTENTIAL.
FT PEPTIDE 58 68 SUBSTANCE P.
FT PEPTIDE 72 107 NEUROPEPTIDE K.
FT PEPTIDE 72 73 NEUROPEPTIDE GAMMA 1ST PART.
FT PEPTIDE 89 107 NEUROPEPTIDE GAMMA 2ND PART.
FT PEPTIDE 98 107 NEUROKININ A.
FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
FT MOD_RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
FT MOD_RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
FT VARSPPLIC 74 88 MISSING (IN ISOFORM GAMMA AND ISOFORM DELTA).
FT VARSPPLIC 97 114 MISSING (IN ISOFORM ALPHA AND ISOFORM DELTA).
FT VARSPPLIC 115 115 V -> M (IN ISOFORM ALPHA AND ISOFORM DELTA).
FT SEQUENCE 130 AA; 15001 MW; B2EF8680DCCD75A CRC64;

Query Match 67.6%; Score 48; DB 1; Length 130;
Best Local Similarity 81.8%; Pred. No. 1.6;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|:|

DB 58 RRPQQFFGLM 68

RESULT 8
TKNA_CHICK STANDARD; PRT; 11 AA.
AC FL9850;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine; PubMed=2452461;
RX MEDLINE=88204263; PubMed=2452461;
RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT "[Arg3]substance P and neurokinin A from chicken small intestine.";
RL Regul. Pept. 20:171-180(1988).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; JN0023; JN0023.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION.
FT SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 63.4%; Score 45; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.44;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
||:||||:|:|

DB 1 RRPQQFFGLM 11

RESULT 9
CYB_RHOCA STANDARD; PRT; 436 AA.
ID CYB_RHOCA
AC P08502; P07057;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOCHROME B.
DE PETB OR CYTB.
GN Rhodobacter capsulatus (Rhodopseudomonas capsulata).
OS Rhodobacter; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SB1003;
RX MEDLINE=88011223; PubMed=2821268;
RA Davidson E., Daldal F.;
RT "Primary structure of the bcl complex of Rhodopseudomonas capsulata.
RT Nucleotide sequence of the pet operon encoding the Rieske cytochrome
RT b, and cytochrome c1 apoproteins.";
RL J. Mol. Biol. 195:13-24(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GA;
RX MEDLINE=86136096; PubMed=3004982;
RA Gabellini N., Seibald W.;
RT "Nucleotide sequence and transcription of the fbc operon from
RT Rhodopseudomonas sphaeroides. Evaluation of the deduced amino acid
RT sequences of the Fes protein, cytochrome b and cytochrome c1.";
RL Eur. J. Biochem. 154:569-579(1986).
RN [3]
RP CORRECTION OF ORGANISM GIVEN IN REF. 2.
RX MEDLINE=88011233; PubMed=2821272;
RA Davidson E., Daldal F.;
RT "fbc operon, encoding the Rieske Fe-S protein cytochrome b, and
RT cytochrome c1 apoproteins previously described from Rhodopseudomonas
RT sphaeroides, is from Rhodopseudomonas capsulata.";
RL J. Mol. Biol. 195:25-29(1987).
RN [4]
RP MUTATIONS CONFERRING RESISTANCE TO QUINOL OXIDATION INHIBITORS.
RX MEDLINE=90076115; PubMed=2556259;
RA Daldal F., Tokito M.K., Davidson E., Faham M.;
RT "Mutations conferring resistance to quinol oxidation (Qz) inhibitors
RT of the cyt bcl complex of Rhodobacter capsulatus.";
RL EMBO J. 8:3951-3961(1989).
RN [5]
RP MUTAGENESIS.
RC STRAIN=MT1131;
RX MEDLINE=91105061; PubMed=2176897;
RA Robertson D.E., Daldal F., Dutton P.L.;
RT "Mutants of ubiquinol-cytochrome c2 oxidoreductase resistant to Qo
RT site inhibitors: consequences for ubiquinone and ubiquinol affinity
RT and catalysis";
RL Biochemistry 29:11249-11260(1990).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS.
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN.
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

RESULT 1
AAP61480
ID AAP61480 standard; peptide; 11 AA.
XX
AC AAP61480;
XX
DT 22-AUG-1991 (first entry)
XX
DE Sequence of undeca peptide substance P1.
XX
KW Hypertension therapy; sleep disorder; anti-stress agent.
XX
FH Key Location/Qualifiers
FT Misc-difference 11
FT /label= Met-NH2
XX
PN DD229593-A.
XX
PD 13-NOV-1985.
XX
PF 28-NOV-1984; 84DD-0269954.
XX
PR 28-NOV-1984; 84DD-0269954.
XX
PA (DEAK) AKAD WISSENSCHAFT DDR.
XX
PI Oehme P, Hecht K, Wachtel E, Roske I, Kolometsewa IA;
PI Airpetjan M, Blenert M, Vogt WE, Hilse H, Gores E, Poppei M;
PI Nieber K, Bergmann J;
XX
DR WPI; 1986-069587/11.
XX
PT Cpd. having N-terminal sequences of undeca-peptide substance P -
PT are medicinal agents with anti-stress activity
XX
PS Claim 1; Page 1; 15pp; German.
XX
CC The inventors claim an antistress compound which contains the N-
CC terminal SQ of AAP61480, pref. Arg-Pro-Lys-Pro-X (X= COOH or NH2).
CC Compared with the full undecapeptide they have much reduced
CC side effects (acute hypotension, spastic effects on the ileum and
CC histamine release from peritoneal mast cells).
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 61; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. NO. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPKPQQFFGLM 11
DB 1 rpkpqgffgllm 11
RESULT 2
AAP80312
ID AAP80312 standard; protein; 11 AA.
XX
AC AAP80312;
XX
DT 14-SEP-1990 (first entry)
XX
DE Sequence of neuropeptide substance P which binds with polypeptide
DE receptor for bombesin type polypeptides.
XX
KW Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
XX substance P.
XX Swiss 3T3 cells.
OS
XX
FH Key Location/Qualifiers
FT
FT /note= "N-terminally glycosylated by 5-acetamido-
FT 2,4,7,8,9-penta-O-acetyl-3,5-deoxy-beta-
FT D-glycero-D-galactononulopyranosyl"
XX

FT Misc-difference 11
FT /label=OTHER
FT /note="Met-NH2"
XX
PN WO8807551-A.
XX
PD 06-OCT-1988.
XX
PF 31-MAR-1988; 88WO-GB00255.
XX
PR 25-NOV-1987; 87GB-0027638.
XX
PA (IMCR) IMPERIAL CANCER RES.
XX
PI Rosengurt E, Zachary I, Woll P;
XX
PN WPI; 1988-292842/41.
XX
PT New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation
XX
PS Disclosure; Table 2; 42pp; English.
XX
CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 61; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. NO. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPKPQQFFGLM 11
DB 1 rpkpqgffgllm 11
RESULT 3
AAR13162
ID AAR13162 standard; Protein; 11 AA.
XX
AC AAR13162;
XX
DT 10-OCT-1991 (first entry)
XX
DE Sialic acid-bonded polypeptide (2).
XX
KW Sialic acid; cataract; immune disorder.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminally glycosylated by 5-acetamido-
FT 2,4,7,8,9-penta-O-acetyl-3,5-deoxy-beta-
FT D-glycero-D-galactononulopyranosyl"
XX

PN JP03151398-A.
XX 27-JUN-1991.
XX
PF 06-NOV-1989; 89JP-0288560.
XX
PR 06-NOV-1989; 89JP-0288560.
XX
PA (MECT-) MECT KK.
XX
DR WPI; 1991-233839/32.
XX
XX New sialic acid derivs. bonded to physiologically active
XX polypeptide - for treatment of cataracts, immune disorders etc.
PT
PT with prolonged half-life
XX
PS Example 4; Page 6; 7pp; Japanese.
XX
XX The prod. has prolonged half-life and is used as a pharmaceutical
CC for treatment of various diseases, such as cataract and immune
CC disorders. It comprises a peptide, N-terminally glycosylated by
CC (opt. acetylated) sialic acid.
CC See also AAR12932, AAR13162 and AAR13201.
XX
XX Sequence 11 AA;
SQ

Query Match 100.0%; Score 61; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
| | | | | | | | | |
Db 1 rpkgqgffglm 11

RESULT 4
AAR11854
ID AAR11854 standard; peptide; 11 AA.
XX
AC AAR11854;
XX
DT 09-JUL-1991 (first entry)
XX
DE Undecapeptide substance P.
XX
KW Undecapeptide; pharmaceutical; stress; sleep.
XX
OS Synthetic.
XX
PN DD285097-A.
XX
PD 05-DEC-1990.
XX
PF 21-JUN-1989; 89DD-0329831.
XX
PR 21-JUN-1989; 89DD-0329831.
XX
PA (DEAK) INST WIRKSTOFF AKAD.
XX
FA (FARF) VEB CHEM BITTERFELD.
XX
PI Beyermann M, Bienert M, Egler H, Haupke K, Krause E;
XX Schwarz J, Walz H;
XX WPI; 1991-133498/19.
DR
XX Undeca-peptide substance pharmaceutical intermediate prepn. - by
PT forming di-peptide between nitro-arginine and proline and
PT reacting with polymer-bound non-peptide
XX
XX Calim 1; Page 1; 8pp; German.
XX
XX The peptide is prepared by solid phase synthesis.

CC It can be used in the preparation of pharmaceuticals which can be
CC used to treat certain stress-induced disturbances of the sleep
CC profile.
XX
SQ Sequence 11 AA;
XX

Query Match 100.0%; Score 61; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
| | | | | | | | | |
Db 1 rpkgqgffglm 11

RESULT 5
AAR21938
ID AAR21938 standard; Protein; 11 AA.
XX
AC AAR21938;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P [Me-Leu 10].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Modified-site 10
FT /label= OTHER
FT /note= "OTHER - Me-Leu"
XX
XX WO9202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991; 91WO-US05323.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 10; Page 21; 35pp; English.
XX
XX The peptide is the tachykinin agonist substance P with Me-Leu
XX substituted at position 10. The peptide was synthesised
XX by standard solid phase synthesis. Neuronal accumulation of
XX beta-amyloid may be treated by administration of tachykinin
XX agonists. The peptides can reduce the neurotoxic effects of a
XX beta-amyloid related polypeptide on cultured neurons. The peptide
XX and its analogues are useful for controlling diseases characterised
XX by beta amyloid accumulation in the brain such as Alzheimer's
XX disease and Down's syndrome.
XX See also AAR21932-75.
XX
XX Sequence 11 AA;
SQ

Query Match 100.0%; Score 61; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
|||||
Db 1 rpkpqffglm 11

RESULT 6
AAR21942
ID AAR21942 standard; Protein; 11 AA.
XX AAR21942;
AC AAR21942;
XX 25-JUN-1992 (first entry)
DT 25-JUN-1992 (first entry)
XX Substance P [MeMet 11].
DE Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX Synthetic.
OS
FH Key Location/Qualifiers
FT Misc-difference 11
FT /label= OTHER
FT /note= "OTHER = Methyl Methionine"
XX
XX W09202248-A.
PN 20-FEB-1992.
PD 29-JUL-1991; 91WO-US05323.
XX 27-JUL-1990; 90US-0559173.
XX (CHIL-) CHILDRENS MED CENT.
XX Yankner BA;
PI WPI; 1992-079804/10.
DR
XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX Claim 10; Page 21; 35pp; English.
XX The peptide is the tachykinin agonist substance P with a methyl
CC methionine residue substituted at position 11. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
|||||
Db 1 rpkpqffglm 11

RESULT 7
AAR21946
ID AAR21946 standard; Protein; 11 AA.
XX

AC AAR21946;
XX 25-JUN-1992 (first entry)
DT 25-JUN-1992 (first entry)
XX Substance P [Me-Phe 8].
DE Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX Synthetic.
OS
FH Key Location/Qualifiers
FT Misc-difference 8
FT /label= OTHER
FT /note= "OTHER = Methyl phenylalanine"
XX
XX W09202248-A.
PN 20-FEB-1992.
PD 29-JUL-1991; 91WO-US05323.
XX 27-JUL-1990; 90US-0559173.
XX (CHIL-) CHILDRENS MED CENT.
XX Yankner BA;
PI WPI; 1992-079804/10.
DR
XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX Claim 10; Page 21; 35pp; English.
XX The peptide is the tachykinin agonist substance P with a methyl
CC phenylalanine residue substituted at position 8. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
|||||
Db 1 rpkpqffglm 11

RESULT 8
AAR21954
ID AAR21954 standard; Protein; 11 AA.
XX AAR21954;
AC AAR21954;
XX 25-JUN-1992 (first entry)
DT 25-JUN-1992 (first entry)
XX Substance P [Me-Gly 9].
DE Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX Synthetic.

```
XX Key Location/Qualifiers
FH Misc-difference 9
FT /label= OTHER
FT /note= "OTHER = Methyl glycine"
XX
XX WO9202248-A.
XX
XX PD 20-FEB-1992.
XX
XX PF 29-JUL-1991; 91WO-US05323.
XX
XX PR 27-JUL-1990; 90US-0559173.
XX
XX PA (CHIL-) CHILDRENS MED CENT.
XX
XX PI Yankner BA;
XX
XX DR WPI; 1992-079804/10.
XX
XX PT Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX PS Claim 10; Page 22; 35pp; English.
XX
XX CC The peptide is the tachykinin agonist substance P with a methyl
XX glycine residue substituted at position 9. The peptide was
XX synthesised by standard solid phase synthesis. Neuronal
XX accumulation of beta-amyloid may be treated by administration of
XX tachykinin agonists. The peptide can reduce the neurotoxic effects
XX of a beta-amyloid related polypeptide on cultured neurons. The
XX peptide and its analogues are useful for controlling diseases
XX characterised by beta amyloid accumulation in the brain such as
XX Alzheimer's disease and Down's syndrome.
XX See also AAR21932-75.
XX
XX SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. NO. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
Db 1 rpqpqffglm 11

RESULT 9
AAR21962
ID AAR21962 standard; Peptide; 11 AA.
XX
XX AC AAR21962;
XX
XX DT 25-JUN-1992 (first entry)
XX
XX DE Substance P [Met Gly 6, Met (O2) 11].
XX
XX KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
FT Misc-difference 6
FT /label= OTHER
FT /note= "OTHER = Methyl glycine"
XX
XX FT Misc-difference 11
XX
XX FT /label= OTHER
XX /note= "OTHER = Met (O2)"
XX
XX PN WO9202248-A.
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XX
XX PD 20-FEB-1992.
XX
XX PF 29-JUL-1991; 91WO-US05323.
XX
XX PR 27-JUL-1990; 90US-0559173.
XX
XX PA (CHIL-) CHILDRENS MED CENT.
XX
XX PI Yankner BA;
XX
XX DR WPI; 1992-079804/10.
XX
XX PT Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX PS Claim 10; Page 22; 35pp; English.
XX
XX CC The peptide is the tachykinin agonist, substance P with methyl
XX glycine substituted at position 9 and Met (O2) at position 11.
XX The peptide was synthesised by standard solid phase synthesis.
XX Neuronal accumulation of beta-amyloid may be treated by administ-
XX ration of tachykinin agonists. The peptide can reduce the neuro-
XX toxic effects of a beta-amyloid related polypeptide on cultured
XX neurons. The peptide and its analogues are useful for controlling
XX diseases characterised by beta amyloid accumulation in the brain
XX such as Alzheimer's disease and Down's syndrome.
XX See also AAR21932-75.
XX
XX SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. NO. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
Db 1 rpqpqffglm 11

RESULT 10
AAR21963
ID AAR21963 standard; Peptide; 11 AA.
XX
XX AC AAR21963;
XX
XX DT 25-JUN-1992 (first entry)
XX
XX DE Substance P [p-Chloro-Phe 7,8].
XX
XX KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
FT Modified-site 7
FT /label= OTHER
FT /note= "OTHER = p-Chloro-phenylalanine"
XX
XX FT Modified-site 8
XX /label= OTHER
XX /note= "OTHER = p-Chloro-phenylalanine"
XX
XX PN WO9202248-A.
XX
XX PD 20-FEB-1992.
XX
XX PF 29-JUL-1991; 91WO-US05323.
XX
XX PR 27-JUL-1990; 90US-0559173.
XX
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PA (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using

PT tachykinin agonists e.g. substance P, physalaemin and neurokinin

PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX Claim 10; Page 22; 35pp; English.

XX The peptide is the tachykinin agonist, substance P fragment

CC with p-Chloro-phenylalanine residues substituted at positions 7 and

CC 8. The peptide was synthesised by standard solid phase synthesis.

CC Neuronal accumulation of beta-amyloid may be treated by administ-

CC ration of tachykinin agonists. The peptide can reduce the neuro-

CC toxic effects of a beta-amyloid related polypeptide on cultured

CC neurons. The peptide and its analogues are useful for controlling

CC diseases characterised by beta amyloid accumulation in the brain

CC such as Alzheimer's disease and Down's syndrome.

XX See also AAR21932-75.

XX Sequence 11 AA;

Query Match

Best Local Similarity 100.0%; Score 61; DB 13; Length 11;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11

DB 1 rpkpqffglm 11

RESULT 11

AAR28442

ID AAR28442 standard; peptide; 11 AA.

XX AAR28442;

XX 22-MAR-1993 (first entry)

XX Substance P.

XX NK1 receptor; tumour; malignant glioma; pheochromocytoma;

KW paraganglia; small cell lung cancer; nerve regeneration; lymphoma;

KW granuloma; Crohn's disease.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 11

FT /note= "amidated"

XX W09218536-A.

XX 29-OCT-1992.

XX 22-APR-1992; 92WO-US03307.

XX 22-APR-1991; 91EP-0200955.

XX (MLCW) MALLINCKRODT MEDICAL INC.

XX Bakker WH, Hagen PM, Krenning EP, Lamberts SWJ, Visser TJ;

XX WPI; 1992-382047/46.

XX Detection and localisation of tissues with neurokinine-1 receptors

PT - for detecting and treating tumours having neurokinine-1

PT receptors e.g. malignant glioma, small cell lung cancer etc.

PS Disclosure; Page 4; 22pp; English.

XX Substance P or its Tyr0 deriv. is a preferred peptide having a

CC selective affinity to neurokinine-1 receptors which (when

CC labelled with a radioactive isotope) can be used in imaging methods.

CC A generic formula for preferred peptides is AAR28441. Such peptides

CC are thus useful in diagnosis and treatment of conditions that are

CC related to NK1 receptors and in visualising NK1 receptors on certain

CC tissues. See also AAR28443-R28446.

XX Sequence 11 AA;

Query Match

Best Local Similarity 100.0%; Score 61; DB 13; Length 11;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11

DB 1 rpkpqffglm 11

RESULT 12

AAR42646

ID AAR42646 standard; peptide; 11 AA.

XX AAR42646;

XX 19-APR-1994 (first entry)

XX Neurokinin 1 receptor affinity-contg. peptide (Substance P).

KW Neurokinin 1; somatostatin; receptor; cytokine; growth factor;

KW hormone; intra-operativ; tumour; low energy gamma photon;

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 11

FT /note= "the C-terminal is amidated"

XX W09318797-A.

XX 30-SEP-1993.

XX 24-MAR-1993; 93WO-US02772.

XX 25-MAR-1992; 92EP-0200848.

XX (MLCW) MALLINCKRODT MEDICAL INC.

XX Doedens BJ, Ensing GJ, Panek KJ;

XX WPI; 1993-320461/40.

XX Intra-operatively detecting and locating tumour tissues - using

PT specific peptide(s) labelled with low energy gamma photon

PT emitting radionuclide

XX Disclosure; Page 4; 31pp; English.

XX The method of intraoperatively detecting and locating tumoral

CC tissues makes use of peptides having selective neurokinin 1

CC receptor affinity (AAR42644; generic formula; AAR42646-R42650;

CC specific examples), peptides having selective somatostatin

CC receptor affinity (AAR42645; generic formula; AAR42651-R42660;

CC specific examples), and peptides selected from cytokines,

CC growth factors and hormones.

XX Sequence 11 AA;

Query Match 100.0%; Score 61; DB 14; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00029;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
 | | | | | | | | | |
 Db 1 rpkpqffglm 11

RESULT 13
 AAR85243
 ID AAR85243 standard; peptide; 11 AA.
 XX
 AC AAR85243;
 DT 18-AUG-1997 (first entry)
 DE Substance P peptide.
 XX
 KW Ligand; antibody; receptor; SELEX; random library; amplification; PCR;
 KW Systematic Evolution of Ligands by Exponential enrichment; primer;
 KW polymerase chain reaction; structure; mimicry; substance P; tachykinin;
 KW neuropeptide; rheumatoid arthritis; atherosclerosis; cancer;
 KW diabetic retinopathy.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 11 /note= "contains C-terminal NH2 group"
 XX
 PN W09530775-A1.
 XX
 PD 16-NOV-1995.
 XX
 PF 03-MAY-1995; 95WO-US05600.
 XX
 PR 21-DEC-1994; 94US-0361795.
 PR 06-MAY-1994; 94US-0238863.
 PR 24-MAY-1994; 94US-0248632.
 PR 09-SEP-1994; 94US-0303362.
 PR 11-JUN-1990; 90US-0536428.
 PR 10-JUN-1991; 91US-0714131.
 PR 21-OCT-1992; 92US-0964624.
 XX
 PA (UYRE-) UNIV RES CORP.
 XX
 PI Allen P, Doudna JA, Feigon J, Gold L, Nieuwlandt D;
 PI Schneider DJ, Sullenger BA, Wecker M;
 XX
 DR WPI; 1995-404132/51.
 XX
 PT Systematic evolution of ligands by exponential enrichment - for
 PT identifying nucleic acid ligands used in the treatment of, e.g. type
 PT B insulin resistance and HIV
 XX
 PS Example 10; Fig 8; 209pp; English.
 XX
 CC The invention relates to a novel method of isolating ligands that bind
 CC to target proteins e.g. antibodies or receptors, which bind other
 CC proteins or ligands. The method, designated Systematic Evolution of
 CC Ligands by Exponential enrichment (SELEX), comprises generating a library
 CC of random oligonucleotide sequences, about 40-60 nucleotides in length,
 CC and binding these sequences to the target proteins. After removal of
 CC unbound material, the remaining bound nucleotide sequences are amplified
 CC e.g. by PCR, and the newly amplified material is bound again with the
 CC target protein. This cycle continues until a sufficiently pure
 CC oligonucleotide sequence is isolated. The method allows the isolation of
 CC oligonucleotide sequences which structurally mimic the target protein's
 CC ligand. Ligands AAR06098-130 are examples of nucleic acid ligands which
 CC bind the tachykinin-family neuropeptide Substance P (this sequence). The
 CC new ligands were split into 2 groups based on their affinities for
 CC Substance P. Class 1 ligands had binding affinities up to 2 micromolar

CC whereas class 2 ligands bound at above 2 micromolar. This sequence
 CC represents the consensus of the class 1 ligands. The ligands can be
 CC used to block the activity of Substance P and is useful in the treatment
 CC of e.g. rheumatoid arthritis, atherosclerosis, diabetic retinopathy or
 CC cancer.
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 16; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00029;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
 | | | | | | | | | |
 Db 1 rpkpqffglm 11

RESULT 14
 AAR77310
 ID AAR77310 standard; peptide; 11 AA.
 XX
 AC AAR77310;
 XX
 DT 08-MAR-1996 (first entry)
 DE Substance P.
 XX
 KW Substance P; neurokinin; neurokinin receptor antagonist;
 KW sensory perception; tachykinin receptor; therapy;
 KW neurodegenerative disorder; Alzheimer's disease; demyelinating disease;
 KW multiple sclerosis; respiratory disease; ocular disease;
 KW addiction disorder; adverse immune reaction; gastrointestinal disorder;
 KW bladder function disorder; fibrosing disease; collagen disease;
 KW diagnosis.
 KW
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 11 /note= "amidated"
 XX
 PN US5434158-A.
 XX
 PD 18-JUL-1995.
 XX
 PF 26-APR-1994; 94US-0233487.
 XX
 PR 26-APR-1994; 94US-0233487.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Shah SK;
 XX
 DR WPI; 1995-268290/35.
 XX
 PT New 1'-substd. spiro-indoline-3,4'-piperidine derivs. - useful as
 PT selective neurokinin-3 antagonists, e.g. for treating CNS disorders,
 PT migraine or esp. asthma.
 XX
 PS Disclosure; Column 1; 16pp; English.
 XX
 CC This sequence represents Substance P. This sequence, and those shown in
 CC AAR77311 and AAR77312 are tachykinins. These three sequences are
 CC pharmacologically active neuropeptides, and are neurokinin receptor
 CC agonists. Neurokinin receptors are widely distributed throughout the
 CC mammalian nervous system, circulatory system and peripheral tissues.
 CC Neurokinin receptors are involved in sensory perception. These
 CC sequences were used in the design and testing of neurokinin antagonists.
 CC These antagonists could be used in the treatment of conditions
 CC characterised by overstimulation of tachykinin receptors. The
 CC antagonists can also be used, for the treatment of neurodegenerative
 CC disorders (e.g. Alzheimer's disease), demyelinating diseases (e.g.

CC multiple sclerosis), respiratory diseases, ophthalmic diseases, addiction
CC disorders, adverse immune reactions, gastrointestinal disorders, bladder
CC function disorders, fibrosis and collagen diseases. The antagonists can
CC also be used as diagnostic agents.

XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGLM 11
| | | | | | | | | | |
Db 1 rpkpqgffglm 11

RESULT 15
AAW33180
ID AAW33180 standard; peptide; 11 AA.

XX
AC AAW33180;

XX 29-JAN-1998 (first entry)

XX Mono-DTPA-Arg1 Substance P.

DE Substance P; radiolabel; diagnostic imaging; therapy;
KW mono-DTPA-Arg1.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "DTPA-Arg"

FT Modified-site 11 /note= "amidated"

XX WO9640292-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US09706.

XX 07-JUN-1995; 95US-0480372.

XX (MLCW) MALLINCKRODT MEDICAL INC.

XX Srinivasan A;

XX WPI; 1997-087027/08.

XX Prepn. of pure radio-labelled peptide, e.g. for diagnostic imaging -
PT by combining protected poly(amino:carboxylate) ligand with peptide
PT and forming complex with radionuclide

XX Example 3; Page 12; 20pp; English.

XX Preparing a radiolabelled peptide composition, comprises combining
CC a triamine or diamine chelating agent with a peptide, e.g. the
CC present peptide, in a solid phase peptide synthesiser, and
CC complexing a radionuclide with the chelate-peptide conjugate.
CC Radiolabelled peptides or peptidomimetics can be used as diagnostic
CC imaging agents, or in therapeutic applications, e.g. iodine(111)
CC labelled pentatreotide can be used for somatostatin receptor
CC imaging of neuroendocrine tumours. The radiolabelled products are
CC obtained efficiently and inexpensively in high purity. The
CC protected polyaminocarboxylate ligands can be added to the peptide
CC by standard solution or solid phase peptide synthesis and
CC deprotected with conventional reagents to give only the
CC mono-addition product, free of di-addition product impurities. The
CC deprotected product can be labelled with medically useful
CC radionuclides, e.g. lanthanides or actinides, at any desired

CC location. Pre-derivatization of individual amino acids is not
CC required.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGLM 11
| | | | | | | | | | |
Db 1 rpkpqgffglm 11

RESULT 16
AAW04616
ID AAW04616 standard; peptide; 11 AA.

XX
AC AAW04616;

XX 13-AUG-1997 (first entry)

XX Substance P peptide for mass spectrometry analysis.

XX Mass spectrometry; polymer analysis; biopolymer analysis.

XX Synthetic.

XX WO9636986-A1.

XX 21-NOV-1996.

XX 17-MAY-1996; 96WO-US07146.

XX 19-MAY-1995; 95US-0447175.

XX 19-MAY-1995; 95US-0446055.

XX (PERS-) PERSEPTIVE BIOSYSTEMS INC.

XX Patterson DH, Tarr GE;

XX WPI; 1997-012308/01.

XX Sequencing polymers, e.g. DNA, RNA, peptide nucleic acids, proteins,
PT etc. - by obtaining mass to charge ratios of polymer fragments,
PT pref. using mass spectrometer, and performing statistical analysis

XX Example 2; Page 32; 86pp; English.

XX A method of obtaining sequence information about a polymer (e.g. DNA,
CC RNA, peptide nucleic acids, proteins, peptides and carbohydrates)
CC comprising monomers of known mass has been claimed. The present
CC sequence represents a substance P peptide, and was used as
CC an example as a digestion before analysis by mass spectrometry.
CC using this novel on-plate strategy. Total sequence information
CC from a nine well digestion can be represented in a single digestion or
CC it is often derived from two or more wells. The methods, apparatus and
CC kit (claimed) can be used for the analysis of polymers, particularly
CC biopolymers, e.g. DNA, RNA, peptide nucleic acids, proteins, peptides
CC and carbohydrates. It provides a rapid, automated and cost effective
CC sequencing of polymers, with a statistical certainty.

XX Sequence 11 AA;

Query Match 100.0%; Score 61; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGLM 11
| | | | | | | | | | |
Db 1 rpkpqgffglm 11

RESULT 17

AAW42973
ID AAW42973 standard; Protein; 11 AA.XX AC
XX DTXX AAW42973;
XX 01-MAY-1998 (first entry)

XX DE Substrate P reporter epitope.

XX KW Beta-amyloid peptide; BAP; extracellular BAP plaque;
KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;KW amyloid precursor protein; APP; secretase; BAP aggregation;
KW abnormal proteolytic cleavage; substrate P reporter epitope.XX OS
XX US5703209-A.XX PN
XX PD 30-DEC-1997.

XX PF 05-JUN-1995; 95US-0464248.

XX PR 20-SEP-1993; 93US-0123659.

XX PR 01-MAY-1992; 92US-0877675.

XX PA (AMCY) AMERICAN CYANAMID CO.

XX PI Jacobsen JS, Vitek MP;

XX DR WPI; 1998-076482/07.

XX PT Amyloid precursor protein fusion polypeptides - comprising APP
PT fragment and marker, useful for research and drug screening

XX PS Disclosure; Column 3; 84pp; English.

XX CC Peptide sequence AAW42978 represents an amyloid precursor protein (APP),
XX which has a deletion of 276 amino acids to within 15 amino acids of the
XX beta-amyloid peptide (BAP) domain. The protein also contains the
XX Met-enkephalin reporter epitope at the carboxy terminus. Abnormal
XX accumulation of extracellular BAP in plaques and cerebrovascular
XX deposits is characteristic in brains of individuals suffering from
XX Alzheimers disease and Downs syndrome. BAP is a poorly soluble,
XX self-aggregating protein which is derived from a larger amyloid precursor
XX protein (APP). APP is expressed as an integral membrane protein, and is
XX cleaved by secretase, between BAP 16lys and 17leu. Cleavage at this site
XX precludes amyloidogenesis and results in the release of the
XX amino-terminal APP fragment. Three major isoforms of APP exist: APP-695,
XX APP-751 and APP-770. These isoforms are derived by alternative splicing.
XX APP-RRP 751 is constructed by ligating restriction fragments representing
XX N- and C-terminal APP-751 cDNA and substrate P reporter epitope
XX sequences (present sequence) APP can be used as a substrate for studying
XX abnormal proteolytic cleavage which results in the release of BAP, and
XX also to screen for drugs that will inhibit such cleavage.

SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 19; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00029;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11

Db 1 rpqpqffglm 11

RESULT 18

RAY30985
ID AAY30985 standard; peptide; 11 AA.

XX AC

XX AAY30985;
XX 21-OCT-1999 (first entry)

XX DE Non-crosslinked protein particle peptide 34.

XX KW Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
KW albumin; haemoglobin; nanometer; micrometer; clearance.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 11
XX /note= "C-terminal amide"

XX PN US5945033-A.

XX PD 31-AUG-1999.

XX PF 12-NOV-1996; 96US-0747137.

XX PR 14-MAR-1994; 94US-0212546.

XX PR 15-JAN-1991; 91US-0641720.

XX PR 13-OCT-1992; 92US-0959560.

XX PR 01-JUN-1993; 93US-0069831.

XX PR 12-NOV-1996; 96US-0747137.

XX PA (HEMO-) HEMOSPHERE INC.

XX PI Yen RCK;

XX DR WPI; 1999-508153/42.

XX PT Non-crosslinked protein particles for therapeutic and diagnostic use

XX PS Example 22; Column 63-64; 65pp; English.

XX CC This invention describes a novel aqueous suspension of monodisperse
XX particles on non-crosslinked, non-denatured albumin (50-5030 nm) which
XX is stable against dissolving upon dilution with an alcohol-free aqueous
XX medium. The method involves (a) forming an aqueous solution containing
XX albumin and hemoglobin and (b) treating the aqueous solution with an
XX alcohol to cause the solution to become turbid. The particles are useful
XX as agents for in vivo administration, either of their own administration
XX or as a vehicle for other therapeutic or diagnostic agents. The method
XX permits the formation of albumin and hemoglobin particles in the
XX nanometer and micrometer size range, in a form closer to their natural
XX form than the forms of the prior art. The particles therefore constitute
XX a more closely controlled agent for in vivo administration, with greater
XX ease of clearance from the body after their period of usefulness.

XX CC AAY30952-Y31135 represent peptides used in the method of the invention.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 20; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00029;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11

Db 1 rpqpqffglm 11

RESULT 19

AAY03156
ID AAY03156 standard; peptide; 11 AA.

XX AC

XX AAY03156;
XX 10-JUN-1999 (first entry)

XX DT

DE Substance P.
XX Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
KW Substance P.
XX Synthetic.
OS US5891842-A.
PN 06-APR-1999.
XX 12-APR-1996; 96US-0631434.
XX 09-APR-1993; 93US-0044954.
PR 12-APR-1996; 96US-0631434.
XX (TUFT) TUFTS COLLEGE.
PA Kream RM;
PI WPI; 1999-253906/21.
DR Synergistic method for enhancing opioid analgesia and anaesthesia
XX within a human
XX Disclosure; Column 14; 20pp; English.
XX This sequence represents substance P used in the method of the
CC invention. The method is for enhancing opioid analgesia within a human
CC subject for a duration of 15 minutes comprises concurrent administration
CC of substance P, or one of its precursors. The method is used to elicit
CC opioid analgesia and anaesthesia, either prior to or after the occurrence
CC of a nociceptive event. The components have a synergistic effect. The
CC method allows use of low doses of opioid that produce little or no
CC physiological effect reducing conventional risks of toxicity and
CC addiction, and allows the use of low doses of substance P and its related
CC analogs that limit their in vivo physiological consequences. The
CC analgesia is naloxone reversible allowing diminishment or complete
CC elimination of opioid analgesia if desired and on demand. The treatment
CC provides a durable analgesic effect, but only minimally disturbs and
CC interrupts the normal metabolic processes of the body.
XX
XX Sequence 11 AA;
SQ

Query Match 100.0%; Score 61; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPKPQOQFFGLM 11
DB 1 rpkpqgffglm 11

RESULT 20
AAW92715
ID AAW92715 standard; peptide; 11 AA.
XX
AC AAW92715;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #61.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 10
FT /label= MeLeu

FT
XX US5876948-A.
PN 02-MAR-1999.
XX 27-JUL-1991; 91US-0737371.
XX 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX Yankner BA;
XX WPI; 1999-189630/16.
DR Screening for neurotoxin inhibitors - by testing compounds for their
XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells
PT Disclosure; Column 37-38; 28pp; English.
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
XX Sequence 11 AA;
SQ

Query Match 100.0%; Score 61; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPKPQOQFFGLM 11
DB 1 rpkpqgffglm 11

RESULT 21
AAW92719
ID AAW92719 standard; peptide; 11 AA.
XX
AC AAW92719;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #65.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 9
FT /label= MeGly
FT /note= "N-methyl-glycine"
XX
XX US5876948-A.
XX 02-MAR-1999.
XX 27-JUL-1991; 91US-0737371.
XX 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX


```
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX beta-amyloid peptide fragments.
SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
   |||||
Db 1 rpkpqgffglm 11

RESULT 24
AAW92680
ID AAW92680 standard; peptide; 11 AA.
XX
AC AAW92680;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #26.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 8 /note= "Residue is N-methyl-phenylalanine"
FT
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
PS Disclosure; Column 21-22; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX beta-amyloid peptide fragments.
SQ Sequence 11 AA;

This invention describes a method for screening compounds for inhibiting
a neurotoxin. The method involves incubating tachykinin agonists with
neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
used for identifying compounds for treating diseases characterised by an
undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
with amyloidosis and non-inherited congophilic angiopathy with cerebral
haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
beta-amyloid peptide fragments.

Query Match 100.0%; Score 61; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
   |||||
Db 1 rpkpqgffglm 11

RESULT 26
AAW92676
ID AAW92676 standard; peptide; 11 AA.
XX
AC AAW92676;
XX
DT 30-APR-1999 (first entry)
XX
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XX DE Human tachykinin agonist beta-amyloid peptide fragment #22.
XX KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Modified-site 9
XX FT /label= MeGly
XX FT /note= "N-methyl-glycine (Sarcosine)"
XX PN US5876948-A.
XX PD 02-MAR-1999.
XX PF 27-JUL-1991; 91US-0737371.
XX PR 29-JUL-1991; 91US-0737371.
XX PR 27-JUL-1990; 90US-0559173.
XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX PI Yankner BA;
XX DR WPI; 1999-189630/16.
XX XX Screening for neurotoxin inhibitors - by testing compounds for their
XX PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX PS Disclosure; Column 19-20; 28pp; English.
XX CC This invention describes a method for screening compounds for inhibiting
XX CC a neurotoxin. The method involves incubating tachykinin agonists with
XX CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
XX CC used for identifying compounds for treating diseases characterised by an
XX CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
XX CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
XX CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
XX CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX CC beta-amyloid peptide fragments.
XX SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
Db 1 rpkpqffglm 11

RESULT 27
AAW92731
ID AAW92731 standard; peptide; 11 AA.
XX AC AAW92731;
XX DT 30-APR-1999 (first entry)
XX DE Human tachykinin agonist beta-amyloid peptide fragment #77.
XX KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX OS Homo sapiens.
XX PN US5876948-A.

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XX PD 02-MAR-1999.
XX XX 27-JUL-1991; 91US-0737371.
XX PF 29-JUL-1991; 91US-0737371.
XX PR 27-JUL-1990; 90US-0559173.
XX XX (CHIL-) CHILDRENS MEDICAL CENT.
XX PI Yankner BA;
XX DR WPI; 1999-189630/16.
XX XX Screening for neurotoxin inhibitors - by testing compounds for their
XX PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX PS Disclosure; Column 43-44; 28pp; English.
XX CC This invention describes a method for screening compounds for inhibiting
XX CC a neurotoxin. The method involves incubating tachykinin agonists with
XX CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
XX CC used for identifying compounds for treating diseases characterised by an
XX CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
XX CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
XX CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
XX CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX CC beta-amyloid peptide fragments.
XX SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
Db 1 rpkpqffglm 11

RESULT 28
AAW79662
ID AAW79662 standard; peptide; 11 AA.
XX AC AAW79662;
XX DT 02-MAR-1999 (first entry)
XX DE Substance P derivative having complex glycosylation.
XX KW Substance P; mannose; glycosylation; solubility.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Region 1..4
XX FT /note= "optionally the first four residues may be
XX FT Modified-site 5 deleted, leaving SP(5-11)"
XX FT /note= "the side chain amide group is N-substituted
XX FT with N-acetyl-D-glucosamine (GlcNAc) which in turn
XX FT is extended in the 4-position with a complex type
XX FT sugar chain, a high mannose type sugar chain or a
XX FT mixed type sugar chain"
XX FT Modified-site 11
XX FT /note= "Met-NH2, i.e. C-terminal amide"
XX PN JPL0306099-A.
XX PD 17-NOV-1998.
XX PF 28-NOV-1997; 97JP-0343979.

```

XX PR 04-MAR-1997; 97JP-0065372.
XX PA (NOGK) ZH NOGUCHI KENKYUSHO.
XX DR WPI; 1999-054306/05.
XX PT New substance P derivatives with side chain containing sugar - has
XX PT improved solubility
XX PS Claim 1; Page 2; 8pp; Japanese.
XX CC The sequence represents the peptide portion of a new Substance P
XX CC derivative having complex glycosylation on the Gln(5) position. The
XX CC derivative has improved solubility compared with Substance P.
XX SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPkpQQFFGLM 11
Db 1 rpkpqqffglm 11

RESULT 29
AAW79663
ID AAW79663 standard; peptide; 11 AA.
XX AC AAW79663;
XX DT 02-MAR-1999 (first entry)
XX DE Substance P derivative having complex glycosylation.
XX KW Substance P; mannose; glycosylation; solubility.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 6
FT /note= "the side chain amide group is N-substituted
FT with N-acetyl-D-glucosamine (GlcNAc) which in turn
FT is extended in the 4-position with a complex type
FT sugar chain, a high mannose type sugar chain or a
FT mixed type sugar chain"
FT Modified-site 11
FT /note= "Met-NH2, i.e. C-terminal amide"
XX JP10306099-A.
XX PD 17-NOV-1998.
XX PF 28-NOV-1997; 97JP-0343979.
XX PR 04-MAR-1997; 97JP-0065372.
XX PA (NOGK) ZH NOGUCHI KENKYUSHO.
XX DR WPI; 1999-054306/05.
XX PT New substance P derivatives with side chain containing sugar - has
XX PT improved solubility
XX PS Claim 1; Page 2; 8pp; Japanese.
XX CC The sequence represents the peptide portion of a new Substance P
XX CC derivative having complex glycosylation on the Gln(6) position. The
XX CC derivative has improved solubility compared with Substance P.

SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPkpQQFFGLM 11
Db 1 rpkpqqffglm 11

RESULT 30
AAB18483
ID AAB18483 standard; peptide; 11 AA.
XX AC AAB18483;
XX DT 15-JAN-2001 (first entry)
XX DE Peptide substrate used to test prolyl-tripeptidyl peptidase activity.
XX KW Prolyl tripeptidyl-peptidase; amidolytic activity; periodontal disease;
XX KW gingivitis; periodontitis.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "hydrogen attached"
FT Modified-site 11
FT /note= "amidated residue"
XX WO200052147-A2.
XX PN 08-SEP-2000.
XX PD 03-MAR-2000; 2000WO-US05551.
XX PF 05-MAR-1999; 99US-0123148.
XX PR (UYGE-) UNIV GEORGIA RES FOUND INC.
XX PA (TRAV/) TRAVIS J.
XX PA (POTE/) POTEPA J.
XX PA (BANB/) BANBULA A.
XX PI Travis J, Potempa J, Banbula A;
XX DR WPI; 2000-594181/56.
XX PT Prolyl tripeptidyl-peptidase, active analog, fragment or variant useful
XX PT for identifying its inhibitor which is useful for protecting an animal
XX PT from a periodontal disease such as gingivitis and periodontitis -
XX PS Example 4; Page 37; 58pp; English.
XX CC The present sequence represents a substrate which was used to test
XX CC the activity of prolyl tripeptidyl-peptidases PRP-A and PRP IV. The
XX CC prolyl tripeptidyl-peptidase has an amidolytic activity, and cleaves
XX CC a peptide bond in a target polypeptide having at least 4 amino acids.
XX CC This bond is between a proline and an amino acid attached to the
XX CC alpha-carboxyl group end of the proline. The polypeptide is useful for
XX CC identifying inhibitors. These inhibitors are then useful for reducing
XX CC the growth of bacterium or for protecting an animal from a periodontal
XX CC disease such as gingivitis and periodontitis caused by Porphyromonas
XX CC gingivalis.
XX SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RPKPQQFFGLM 11
|||||
Db 1 rpkpqffglm 11

RESULT 31

AAB23027
ID AAB23027 standard; peptide: 11 AA.

XX AC AAB23027;

XX DT 16-JAN-2001 (first entry)

XX DE Human/rat tachykinin Substance P.

XX KW Substance P; tachykinin; human; rat; magnesium binding defect;
KW sodium sensitive essential hypertension; insulin resistance;
KW type 2 diabetes; antibody; immunoassay; quantification.

XX OS Homo sapiens.

XX OS Rattus sp.

XX FH Key Location/Qualifiers

FT Modified-site 11

FT /note= "C-terminal amide"

PN WO200054053-A1.

XX PD 14-SEP-2000.

XX PF 09-MAR-2000; 2000WO-US03707.

XX PR 10-MAR-1999; 99US-0265690.

XX PA (WELL)/ WELLS I C.

XX PI Wells IC;

XX DR WPI; 2000-587457/55.

XX PT Detecting magnesium binding defects associated with abnormal
PT physiological states such as sodium-sensitive essential hypertension
PT and type 2 insulin-resistant diabetes mellitus, comprises measuring a
PT specific pentapeptide in blood -

XX PS Disclosure; Page 5; 21pp; English.

XX CC The invention relates to a method for detecting magnesium binding
CC defects. The method comprises quantitating a tachykinin C-terminal
CC pentapeptide (e.g., AAB23025) and its degradation products (e.g.,
CC AAB23026) in blood using an antibody specific for the generalised
CC mammalian tachykinin C-terminal pentapeptide
CC Phe-(Phe/Val)-Gly-Leu-Met-NH₂ (AAB23028). The method is useful for
CC detecting cellular magnesium binding defects which are associated with
CC abnormal physiological states such as sodium-sensitive essential
CC hypertension and type 2 diabetes mellitus. The present sequence
CC represents the tachykinin Substance P from human and rat. C-terminal
CC fragments (AAB23025, AAB23026) of the present sequence may be assayed
CC according to the method of the invention.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RPKPQQFFGLM 11
|||||
Db 1 rpkpqffglm 11

RESULT 32

AAY32382

ID AAY32382 standard; Peptide; 11 AA.

XX AC AAY32382;

XX DT 28-FEB-2000 (first entry)

XX DE Cell differentiation, proliferation and maintenance factor peptide.

XX KW Cell differentiation; cell proliferation; cell maintenance;
KW ectoderm-like cell; embryonic stem cell; pluripotent cell;
KW gene therapy; cell therapy; tissue transplant; organ transplant;
KW xerograft; allotransplant; concomitant transplantation;
KW transgenic animal; substance P.

XX OS Synthetic.

XX PN WO9953021-A1.

XX PD 21-OCT-1999.

XX PF 09-APR-1999; 99WO-AU00265.

XX PR 09-APR-1998; 98AU-0002912.

XX PR 23-SEP-1998; 98AU-0006097.

XX PA (BRES-) BRESAGEN LTD.

XX PI Bettess MD, Rathjen PD, Rathjen J;

XX DR WPI; 2000-061970/05.

XX PT New isolated biologically active factor capable of influencing
PT differentiation, proliferation or maintenance of pluripotent cells

XX PS Claim 3; Page 123; 189pp; English.

XX CC This sequence represents a peptide (substance P free acid) that can
CC form the low mol.wt. component of a novel biologically active factor
CC that is capable of influencing the differentiation, proliferation
CC and/or maintenance of pluripotent cells. The factor consists of a
CC low mol.wt. component selected from Pro, Pro-Ala, Ala-Pro-Gly,
CC Pro-OH-Pro, Gly-Pro-Ala, Gly-Pro-OH-Pro, a peptide given in
CC AAY32378-82, or a protease digested (including collagenase digested)
CC collagen fragment, and a high mol.wt. component such as fibronectin.
CC The biologically active factor is obtained from conditioned media of
CC hepatic or hepatoma cells or cell lines or extraembryonic endodermal
CC cells or cell lines. The factor is capable of causing the
CC transition of pluripotent cells (e.g. embryonic stem cells in
CC adherent culture and in suspension culture) to pluripotent cells
CC having different properties, more specifically primitive of
CC ectoderm-like (EPL) cells. The factor is also capable of
CC maintaining and supporting proliferation of these cells in vitro.
CC It also allows the isolation and maintenance of EPL cells derived
CC from in vitro and in vivo primitive ectoderm. These cells can be
CC used in allo-, concomitant- or xeno-transplantation, cell therapy,
CC tissue and organ augmentation or replacement, and gene therapy.
CC They can also be used for producing chimeric or transgenic animals.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RPKPQQFFGLM 11
|||||
Db 1 rpkpqffglm 11

RESULT 33

AAG62768
ID AAG62768 standard; peptide; 11 AA.

XX
AC AAG62768;

XX
DT 17-SEP-2001 (first entry)

XX
DE Amino acid sequence of substance P.

XX
KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.

XX
OS Unidentified.

XX
FH Key Location/Qualifiers

FT Modified-site 11

FT /note= "amidated residue"

XX
PN WO200153336-A1.

XX
PD 26-JUL-2001.

XX
PF 17-JAN-2001; 2001WO-US01529.

XX
PR 19-JAN-2000; 2000US-0489667.

XX
PA (ALLR) ALLERGAN SALES INC.

XX
PI Donovan S;

XX
DR WPI; 2001-451900/48.

XX
XX Agent useful for treating pain comprises a clostridial neurotoxin (or component) attached to a targeting moiety

XX
PS Disclosure; Page 61; 77pp; English.

XX
CC The specification describes an agent, comprising a clostridial neurotoxin attached to a targeting moiety, where the targeting moiety is selected from transmission compounds, and compounds substantially similar to the transmission compounds. The agent may be used for treating pain, where the clostridial neurotoxin component is derived from botulinum toxin selected from botulinum types A, B, C, D, E, F, G and mixtures of these. The targeting moiety comprises a light chain and an amine end segment of a heavy chain and comprises substance P as the targeting moiety. The pain alleviating effects persist for 2-6 months. The present sequence represents substance P, and is used in the course of the invention.

XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGLM 11
Db 1 rpkpqqffgilm 11

RESULT 34

AAG99354

ID AAG99354 standard; Peptide; 11 AA.

XX
AC AAG99354;

XX
DT 25-SEP-2001 (first entry)

XX
DE Substance P peptide.

XX
KW Atypical tachykinin; ATT; human; hypertension.

XX
OS Unidentified.

PN WO200146415-A1.

XX
PD 28-JUN-2001.

XX
PF 21-DEC-2000; 2000WO-JP09083.

XX
PR 21-DEC-1999; 99JP-0362638.

XX
PR 10-MAR-2000; 2000JP-0066714.

XX
PA (TAKE) TAKEDA CHEM IND LTD.

XX
XX Itoh Y, Nishi K, Kitada C, Inatomi N;

XX
PI WPI; 2001-441676/47.

XX
DR Atypical tachykinin peptides of human origin and DNA encoding them for screening potential agents for treatment of hypertension

XX
PT Disclosure; Page 9; 153pp; Japanese.

XX
CC The present invention relates to atypical tachykinin proteins of human origin and their esters, amides, salts and partial peptides. These can be used in the treatment, prevention and diagnosis of hypertension. The present sequence is a protein fragment described in the exemplification of the invention.

XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00029;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGLM 11
Db 1 rpkpqqffgilm 11

RESULT 35

AAB84527

ID AAB84527 standard; peptide; 11 AA.

XX
AC AAB84527;

XX
DT 05-SEP-2001 (first entry)

XX
DE Amino acid sequence of human substance P.

XX
KW Substance P; cell toxin; Pseudomonas exotoxin; cell ablation;
KW NK-1 receptor; chronic pain; tumour; neurological dysfunction;
KW basal ganglia; cholinergic interneuron; Parkinson's disease.

XX
XX Homo sapiens.

XX
PN WO200131020-A1.

XX
PD 03-MAY-2001.

XX
PF 20-OCT-2000; 2000WO-US29064.

XX
PR 22-OCT-1999; 99US-0161159.

XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
PI Fitzgerald DJ, Iadarola MJ;

XX
WPI; 2001-417560/44.

XX
PT Making cell toxin to treat chronic pain, by forming substance
PT P-pseudomonas exotoxin disulfide-linked conjugate, by reacting modified
PT exotoxin and substance P having additional cysteine residue at its
PT N-terminus

PS Disclosure; Page 10; 54pp; English.

XX The present sequence represents a human substance P. The peptide is
CC used to produce a cell toxin. The cell toxin comprises a substance
CC P-pseudomonas exotoxin disulfide-linked conjugate. The cell toxin is
CC useful for ablating NK-1 receptor expressing cells, such as dorsal horn
CC cell, a stratum cell or a brain parenchyma cell, for treating chronic
CC pain in epineurium cells, perineurium cells, nerve ganglia, nerve
CC sheaths, nerve linings, meninges, planar cells, arachnoid membrane
CC cells, duramembrane cells, cells lining a joint or brain or spinal cord
CC parenchymal cells, without significantly affecting basal nociceptive
CC responses. The cell toxin is thus useful for treating chronic pain or
CC tumours that binds substance P. It is also useful for neurological
CC dysfunctions of the basal ganglia by targeting cholinergic interneurons
CC that express substance P e.g. Parkinson's disease.

XX Sequence 11 AA;

Query Match 100.0%; Score 61; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
Db 1 rpkpqffgflm 11

RESULT 36

AAB98866
ID AAB98866 standard; Peptide; 11 AA.

AC AAB98866;

DT 14-AUG-2001 (first entry)

DE Chimeric analgesic peptide #22.

KW Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.

OS Synthetic.

FH Key Location/Qualifiers
FT Modified-site 11
FT /label= OTHER
FT /note= "C-terminal amide"

PN WO200130371-A2.

XX 03-MAY-2001.

XX 27-OCT-2000; 2000WO-US29789.

XX 28-OCT-1999; 99US-0428692.

XX (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

XX WPI; 2001-397593/42.

XX New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group

XX Claim 10; Page 15; 34pp; English.

XX The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.

XX Sequence 11 AA;

Query Match 100.0%; Score 61; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
Db 1 rpkpqffgflm 11

RESULT 37

AAB82070
ID AAB82070 standard; peptide; 11 AA.

AC AAB82070;

XX 22-JUN-2001 (first entry)

XX Substance P.

XX Antigen; immunostimulant; vaccine; pharmaceutical composition; antiviral;
KW viral infection; substance P.

OS Unidentified.

FH Key Location/Qualifiers
FT Modified-site 11
FT /note= "C-terminal amide"

XX WO200124822-A2.

XX 12-APR-2001.

XX 02-OCT-2000; 2000WO-EF09657.

XX 01-OCT-1999; 99AT-0001680.

XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

XX Fleitmann J, Mattner F, Buschle M, Melling J;

XX WPI; 2001-290577/30.

XX New pharmaceutical composition comprising an antigen, an
PT immunostimulating substance and a polycationic polymer, useful in
PT manufacturing vaccines

XX Example 3; Page 14; 20pp; English.

XX The present invention relates to a pharmaceutical composition comprising
CC (a) an antigen; (b) an immunostimulating substance consisting of
CC neuroactive compounds, hormones, compounds having growth hormone activity
CC or their mixtures; and (c) a polycationic polymer. The composition is
CC useful in manufacturing vaccines. To illustrate the present invention, a
CC murine tyrosinase related protein-2 peptide (TRP-2 peptide; see
CC AAB82064), was used. Mice were injected subcutaneously with either the
CC TRP-2 peptide, TRP-2 peptide + poly-L-arginine 60 (pR60) or TRP-2 peptide
CC + pR60 + substance P (the present peptide). Animals were sacrificed 10
CC days post injection, and spleen tissue was harvested. Lymphocytes were
CC prepared from the spleen tissue and were re-stimulated with TRP-2 peptide
CC or with an ovalbumin-derived peptide (AAB82065), with the same major
CC histocompatibility complex (MHC) restriction serving as negative control.
CC Spots representing single T cells specific for the peptide used for
CC re-stimulation were counted. No spots were detected when the ovalbumin
CC derived peptide was used, while TRP-2 peptide + pR60 + substance P showed
CC the highest number of spots or single T cells.

XX Sequence 11 AA;

Query Match 100.0%; Score 61; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
| | | | | | | | | |
Db 1 rp*pgqffglm 11

RESULT 38
AAB91436
ID AAB91436 standard; Peptide; 11 AA.

XX AC AAB91436;

DT 22-JUN-2001 (first entry)

XX Tachykinins peptide SEQ ID NO:612.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
OS Synthetic.

PN WO200069900-A2.

XX 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT

PS Disclosure; Page 399; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 11 AA;

Query Match 100.0%; Score 61; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
| | | | | | | | | |
Db 1 rp*pgqffglm 11

RESULT 39
AAB91449
ID AAB91449 standard; Peptide; 11 AA.

XX AC AAB91449;

DT 22-JUN-2001 (first entry)

XX Tachykinins peptide SEQ ID NO:625.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
OS Synthetic.

PN WO200069900-A2.

XX 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT

PS Disclosure; Page 403; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 11 AA;

Query Match 100.0%; Score 61; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
| | | | | | | | | |
Db 1 rp*pgqffglm 11

RESULT	40
AAB91450	
ID	AAB91450 standard; Peptide; 11 AA.
XX	
AC	AAB91450;
XX	
DT	22-JUN-2001 (first entry)
XX	
DE	Tachykinins peptide SPQ ID NO:626.
XX	
KW	Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW	blood component; modification; succinimidyl; maleimido group; amino;
KW	hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX	
OS	Homo sapiens.
OS	Synthetic.
PN	WO200069900-A2.
PD	
XX	23-NOV-2000.
XX	
PF	17-MAY-2000; 2000WO-US13576.
XX	
PR	17-MAY-1999; 99US-0134406.
PR	10-SEP-1999; 99US-0153406.
PR	15-OCT-1999; 99US-0159783.
XX	
PA	(CONJ-) CONJUCHEM INC.
XX	
PI	Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX	
DR	WPI; 2001-112059/12.
XX	
PT	Modifying and attaching therapeutic peptides to albumin prevents
PT	peptidase degradation, useful for increasing length of in vivo activity
PT	-
XX	
PS	Disclosure; Page 403; 733pp; English.
XX	
CC	The present invention describes a modified therapeutic peptide (I)
CC	comprising a therapeutically active amino acid region (III) and a
CC	reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC	a less therapeutically active amino acid region (IV), which covalently
CC	bonds with amino/hydroxyl/thiol groups on blood components to form a
CC	peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC	(I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC	factors and neurotransmitters, to protect them from peptidase activity
CC	in vivo for the treatment of various disorders. Endogenous therapeutic
CC	peptides are not suitable as drug candidates as they require frequent
CC	administration due to rapid degradation by peptidases in the body.
CC	Modifying and attaching therapeutic peptides to albumin prevents or
CC	reduces the action of peptidases to increase length of activity (half
CC	life) and specificity as bonding to large molecules decreases
CC	intracellular uptake and interference with physiological processes.
CC	AAB90829 to AAB92441 represent peptides which can be used in the
CC	exemplification of the present invention.
XX	
SQ	Sequence 11 AA;
Query Match	100.0%; Score 61; DR 22; Length 11;
Best Local Similarity	100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 RPKPQQFFGLM 11
Db	
	1 rpkpqffglm 11
RESULT	41
AAB50544	
ID	AAB50544 standard; peptide; 11 AA.

CC target protein. This cycle continues until a sufficiently pure
CC oligonucleotide sequence is isolated. The method allows the isolation of
CC oligonucleotide sequences which structurally mimic the target protein's
CC ligand. This peptide represents an analogue of Substance P (AAR85243) in
CC which the N-terminal amine has been acylated in order to determine
CC whether this functional group interacts with nucleic acid ligands binding
CC substance P (see AAR06098-130). The ligands can be used to block the
CC activity of Substance P and is useful in the treatment of e.g. rheumatoid
CC arthritis, atherosclerosis, diabetic retinopathy or cancer.

XX Sequence 12 AA;

Query Match 100.0%; Score 61; DB 16; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RPKPQQFFGLM 11
| | | | | | | | | |
Db 1 rpkpqffglm 11

RESULT 45

AA03157
ID AAY03157 standard; peptide: 12 AA.

XX AC AAY03157;

XX DT 10-JUN-1999 (first entry)

XX DE Substance P-Glycine.

XX KW Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
substance P.

XX OS Synthetic.

XX PN US5891842-A.

XX PD 06-APR-1999.

XX PF 12-APR-1996; 96US-0631434.

XX PR 09-APR-1993; 93US-0044954.

XX PR 12-APR-1996; 96US-0631434.

XX PA (TUFT) TUFTS COLLEGE.

XX PI Kream RM;

XX DR WPI; 1999-253906/21.

XX PT Synergistic method for enhancing opioid analgesia and anaesthesia
within a human

XX PS Disclosure; Column 14; 20pp; English.

XX This sequence represents substance P used in the method of the
CC invention. The method is for enhancing opioid analgesia within a human
CC subject for a duration of 15 minutes comprises concurrent administration
CC of substance P, or one of its precursors. The method is used to elicit
CC opioid analgesia and anaesthesia, either prior to or after the occurrence
CC of a nociceptive event. The components have a synergistic effect. The
CC method allows use of low doses of opioid that produce little or no
CC physiological effect reducing conventional risks of toxicity and
CC addiction, and allows the use of low doses of substance P and its related
CC analogs that limit their in vivo physiological consequences. The
CC analgesia is naloxone reversible allowing diminishment or complete
CC elimination of opioid analgesia if desired and on demand. The treatment
CC provides a durable analgesic effect, but only minimally disturbs and
CC interrupts the normal metabolic processes of the body.

XX Sequence 12 AA;

Query Match 100.0%; Score 61; DB 20; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RPKPQQFFGLM 11
| | | | | | | | | |
Db 1 rpkpqffglm 11

RESULT 46

AAW94412
ID AAW94412 standard; peptide: 12 AA.

XX AC AAW94412;

XX DT 15-APR-1999 (first entry)

XX DE Cancer protease-sensitive amino acid linker pAP-215 and pAP-216.

XX KW Ricin-like toxin; cancer; viral infection; parasitic infection;
linker; B chain; A chain; protease; fungal infection; malaria;
KW leucocyte proliferation; cytomegalovirus; herpes; hepatitis;
KW rhinovirus; laryngeotracheitis; poliomyelitis; varicella zoster;
KW cystic fibrosis; multiple sclerosis.

XX OS Unidentified.

XX OS Synthetic.

XX PN W09849311-A2.

XX PD 05-NOV-1998.

XX PF 30-APR-1998; 98WO-CA00394.

XX PR 29-OCT-1997; 97US-0063715.

XX PR 30-APR-1997; 97US-0045148.

XX PA (DNOV-) DE NOVO ENZYME CORP.

XX PI Borgford T;

XX DR WPI; 1999-009431/01.

XX PT New nucleic acid encoding ricin-like toxin with an interchain linker
cleaved by protease - is specific for diseased cells, useful for,
PT e.g. killing selectively cancer or infected cells

XX PS Claim 24; Fig 21; 352pp; English.

XX The present invention describes new purified and isolated nucleic acids
CC (i) encoding: (i) the A and B chains of a ricin-like toxin (II); and
CC (ii) a heterologous linker, joining the two chains and including a
CC cleavage recognition site for a disease-specific protease (III). Also
CC described are: (1) plasmids or baculovirus transfer vectors that contain
CC (i); and (2) recombinant protein (IV) consisting of the A and B chains
CC of (II) joined by the specified linker. (IV), produced by expression of
CC (I) in host cells, are used to inhibit or kill diseased cells that
CC produce (III), particularly for treating cancers (e.g. leucocyte
CC proliferation; cancer of ovary, pancreas, breast or prostate; glioma) or
CC infections caused by fungi, parasites (e.g. malaria) or viruses (e.g.
CC cytomegalovirus (CMV), herpes, hepatitis, rhinovirus, laryngeotracheitis,
CC poliomyelitis or varicella zoster), also cystic fibrosis and multiple
CC sclerosis. Alternatively, (I) is used to express (IV) in vivo. (IV) is
CC toxic specifically for (III)-expressing cells and does not depend for
CC specificity on a cell-binding component. When used to treat virus-
CC infected cells, transcytosis and cytotoxicity of (IV) are increased by
CC retrograde translocation from endoplasmic reticulum to cytoplasm (which
CC some viruses exploit to avoid immune detection), so selectivity and
CC safety are further improved. (IV) are not toxic until chain A is
CC released and this occurs only in target cells. The present sequence
CC represents a specifically claimed cancer protease-sensitive amino acid

CC linker from the present invention.

XX Sequence 12 AA;

Query Match 100.0%; Score 61; DB 20; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
| | | | | | | | | |
Db 1 rpkpqgffglm 11

RESULT 47

AAG62769

ID AAG62769 standard; peptide; 12 AA.

XX Sequence 12 AA;

AC AAG62769;

XX 17-SEP-2001 (first entry)

XX Amino acid sequence of substance P precursor.

XX Clostridial neurotoxin; pain; botulinum toxin; Substance P.

XX Unidentified.

XX WO200153336-A1.

XX 26-JUL-2001.

XX 17-JAN-2001; 2001WO-US01529.

XX 19-JAN-2000; 2000US-0489667.

XX (ALLR) ALLERGAN SALES INC.

XX Donovan S;

XX WPI; 2001-451900/48.

XX Agent useful for treating pain comprises a clostridial neurotoxin (or component) attached to a targeting moiety -
PS Disclosure; Page 62; 77pp; English.

XX The specification describes an agent, comprising a clostridial neurotoxin attached to a targeting moiety, where the targeting moiety is selected from transmission compounds, and compounds substantially similar to the transmission compounds. The agent may be used for treating pain, where the clostridial neurotoxin component is derived from botulinum toxin selected from botulinum types A, B, C, D, E, F, G and mixtures of these. The targeting moiety comprises a light chain and an amine end segment of a heavy chain and comprises Substance P as the targeting moiety. The pain alleviating effects persist for 2-6 months. The present sequence represents substance P precursor, and is used in the course of the invention.

XX Sequence 12 AA;

Query Match 100.0%; Score 61; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
| | | | | | | | | |
Db 1 rpkpqgffglm 11

RESULT 48

AAG62772

ID AAG62772 standard; peptide; 12 AA.

XX Sequence 12 AA;

XX 17-SEP-2001 (first entry)

XX Amino acid sequence of carboxy-ester substance P precursor.

XX Clostridial neurotoxin; pain; botulinum toxin; Substance P.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site 12

XX /note= "methylated residue"

XX WO200153336-A1.

XX 26-JUL-2001.

XX 17-JAN-2001; 2001WO-US01529.

XX 19-JAN-2000; 2000US-0489667.

XX (ALLR) ALLERGAN SALES INC.

XX Donovan S;

XX WPI; 2001-451900/48.

XX Agent useful for treating pain comprises a clostridial neurotoxin (or component) attached to a targeting moiety -
PS Disclosure; Page 64; 77pp; English.

XX The specification describes an agent, comprising a clostridial neurotoxin attached to a targeting moiety, where the targeting moiety is selected from transmission compounds, and compounds substantially similar to the transmission compounds. The agent may be used for treating pain, where the clostridial neurotoxin component is derived from botulinum toxin selected from botulinum types A, B, C, D, E, F, G and mixtures of these. The targeting moiety comprises a light chain and an amine end segment of a heavy chain and comprises Substance P as the targeting moiety. The pain alleviating effects persist for 2-6 months. The present sequence represents a substance P precursor, and is used in the course of the invention.

XX Sequence 12 AA;

Query Match 100.0%; Score 61; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
| | | | | | | | | |
Db 1 rpkpqgffglm 11

RESULT 49

AAG62775

ID AAG62775 standard; peptide; 12 AA.

XX Sequence 12 AA;

XX 17-SEP-2001 (first entry)

XX Amino acid sequence of carboxy-ester substance P precursor.

XX Clostridial neurotoxin; pain; botulinum toxin; Substance P.

XX Synthetic.

FH Key Location/Qualifiers
FT Modified-site 12
FT /note= "ethylated residue"
XX
XX WO200153336-A1.
XX
XX 26-JUL-2001.
XX
XX 17-JAN-2001; 2001WO-US01529.
XX
XX 19-JAN-2000; 2000US-0489667.
XX
XX (ALLR) ALLERGAN SALES INC.
XX
XX Donovan S;
XX
XX WPI; 2001-451900/48.
XX
XX Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety .
XX
XX Disclosure; Page 67; 77pp; English.
XX
XX The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin
CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
CC The targeting moiety comprises a light chain and an amine end segment of
CC a heavy chain and comprises Substance P as the targeting moiety. The pain
CC alleviating effects persist for 2-6 months. The present sequence
CC represents a substance P precursor, and is used in the course of the
CC invention.
XX
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 61; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQQFFGLM 11
| | | | | | | | | |
Db 1 rpkpqgffglm 11

RESULT 50
AAB84528
ID AAB84528 standard; peptide; 12 AA.
XX
XX AAB84528;
XX
XX 05-SEP-2001 (first entry)
XX
XX Amino acid sequence of a modified substance P.
XX
XX Substance P; cell toxin; Pseudomonas exotoxin; cell ablation;
KW NK-1 receptor; chronic pain; tumour; neurological dysfunction;
KW basal ganglia; cholinergic interneuron; Parkinson's disease.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200131020-A1.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-US29064.
XX
XX 22-OCT-1999; 99US-0161159.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX

XX Fitzgerald DJ, Iadarola MJ;
XX WPI; 2001-417560/44.
XX
XX Making cell toxin to treat chronic pain, by forming substance
PT P-pseudomonas exotoxin disulfide-linked conjugate, by reacting modified
PT exotoxin and substance P having additional cysteine residue at its
PT N-terminus .
XX
XX Example 1; Page 10; 54pp; English.
XX
XX The present sequence represents a modified substance P. The peptide is
CC used to produce a cell toxin. The cell toxin comprises a substance
CC P-pseudomonas exotoxin disulfide-linked conjugate. The cell toxin is
CC useful for ablating NK-1 receptor expressing cells, such as dorsal horn
CC cell, a stratum cell or a brain parenchyma cell, for treating chronic
CC pain in epineurium cells, perineurium cells, nerve ganglia, nerve
CC sheaths, nerve linings, meninges, pia mater cells, arachnoid membrane
CC cells, duramembrane cells, cells lining a joint or brain or spinal cord
CC parenchymal cells, without significantly affecting basal nociceptive
CC responses. The cell toxin is thus useful for treating chronic pain or
CC tumours that binds substance P. It is also useful for neurological
CC dysfunctions of the basal ganglia by targeting cholinergic interneurons
CC that express substance P e.g. Parkinson's disease.
XX
XX Sequence 12 AA;
SQ

Query Match 100.0%; Score 61; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQQFFGLM 11
| | | | | | | | | |
Db 2 rpkpqgffglm 12

RESULT 51
AAB98867
ID AAB98867 standard; Peptide; 12 AA.
XX
XX AAB98867;
XX
XX 14-AUG-2001 (first entry)
XX
XX Chimeric analgesic peptide #23.
XX
XX Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 12
FT /label= OTHER
FT /note= "C-terminal amide"
XX
XX WO200130371-A2.
XX
XX 03-MAY-2001.
XX
XX 27-OCT-2000; 2000WO-US29789.
XX
XX 28-OCT-1999; 99US-0428692.
XX
XX (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
XX Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX WPI; 2001-397593/42.
XX
XX New chimeric peptides used for treating pain comprise oploid receptor
PT

PT binding group and nociceptive receptor binding group -
PS Claim 10; Page 15; 34pp; English.

XX The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 61; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
DB 1 rpkgqffglm 11
|||||

RESULT 52
AAB98870
ID AAB98870 standard; Peptide; 12 AA.

XX AC AAB98870;

XX DT 14-AUG-2001 (first entry)

XX DE Chimeric analgesic peptide #26.

XX KW Opioid receptor binding; nociceptive receptor binding; analgesic;
XX KW pain; chimeric peptide.

XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT Modified-site 12
XX FT /label= OTHER
XX FT /note= "modified by OMe"

XX PN WO200130371-A2.

XX PD 03-MAY-2001.

XX PF 27-OCT-2000; 2000WO-US29789.

XX PR 28-OCT-1999; 99US-0428692.

XX PA (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

XX PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

XX DR WPI; 2001-397593/42.

XX PT New chimeric peptides used for treating pain comprise opioid receptor
XX PT binding group and nociceptive receptor binding group -

XX PS Claim 10; Page 15; 34pp; English.

XX The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 61; DB 22; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
DB 1 rpkgqffglm 11
|||||

RESULT 53
AAB98873
ID AAB98873 standard; Peptide; 12 AA.

XX AC AAB98873;

XX DT 14-AUG-2001 (first entry)

XX DE Chimeric analgesic peptide #29.

XX KW Opioid receptor binding; nociceptive receptor binding; analgesic;
XX KW pain; chimeric peptide.

XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT Modified-site 12
XX FT /label= OTHER
XX FT /note= "modified by Oeth"

XX PN WO200130371-A2.

XX PD 03-MAY-2001.

XX PF 27-OCT-2000; 2000WO-US29789.

XX PR 28-OCT-1999; 99US-0428692.

XX PA (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

XX PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

XX DR WPI; 2001-397593/42.

XX PT New chimeric peptides used for treating pain comprise opioid receptor
XX PT binding group and nociceptive receptor binding group -

XX PS Claim 10; Page 15; 34pp; English.

XX The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 61; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
DB 1 rpkgqffglm 11
|||||

RESULT 54
AAY03158
ID AAY03158 standard; peptide; 13 AA.

XX AC AAY03158;

XX DT 10-JUN-1999 (first entry)

```

XX      Substance P-Glycine-Lysine.
XX
XX      Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
KW      substance P.
XX
XX      Synthetic.
XX
XX      US5891842-A.
XX
XX      06-APR-1999.
XX
XX      12-APR-1996; 96US-0631434.
XX
XX      09-APR-1993; 93US-0044954.
XX      12-APR-1996; 96US-0631434.
XX
XX      (TUFT ) TUFTS COLLEGE.
XX
XX      Kream RM;
PI
XX
XX      WPI; 1999-253906/21.
XX
XX      Synergistic method for enhancing opioid analgesia and anaesthesia
PT      within a human
XX
XX      Disclosure; Column 14; 20pp; English.
XX
XX      This sequence represents substance P used in the method of the
CC      invention. The method is for enhancing opioid analgesia within a human
CC      subject for a duration of 15 minutes comprises concurrent administration
CC      of substance P, or one of its precursors. The method is used to elicit
CC      opioid analgesia and anaesthesia, either prior to or after the occurrence
CC      of a nociceptive event. The components have a synergistic effect. The
CC      method allows use of low doses of opioid that produce little or no
CC      physiological effect reducing conventional risks of toxicity and
CC      addiction, and allows the use of low doses of substance P and its related
CC      analogs that limit their in vivo physiological consequences. The
CC      analgesia is naloxone reversible allowing diminishment or complete
CC      elimination of opioid analgesia if desired and on demand. The treatment
CC      provides a durable analgesic effect, but only minimally disturbs and
CC      interrupts the normal metabolic processes of the body.
XX
XX      Sequence 13 AA;
SQ
      Query Match 100.0%; Score 61; DB 20; Length 13;
      Best Local Similarity 100.0%; Pred. NO. 0.00034;
      Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0
      QY 1 RPKPQQFFGLM 11
      |||||
      Db 1 rpKpqffglm 11
      RESULT 55
      AAG62770
      ID AAG62770 standard; peptide; 13 AA.
      XX
      XX AAG62770;
      XX
      XX 17-SEP-2001 (first entry)
      XX
      XX Amino acid sequence of substance P precursor.
      DE
      XX Clostridial neurotoxin; pain; botulinum toxin; Substance P.
      KW
      XX Unidentified.
      OS
      XX WC200153336-A1.
      PN
      XX 26-JUL-2001.
      PD
      XX
      XX

```


XX Disclosure: Page 65; 77pp; English.

XX The specification describes an agent, comprising a clostridial neurotoxin

CC attached to a targeting moiety, where the targeting moiety is selected

CC from transmission compounds, and compounds substantially similar to the

CC transmission compounds. The agent may be used for treating pain, where

CC the clostridial neurotoxin component is derived from botulinum toxin

CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.

CC The targeting moiety comprises a light chain and an amine end segment of

CC a heavy chain and comprises Substance P as the targeting moiety. The pain

CC alleviating effects persist for 2-6 months. The present sequence

CC represents a substance P precursor, and is used in the course of the

CC invention.

XX Sequence 13 AA;

Query Match , 100.0%; Score 61; DB 22; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00034;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11

Db 1 rpkpqffglm 11

RESULT 57

AAG62776

ID AAG62776 standard; peptide; 13 AA.

XX

AC AAG62776;

XX

DT 17-SEP-2001 (first entry)

XX

DE Amino acid sequence of carboxy-ester substance P precursor.

XX

KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 13

FT /note= "ethylated residue"

XX

PN WO200153336-A1.

XX

PD 26-JUL-2001.

XX

PF 17-JAN-2001; 2001WO-US01529.

XX

PR 19-JAN-2000; 2000US-0489667.

XX

PA (ALLR) ALLERGAN SALES INC.

XX

PI Donovan S;

XX

XX WPI; 2001-451900/48.

DR Agent useful for treating pain comprises a clostridial neurotoxin (or

PT component) attached to a targeting moiety -

XX

PS Disclosure: Page 68; 77pp; English.

XX

CC The specification describes an agent, comprising a clostridial neurotoxin

CC attached to a targeting moiety, where the targeting moiety is selected

CC from transmission compounds, and compounds substantially similar to the

CC transmission compounds. The agent may be used for treating pain, where

CC the clostridial neurotoxin component is derived from botulinum toxin

CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.

CC The targeting moiety comprises a light chain and an amine end segment of

CC a heavy chain and comprises Substance P as the targeting moiety. The pain

CC alleviating effects persist for 2-6 months. The present sequence

CC represents a substance P precursor, and is used in the course of the

CC invention.

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 61; DB 22; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00034;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11

Db 1 rpkpqffglm 11

RESULT 58

AAB98868

ID AAB98868 standard; Peptide; 13 AA.

XX

AC AAB98868;

XX

DT 14-AUG-2001 (first entry)

XX

DE Chimeric analgesic peptide #24.

XX

KW Opioid receptor binding; nociceptive receptor binding; analgesic;

XX

KW pain; chimeric peptide.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 13

FT /label= OTHER

FT /note= "C-terminal amide"

XX

PN WO200130371-A2.

XX

PD 03-MAY-2001.

XX

PF 27-OCT-2000; 2000WO-US29789.

XX

PR 28-OCT-1999; 99US-0428692.

XX

PA (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

XX

PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

XX

DR WPI; 2001-397593/42.

XX

PT New chimeric peptides used for treating pain comprise opioid receptor

PT binding group and nociceptive receptor binding group -

XX

PS Claim 10; Page 15; 34pp; English.

XX

CC The present invention describes a number of chimeric peptides comprising

CC an opioid receptor binding moiety and a nociceptive receptor binding

CC moiety. These can be used as analgesics for the treatment of pain. Unlike

CC opioid receptor based peptides alone, tolerance does not result from

CC their long-term use. The present sequence is one of the peptides of the

CC invention.

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 61; DB 22; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00034;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11

Db 1 rpkpqffglm 11

```
RESULT 59
AAB98871
ID AAB98871 standard; Peptide; 13 AA.
XX
XX AAB98871;
AC
XX 14-AUG-2001 (first entry)
XX
XX Chimeric analgesic peptide #27.
XX
XX Opioid receptor binding; nociceptive receptor binding; analgesic;
XX pain; chimeric peptide.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 13
XX /label= OTHER
XX /note= "modified by Ome"
XX
XX WO200130371-A2.
XX
XX 03-MAY-2001.
XX
XX 27-OCT-2000; 2000WO-US29789.
XX
XX 28-OCT-1999; 99US-0428692.
XX
XX (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
XX Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX WPI; 2001-397593/42.
XX
XX New chimeric peptides used for treating pain comprise opioid receptor
XX binding group and nociceptive receptor binding group
XX
XX Claim 10; Page 15; 34pp; English.
XX
XX The present invention describes a number of chimeric peptides comprising
XX an opioid receptor binding moiety and a nociceptive receptor binding
XX moiety. These can be used as analgesics for the treatment of pain. Unlike
XX opioid receptor based peptides alone, tolerance does not result from
XX their long-term use. The present sequence is one of the peptides of the
XX invention.
XX
XX Sequence 13 AA;
XX
XX Query Match 100.0%; Score 61; DB 22; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 0.00034;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RPKPQQFFGLM 11
XX |
XX Db 1 rpkpqffglm 11
XX
XX RESULT 60
XX AAB98874
XX ID AAB98874 standard; Peptide; 13 AA.
XX
XX AAB98874;
XX
XX 14-AUG-2001 (first entry)
XX
XX Chimeric analgesic peptide #30.
XX
XX Opioid receptor binding; nociceptive receptor binding; analgesic;
XX pain; chimeric peptide.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 13
XX /label= OTHER
XX /note= "modified by Ome"
XX
XX WO200130371-A2.
XX
XX 03-MAY-2001.
XX
XX 27-OCT-2000; 2000WO-US29789.
XX
XX 28-OCT-1999; 99US-0428692.
XX
XX (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
XX Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX WPI; 2001-397593/42.
XX
XX New chimeric peptides used for treating pain comprise opioid receptor
XX binding group and nociceptive receptor binding group
XX
XX Claim 10; Page 15; 34pp; English.
XX
XX The present invention describes a number of chimeric peptides comprising
XX an opioid receptor binding moiety and a nociceptive receptor binding
XX moiety. These can be used as analgesics for the treatment of pain. Unlike
XX opioid receptor based peptides alone, tolerance does not result from
XX their long-term use. The present sequence is one of the peptides of the
XX invention.
XX
XX Sequence 13 AA;
XX
XX Query Match 100.0%; Score 61; DB 22; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 0.00034;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RPKPQQFFGLM 11
XX |
XX Db 1 rpkpqffglm 11
XX
XX RESULT 60
XX AAB98874
XX ID AAB98874 standard; Peptide; 13 AA.
XX
XX AAB98874;
XX
XX 14-AUG-2001 (first entry)
XX
XX Chimeric analgesic peptide #30.
XX
XX Opioid receptor binding; nociceptive receptor binding; analgesic;
XX pain; chimeric peptide.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 13
XX /label= OTHER
XX /note= "modified by Oeth"
XX
XX WO200130371-A2.
XX
XX 03-MAY-2001.
XX
XX 27-OCT-2000; 2000WO-US29789.
XX
XX 28-OCT-1999; 99US-0428692.
XX
XX (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
XX Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX WPI; 2001-397593/42.
XX
XX New chimeric peptides used for treating pain comprise opioid receptor
XX binding group and nociceptive receptor binding group
XX
XX Claim 10; Page 15; 34pp; English.
XX
XX The present invention describes a number of chimeric peptides comprising
XX an opioid receptor binding moiety and a nociceptive receptor binding
XX moiety. These can be used as analgesics for the treatment of pain. Unlike
XX opioid receptor based peptides alone, tolerance does not result from
XX their long-term use. The present sequence is one of the peptides of the
XX invention.
XX
XX Sequence 13 AA;
XX
XX Query Match 100.0%; Score 61; DB 22; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 0.00034;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RPKPQQFFGLM 11
XX |
XX Db 1 rpkpqffglm 11
XX
XX RESULT 61
XX AAY03159
XX ID AAY03159 standard; peptide; 14 AA.
XX
XX AAY03159;
XX
XX 10-JUN-1999 (first entry)
XX
XX Substance P-Glycine-Lysine-Arginine.
XX
XX Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
XX substance P.
XX
XX Synthetic.
XX
XX US5891842-A.
XX
XX 06-APR-1999.
XX
XX 12-APR-1996; 96US-0631434.
XX
XX 09-APR-1993; 93US-0044954.
XX
XX 12-APR-1996; 96US-0631434.
XX
XX (TUFT ) TUFTS COLLEGE.
XX
XX Kream RM;
XX
XX WPI; 1999-253906/21.
XX
```

PT Synergistic method for enhancing opioid analgesia and anaesthesia
PT within a human
XX
PS Disclosure; Column 14; 20pp; English.
XX
CC This sequence represents substance P used in the method of the
CC invention. The method is for enhancing opioid analgesia within a human
CC subject for a duration of 15 minutes comprises concurrent administration
CC of substance P, or one of its precursors. The method is used to elicit
CC of opioid analgesia and anaesthesia, either prior to or after the occurrence
CC of a nociceptive event. The components have a synergistic effect. The
CC method allows use of low doses of opioid that produce little or no
CC physiological effect reducing conventional risks of toxicity and
CC addiction, and allows the use of low doses of substance P and its related
CC analogs that limit their in vivo physiological consequences. The
CC analgesia is naloxone reversible allowing diminishment or complete
CC elimination of opioid analgesia if desired and on demand. The treatment
CC provides a durable analgesic effect, but only minimally disturbs and
CC interrupts the normal metabolic processes of the body.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 61; DB 20; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGLM 11
DB 1 rpkpqffglm 11
|||||

RESULT 62
AAG62771
ID AAG62771 standard; peptide; 14 AA.
XX
AC AAG62771;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of substance P precursor.
XX
KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX
OS Unidentified.
XX
PN WO200153336-A1.
XX
PD 26-JUL-2001.
XX
PF 17-JAN-2001; 2001WO-US01529.
XX
DE Amino acid sequence of substance P precursor.
XX
KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX
OS Unidentified.
XX
PN WO200153336-A1.
XX
PD 26-JUL-2001.
XX
PF 17-JAN-2001; 2001WO-US01529.
XX
PR 19-JAN-2000; 2000US-0489667.
XX
PA (ALLR) ALLERGAN SALES INC.
XX
PI Donovan S;
XX
DR WPI; 2001-451900/48.
XX
PT 26-JUL-2001.
XX
PF 17-JAN-2001; 2001WO-US01529.
XX
PR 19-JAN-2000; 2000US-0489667.
XX
PA (ALLR) ALLERGAN SALES INC.
XX
PI Donovan S;
XX
DR WPI; 2001-451900/48.
XX
PT Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -
XX
PS Disclosure; Page 63; 77pp; English.
XX
CC The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin
CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
CC The targeting moiety comprises a light chain and an amine end segment of
CC a heavy chain and comprises Substance P as the targeting moiety. The pain
CC alleviating effects persist for 2-6 months. The present sequence
CC represents a substance P precursor, and is used in the course of the
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 61; DB 20; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGLM 11
DB 1 rpkpqffglm 11
|||||

CC alleviating effects persist for 2-6 months. The present sequence
CC represents substance P precursor, and is used in the course of the
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 61; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGLM 11
DB 1 rpkpqffglm 11
|||||

RESULT 63
AAG62774
ID AAG62774 standard; peptide; 14 AA.
XX
AC AAG62774;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of carboxy-ester substance P precursor.
XX
KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 14 /note- "methylated residue"
FT
XX
PN WO200153336-A1.
XX
PD 26-JUL-2001.
XX
PF 17-JAN-2001; 2001WO-US01529.
XX
PR 19-JAN-2000; 2000US-0489667.
XX
PA (ALLR) ALLERGAN SALES INC.
XX
PI Donovan S;
XX
DR WPI; 2001-451900/48.
XX
PT Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -
XX
PS Disclosure; Page 66; 77pp; English.
XX
CC The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin
CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
CC The targeting moiety comprises a light chain and an amine end segment of
CC a heavy chain and comprises Substance P as the targeting moiety. The pain
CC alleviating effects persist for 2-6 months. The present sequence
CC represents a substance P precursor, and is used in the course of the
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 61; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGLM 11

```
Db      1 rpkpqffgglm 11
RESULT 64
AAG62777
ID      AAG62777 standard; peptide; 14 AA.
XX
AC      AAG62777;
XX
DT      17-SEP-2001 (first entry)
XX
DE      Amino acid sequence of carboxy-ester substance P precursor.
XX
KW      Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX
OS      Synthetic.
XX
FH      Key Location/Qualifiers
FT      Modified-site 14
FT      /label= OTHER
FT      /note= "ethylated residue"
XX
PN      WO200153336-A1.
XX
PD      26-JUL-2001.
XX
PF      17-JAN-2001; 2001WO-US01529.
XX
PR      19-JAN-2000; 2000US-0489667.
XX
PA      (ALLR ) ALLERGAN SALES INC.
XX
PI      Donovan S;
XX
DR      WPI; 2001-451900/48.
XX
FT      Agent useful for treating pain comprises a clostridial neurotoxin (or
FT      component) attached to a targeting moiety -
XX
PS      Disclosure; Page 69; 77pp; English.
XX
CC      The specification describes an agent, comprising a clostridial neurotoxin
CC      attached to a targeting moiety, where the targeting moiety is selected
CC      from transmission compounds, and compounds substantially similar to the
CC      transmission compounds. The agent may be used for treating pain, where
CC      the clostridial neurotoxin component is derived from botulinum toxin
CC      selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
CC      The targeting moiety comprises a light chain and an amine end segment of
CC      a heavy chain and comprises Substance P as the targeting moiety. The pain
CC      alleviating effects persist for 2-6 months. The present sequence
CC      represents a substance P precursor, and is used in the course of the
CC      invention.
XX
SQ      Sequence 14 AA;

Query Match 100.0%; Score 61; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RPKPQQFFGLM 11
Db      1 rpkpqffgglm 11

RESULT 66
AAB98872
ID      AAB98872 standard; Peptide; 14 AA.
XX
AC      AAB98872;
XX
DT      14-AUG-2001 (first entry)
XX
DE      Chimeric analgesic peptide #28.
XX
KW      Opioid receptor binding; nociceptive receptor binding; analgesic;
KW      pain; chimeric peptide.
XX
OS      Synthetic.
XX
FH      Key Location/Qualifiers
FT      Modified-site 14
FT      /label= OTHER
FT      /note= "modified by Ome"
XX
PN      WO200130371-A2.
XX
PD      03-MAY-2001.

Query Match 100.0%; Score 61; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RPKPQQFFGLM 11
Db      1 rpkpqffgglm 11

RESULT 65
AAB98869
ID      AAB98869 standard; Peptide; 14 AA.
XX
AC      AAB98869;
XX
DT      14-AUG-2001 (first entry)
XX
```

Chimeric analgesic peptide #25.

Opioid receptor binding; nociceptive receptor binding; analgesic; pain; chimeric peptide.

Synthetic.

Key Location/Qualifiers
Modified-site 14
/label= OTHER
/note= "C-terminal amide"

WO200130371-A2.

03-MAY-2001.

27-OCT-2000; 2000WO-US29789.

28-OCT-1999; 99US-0428692.

(NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

WPI; 2001-397593/42.

New chimeric peptides used for treating pain comprise opioid receptor binding group and nociceptive receptor binding group.

Claim 10; Page 15; 34pp; English.

The present invention describes a number of chimeric peptides comprising an opioid receptor binding moiety and a nociceptive receptor binding moiety. These can be used as analgesics for the treatment of pain. Unlike opioid receptor based peptides alone, tolerance does not result from their long-term use. The present sequence is one of the peptides of the invention.

Sequence 14 AA;

Query Match 100.0%; Score 61; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
Db 1 rpkpqffgglm 11

RESULT 66
AAB98872
ID AAB98872 standard; Peptide; 14 AA.
XX
AC AAB98872;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #28.
XX
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 14
FT /label= OTHER
FT /note= "modified by Ome"
XX
PN WO200130371-A2.
XX
PD 03-MAY-2001.

Agent useful for treating pain comprises a clostridial neurotoxin (or component) attached to a targeting moiety -

Disclosure; Page 69; 77pp; English.

The specification describes an agent, comprising a clostridial neurotoxin attached to a targeting moiety, where the targeting moiety is selected from transmission compounds, and compounds substantially similar to the transmission compounds. The agent may be used for treating pain, where the clostridial neurotoxin component is derived from botulinum toxin selected from botulinum types A, B, C, D, E, F, G and mixtures of these. The targeting moiety comprises a light chain and an amine end segment of a heavy chain and comprises Substance P as the targeting moiety. The pain alleviating effects persist for 2-6 months. The present sequence represents a substance P precursor, and is used in the course of the invention.

Sequence 14 AA;

Query Match 100.0%; Score 61; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
Db 1 rpkpqffgglm 11

RESULT 65
AAB98869
ID AAB98869 standard; Peptide; 14 AA.
XX
AC AAB98869;
XX
DT 14-AUG-2001 (first entry)
XX

XX PF 27-OCT-2000; 2000WO-US29789.
XX PR 28-OCT-1999; 99US-0428692.
XX PA (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX WPI; 2001-397593/42.
DR New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group
XX Claim 10; Page 15; 34pp; English.
XX The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX SQ Sequence 14 AA;
Query Match 100.0%; Score 61; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RPKPQQFFGLM 11
DB 1 rpkpqffglm 11
RESULT 67
AAB98875
ID AAB98875 standard; Peptide; 14 AA.
XX AC AAB98875;
XX DT 14-AUG-2001 (first entry)
XX Chimeric analgesic peptide #31.
XX Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 14
FT /label= OTHER
FT /note= "modified by Oeth"
XX WO200130371-A2.
XX PD 03-MAY-2001.
XX PF 27-OCT-2000; 2000WO-US29789.
XX PR 28-OCT-1999; 99US-0428692.
XX PA (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX WPI; 2001-397593/42.
XX New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group
XX Claim 10; Page 15; 34pp; English.

XX CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX SQ Sequence 14 AA;
Query Match 100.0%; Score 61; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RPKPQQFFGLM 11
DB 1 rpkpqffglm 11
RESULT 68
AAB91440
ID AAB91440 standard; Peptide; 14 AA.
XX AC AAB91440;
XX DT 22-JUN-2001 (first entry)
XX Tachykinins peptide SEQ ID NO:616.
DE Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200069900-A2.
XX PD 23-NOV-2000.
XX PF 17-MAY-2000; 2000WO-US13576.
XX PR 17-MAY-1999; 99US-0134406.
XX PR 10-SEP-1999; 99US-0153406.
XX PR 15-OCT-1999; 99US-0159783.
XX PA (CONJ-) CONJUCHEM INC.
XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX WPI; 2001-112059/12.
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX Disclosure; Page 400; 733pp; English.
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases

CC Intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 14 AA;

Query Match 100.0%; Score 61; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
|||||
Db 1 rpkpqqffglm 11

RESULT 69
AAB06258
ID AAB06258 standard; peptide; 20 AA.

XX AC AAB06258;

DT 16-OCT-2000 (first entry)

XX DE Substance P analogue #2.

XX KW Substance P; SP; neurokinin-1 receptor; NK-1R; nociception; NTE-SAP;
KW saporin; SAP; analgesic; anti-inflammatory; neuroprotective;
KW anti-asthmatic; anti-allergic; dermatological; anti-ulcer;
KW tranquiliser; immunosuppressive; anti-migraine; cytostatic;
KW substance P antagonist; cytotoxic; ribosome inactivator;
KW prostaglandin antagonist; cancer; respiratory disease; asthma;
KW allergic rhinitis; ophthalmic disease; conjunctivitis;
KW allergic dermatitis; psoriasis; ulcerative colitis; Crohn's disease;
KW gastrointestinal disorder; anxiety; psychosis; rheumatoid arthritis;
KW carcinoma; lupus erythematosus conjunctivitis.

XX OS Synthetic.

XX FH Key Location/Qualifiers
FT Modified-site 20 /note= "C-terminal amide"

XX US6063758-A.

XX PD 16-MAY-2000.

XX PF 09-JUL-1997; 97US-0890157.

XX PR 09-JUL-1997; 97US-0890157.

XX PA (ADTA-) ADVANCED TARGETING SYSTEMS INC.

XX PI Lappi DA, Wiley RG;

XX WPI; 2000-430049/37.

XX PT New conjugates comprising substance P or its analog, and a
PT ribosome-inactivating protein (for example saporin), for alleviating
PT pain and treating disorders associated with neurokinin-1 receptor -

XX PS Claim 1; Column 2; 21pp; English.

XX CC The present sequence is an analogue of substance P (SP). SP, which binds
CC to the neurokinin-1 receptor (NK-1R), is best known for its role in
CC nociception. It is secreted by small unmyelinated C-fibres of the
CC peripheral nervous system that are thought to be primary nociceptive
CC neurons. The present sequence may be conjugated to saporin (SAP), a
CC ribosome-inactivating protein, to produce NTP-SAP. The conjugate may be
CC used to control chronic pain by specifically targeting cells having NK1
CC receptors, and inhibiting proliferation of or causing death of these
CC cells. It may also be used to treat NK-1R-associated disorders
CC including respiratory conditions (e.g. asthma, allergic rhinitis),

CC ophthalmic conditions (e.g. conjunctivitis), cutaneous conditions (e.g.
CC allergic dermatitis, psoriasis), intestinal conditions (e.g. ulcerative
CC colitis, Crohn's disease), gastrointestinal disorders, central nervous
CC system disorders (e.g. anxiety, psychosis), inflammatory diseases (e.g.
CC rheumatoid arthritis), proliferative conditions (e.g. carcinoma),
CC disorders related to immune enhancement or suppression (e.g. lupus
CC erythematosus conjunctivitis), and especially migraine.

SQ Sequence 20 AA;

Query Match 100.0%; Score 61; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
|||||
Db 10 rpkpqqffglm 20

RESULT 70

AAP70431

ID AAP70431 standard; protein; 129 AA.

XX AC AAP70431;

XX DT 17-JAN-1991 (first entry)

XX DE Human beta-preprotachykinin.

XX KW Preprotachykinin; substance P; neurokinin A; tachykinin;

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Region 20..56
FT /label=claimed polypeptide
FT Region 1..126
FT /label=claimed polypeptide
FT Region 111..126
FT /label=claimed polypeptide

XX WO8707643-A.

XX PD 17-DEC-1987.

XX PF 03-JUN-1987; 87WO-GE00382.

XX PR 03-JUN-1986; 86GB-0013431.

XX PA (RESE) RESEARCH CORPORATION LTD.

XX PI Harmar AJ, Pascall J, McKeown A;

XX WPI; 1987-362730/51.

XX DR N-PSDB; AAN70688.

XX PT New DNA sequence coding for the new polypeptide preprotachykinin -
PT a precursor for substance P, etc., useful as neurotransmitters,
PT diagnostic reagents, etc.

XX PS Claim 1; page 15; 25pp; English.

XX CC Beta-preprotachykinin includes sequences identical to tachykinins, eg
CC substance P, neurokinin A, or other biologically active peptides, eg
CC neuropeptide K. These peptides are, eg neurotransmitters, hormones,
CC analgesics and anti-inflammatories. The polypeptides can be used
CC as reagents in RIA, eg to monitor or diagnose carcinoid syndrome.

XX SQ Sequence 129 AA;

Query Match 100.0%; Score 61; DB 8; Length 129;

Best Local Similarity 100.0%; Pred. NO. 0.0031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
|||||
Db 58 rpkpqgffglm 68

RESULT 71

AAG99353
ID AAG99353 standard; Protein; 129 AA.

XX AC AAG99353;

XX 25-SEP-2001 (first entry)

DE Human atypical tachykinin protein fragment SEQ ID NO: 63.

XX KW Atypical tachykinin; ATT; human; hypertension.

XX OS Homo sapiens.

PN WO200146415-A1.

XX 28-JUN-2001.

XX PF 21-DEC-2000; 2000WO-JP09083.

XX PR 21-DEC-1999; 99JP-0362638.

XX PR 10-MAR-2000; 2000JP-0066714.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Itoh Y, Nishi K, Kitada C, Inatomi N;

XX WPI; 2001-441676/47.

XX Atypical tachykinin peptides of human origin and DNA encoding them for
screening potential agents for treatment of hypertension

PS Example 14; Page 143; 153pp; Japanese.

XX The present invention relates to atypical tachykinin proteins of human
origin and their esters, amides, salts and partial peptides. These can be
used in the treatment, prevention and diagnosis of hypertension. The
present sequence is a protein fragment described in the exemplification
of the invention.

SQ Sequence 129 AA;

Query Match 100.0%; Score 61; DB 22; Length 129;
Best Local Similarity 100.0%; Pred. NO. 0.0031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
|||||
Db 58 rpkpqgffglm 68

RESULT 72

AAW16339
ID AAW16339 standard; Protein; 401 AA.

XX AC AAW16339;

XX 05-SEP-1997 (first entry)

DE DAB389-SP-Gly fusion toxin.

XX KW DAB389-SP-Gly; amidated polypeptide binding ligand; drug delivery;
XX diphtheria toxin; substance P; cancer; therapy.

OS Synthetic.

PN WO9713410-A1.

XX 17-APR-1997.

XX 11-OCT-1996; 96WO-US16237.

PR 13-OCT-1995; 95US-0005431.

PA (BOST-) BOSTON MEDICAL CENT CORP.

PI Fisher CE, Leeman SE, Murphy JR, Vanderspek JC;

WPI; 1997-235583/21.

N-PSDB; AAF63359.

XX Hybrid molecule for targeting compound, especially a toxin, into
cells - includes polypeptide able to transport the compound across
cytoplasmic membranes and amidated ligand, useful for treatment of
cancer

PS Example 1; Page 22-23; 51pp; English.

XX DAB389-SP-Gly (AAW16339) is a hybrid toxin comprising DAB389 (i.e.
amino acids 1-386 plus His-484 and Ala-485 of mature diphtheria
toxin) fused to C-terminal glycine-extended substance P. It was
expressed in E. coli HMS174 (DE3) transformants using a vector
that carried DAB389-SP-Gly DNA (see also AAF63359). The fusion
protein was then amidated using peptidylglycine-alpha-amidating
monooxygenase. The amidated fusion protein used to target DAB389
toxin to specific cells contg. substance P receptors, esp. cancer
cells. For human IM9 (chronic myelogenous leukaemia) cells contg.
approx. 4000 substance P receptors per cell, the IC50 for amidated
DAB389-SP-Gly was 18 pM.

SQ Sequence 401 AA;

Query Match 100.0%; Score 61; DB 18; Length 401;
Best Local Similarity 100.0%; Pred. NO. 0.0092;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
|||||
Db 390 rpkpqgffglm 400

RESULT 73

AAW26510
ID AAW26510 standard; Protein; 487 AA.

XX AC AAW26510;

XX 06-JAN-1998 (first entry)

DE Amyloid precursor protein substrate APP-REP 751.

XX KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;
XX substrate; mutein; secretase; Alzheimer's disease; human;
KW APP-REP 751; pCLL621.

XX Chimeric Homo sapiens.

OS Chimeric synthetic.

XX Key Location/Qualifiers

FT Peptide 362..372

FT /label= SP

FT /note= "substance P reporter epitope"

FT Domain 389..430

FT /label= BAP

FT /note= "beta-amyloid protein"

FT Cleavage-site 404..405

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FT FT /note= "secretase cleavage site"
FT FT 417..440
FT FT /label= Transmembrane
XX
PN US5656477-A.
XX
PD 12-AUG-1997.
XX
PF 01-MAY-1992; 92US-0877675.
XX
PR 20-SEP-1993; 93US-0123659.
PR 01-MAY-1992; 92US-0877675.
XX
PA (AMCY ) AMERICAN CYANAMID CO.
XX
PI Jacobsen JS, Vitek MP;
XX
DR WPI; 1997-414594/38.
DR P-PSDB; AAT87083.
XX
PT Nucleic acid encoding amyloid precursor mutin(s) - comprising
PT reporter gene and coding sequence, for identifying compounds which
PT modify the activity of proteolytic enzymes which cleave APP
XX
PS Disclosure; Fig 8; 84pp; English.
XX
CC This polypeptide, designated APP-REP 761, comprises an amyloid
CC precursor protein (APP) that has a 276-amino acid deletion of the
CC native APP and which carries a Substance P epitope markers placed
CC N-terminal to the beta-amyloid protein (BAP) domain. APP-REP 751
CC can be used in a claimed method for screening for a compound which
CC reduces the formation of beta-amyloid protein, determined by
CC measuring the amount of marker in a medium containing transfected
CC cells. The method is used to detect compounds which inhibit the
CC activity of proteolytic enzymes which cleave APP to generate BAP
CC fragments. Such compounds can be used in the treatment of e.g.
CC Alzheimer's disease. The deletion of a 276 amino acid portion of
CC APP distinguishes the construct from endogenously expressed APP,
CC and beneficially increases the resolution of APP-REP fragments
CC resulting from the proteolytic cleavage by secretase or other
CC amyloidogenic, BAP-generating cleavage events.
XX
SQ Sequence 487 AA;

Query Match 100.0%; Score 61; DB 18; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
DB 362 rpkpqffglm 372
|||||

RESULT 74
AAW26394
ID AAW26394 standard; Protein; 487 AA.
XX
AC AAW26394;
XX
DT 15-DEC-1997 (first entry)
XX
DE Amyloid precursor protein substrate APP-REP 751.
XX
KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KW substrate; mutin; secretase; Alzheimer's disease; human;
KW APP-REP 751; pCLL621.
XX
OS Chimeric Homo sapiens;
OS Chimeric synthetic.
XX
PH Key Location/Qualifiers
FT Peptide 362..372

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FT FT /label= SP
FT FT /note= "substance P reporter epitope"
FT FT 389..430
FT FT /label= BAP
FT FT /note= "Beta-amyloid protein"
FT FT 404..405
FT FT /note= "secretase cleavage site"
FT FT 417..440
FT FT /label= Transmembrane
XX
PN US5652092-A.
XX
PD 29-JUL-1997.
XX
PF 01-MAY-1992; 92US-0877675.
XX
PR 20-SEP-1993; 93US-0123659.
PR 01-MAY-1992; 92US-0877675.
PR 05-JUN-1995; 95US-0462859.
XX
PA (AMCY ) AMERICAN CYANAMID CO.
XX
PI Jacobsen JS, Vitek MP;
XX
DR WPI; 1997-392937/36.
DR N-PSDB; AAT84562.
XX
CC Screening for compounds which reduce beta-amyloid protein formation
CC - using cells which express a construct encoding a marker and an
CC amyloid precursor mutin derived from APP isoforms
XX
PS Disclosure; Fig 8; 84pp; English.
XX
CC This polypeptide, designated APP-REP 761, comprises an amyloid
CC precursor protein (APP) that has a 276-amino acid deletion of the
CC native APP and which carries a Substance P epitope markers placed
CC N-terminal to the beta-amyloid protein (BAP) domain. APP-REP 751
CC can be used in a claimed method for screening for a compound which
CC reduces the formation of beta-amyloid protein, determined by
CC measuring the amount of marker in a medium containing transfected
CC cells. The method is used to detect compounds which inhibit the
CC activity of proteolytic enzymes which cleave APP to generate BAP
CC fragments. Such compounds can be used in the treatment of e.g.
CC Alzheimer's disease. The deletion of a 276 amino acid portion of
CC APP distinguishes the construct from endogenously expressed APP,
CC and beneficially increases the resolution of APP-REP fragments
CC resulting from the proteolytic cleavage by secretase or other
CC amyloidogenic, BAP-generating cleavage events.
XX
SQ Sequence 487 AA;

Query Match 100.0%; Score 61; DB 18; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
DB 362 rpkpqffglm 372
|||||

RESULT 75
AAW44745
ID AAW44745 standard; Protein; 487 AA.
XX
AC AAW44745;
XX
DT 01-JUN-1998 (first entry)
XX
DE APP-REP 751 protein from pCLL621.
XX
KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;

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KW Alzheimer's disease; cleavage.

XX Homo sapiens.

OS Synthetic.

PN US5693478-A.

XX 02-DEC-1997.

PD 05-JUN-1995; 95US-0464247.

XX 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

XX 05-JUN-1995; 95US-0464247.

PA (AMCY) AMERICAN CYANAMID CO.

PI Jacobsen JS, Vitek MP;

XX N-PSDB; AAV05850.

PT Amyloid precursor muterin reporter molecule assay containing antibody

PT recognised marker - used to study pathways associated with

PT Alzheimer's disease

XX Disclosure; Fig 8; 84pp; English.

XX This is the amino acid sequence of a novel amyloid precursor protein
CC (APP) designated APP-REP 751, contained in construct pCLL621. The
CC sequence comprises a mutant version of the APP 751 isoform of human APP
CC which contains a deletion of 276 amino acids from the central region.
CC The deleted region is replaced by a substrate P reporter epitope
CC sequence (RPKPQQFFGLM). In contrast to the APP-REP 751 encoded by the
CC construct pCLL602 (AAW44744), this sequence does not contain a
CC Met-enkephalin reporter epitope (YGGFM) fused at the C-terminus of the
CC coding sequence. The shorter protein is generated for ease of detection
CC based on size difference with the wild type APP protein and also by
CC detection of the reporter epitopes. The mutant protein can be used in a
CC method to study secretase and beta-amyloid protein (BAP)-generating
CC pathways associated with Alzheimer's disease by studying proteolytic
CC cleavage of the reporter polypeptides.

XX Sequence 487 AA;

Query Match 100.0%; Score 61; DB 19; Length 487;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11

Db 362 rpkpqqffglm 372

RESULT 76

AAW42979

ID AAW42979 standard; Protein; 487 AA.

XX AAW42979;

XX 01-MAY-1998 (first entry)

DE Amyloid precursor protein mutant APP-ARP 751.

XX Beta-amyloid peptide; BAP; extracellular BAP plaque;
KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;
KW amyloid precursor protein; APP; secretase; BAP aggregation;
KW abnormal proteolytic cleavage.

XX Synthetic.

OS Homo sapiens.

PN US5703209-A.

XX 30-DEC-1997.

XX 05-JUN-1995; 95US-0464248.

XX 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobsen JS, Vitek MP;

XX WPI; 1998-076482/07.

DR N-PSDB; AAV04866.

XX Amyloid precursor protein fusion polypeptides - comprising APP

PT fragment and marker, useful for research and drug screening

PS Disclosure; Fig 8A-Q; 84pp; English.

XX The present sequence represents an amyloid precursor protein (APP),
CC which has a deletion of 276 amino acids to within 15 amino acids of the
CC beta-amyloid peptide (BAP) domain. The protein also contains the Abnormal
CC accumulation of extracellular BAP in plaques and cerebrovascular deposits
CC is characteristic in brains of individuals suffering from Alzheimers
CC disease and Downs syndrome. BAP is a poorly soluble, self-aggregating
CC protein which is derived from a larger amyloid precursor protein (APP).
CC APP is expressed as an integral membrane protein, and is cleaved by
CC secretase, between BAP 16lys and 17leu. Cleavage at this site precludes
CC amyloidogenesis and results in the release of the amino-terminal APP
CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and
CC APP-770. These isoforms are derived by alternative splicing. APP-RRP 751
CC is constructed by ligating restriction fragments representing N- and
CC C-terminal APP-751 cDNA and substrate P reporter epitope sequences.
CC APP can be used as a substrate for studying abnormal proteolytic cleavage
CC which results in the release of BAP, and also to screen for drugs that
CC will inhibit such cleavage.

XX Sequence 487 AA;

Query Match 100.0%; Score 61; DB 19; Length 487;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11

Db 362 rpkpqqffglm 372

RESULT 77

AAW45229

ID AAR45229 standard; Protein; 492 AA.

XX AAR45229;

XX 20-JUN-1994 (first entry)

DE APP-REP 751 amyloid precursor protein/reporter protein.

XX Amyloid precursor protein; APP; beta amyloid protein; BAP;

XX detection; Alzheimer's disease; Down's syndrome.

XX Homo sapiens.

XX AU9338358-A.

XX 04-NOV-1993.

XX 03-MAY-1993; 93AU-0038358.

XX 01-MAY-1992; 92US-0877675.

PR

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XX PA (AMCY ) AMERICAN CYANAMID CO.
XX PI Jacobsen JS, Vitek MP;
XX DR WPI; 1993-406194/51.
XX DR N-PSDB; AAQ54257.
XX PT New mutant forms of amyloid precursor protein - for detecting
XX PT cpds. that modify activity of enzymes involved in precursor
XX PT cleavage, also new nucleic acid encoding them
XX PS Claim 5; Figure 7; 66pp; English.
XX CC This mutant form of amyloid precursor protein comprises from the 5'
XX CC to the 3' end a sequence encoding a marker and either (1) a
XX CC sequence encoding the N-terminus of an amyloid precursor protein
XX CC (APP) up to, but not including, the nucleotides encoding the beta
XX CC amyloid protein (BAP) domain or (2) the BAP domain. Recombinant
XX CC polypeptides generated from this proteins coding sequence can be
XX CC used to detect drugs or compounds that inhibit/augment the
XX CC activity of proteolytic enzymes which cleave APP to generate BAP
XX CC fragments (deposition of which occurs in patients with Alzheimers
XX CC disease and Down's syndrome).
XX SQ Sequence 492 AA;

Query Match 100.0%; Score 61; DB 14; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQPFGLM 11
DB 362 rpkpqffg1m 372

RESULT 78
AAW26509
ID AAW26509 standard; Protein; 492 AA.
XX AC AAW26509;
XX DT 06-JAN-1998 (first entry)
XX DE Amyloid precursor protein substrate APP-REP 751.
XX KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;
XX KW substrate; muten; secretase; Alzheimer's disease; human;
XX KW APP-REP 751; pCLL602.
XX OS Chimeric Homo sapiens.
XX OS Chimeric synthetic.
XX FH Key Location/Qualifiers
XX FT Peptide 362..372
XX FT /label= SP
XX FT /note= "substance P reporter epitope"
XX FT Domain 389..430
XX FT /label= BAP
XX FT /note= "beta-amyloid protein"
XX FT Cleavage-site 404..405
XX FT /note= "secretase cleavage site"
XX FT Domain 417..440
XX FT /label= Transmembrane
XX FT Peptide 488..492
XX FT /label= ME
XX FT /note= "Met-enkephalin reporter epitope"
XX PN US5656477-A.
XX PD 12-AUG-1997.
XX

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PF 01-MAY-1992; 92US-0877675.
XX 20-SEP-1993; 93US-0123659.
PR 01-MAY-1992; 92US-0877675.
XX (AMCY ) AMERICAN CYANAMID CO.
XX Jacobsen JS, Vitek MP;
XX WPI; 1997-414594/38.
DR P-PSDB; AAT87083.
XX Nucleic acid encoding amyloid precursor muten(s) - comprising
XX reporter gene and coding sequence, for identifying compounds which
XX modify the activity of proteolytic enzymes which cleave APP
XX Disclosure; Fig 7; 84pp; English.
XX This polypeptide, designated APP-REP 761, comprises an amyloid
XX precursor protein (APP) that has a 276-amino acid deletion of the
XX native APP and which carries Substance P and Met-enkephalin epitope
XX markers placed, respectively, on the N-terminal and C-terminal
XX sites of the beta-amyloid protein (BAP) domain. APP-REP 751 can
XX be used in a claimed method for screening for a compound which
XX reduces the formation of beta-amyloid protein, determined by
XX measuring the amount of marker in a medium containing transfected
XX cells. The method is used to detect compounds which inhibit the
XX activity of proteolytic enzymes which cleave APP to generate BAP
XX fragments. Such compounds can be used in the treatment of e.g.
XX Alzheimer's disease. The deletion of a 276 amino acid portion of
XX APP distinguishes the construct from endogenously expressed APP,
XX and beneficially increases the resolution of APP-REP fragments
XX resulting from the proteolytic cleavage by secretase or other
XX amyloidogenic, BAP-generating cleavage events.
XX SQ Sequence 492 AA;

Query Match 100.0%; Score 61; DB 18; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQPFGLM 11
DB 362 rpkpqffg1m 372

RESULT 79
AAW26393
ID AAW26393 standard; Protein; 492 AA.
XX AC AAW26393;
XX DT 15-DEC-1997 (first entry)
XX DE Amyloid precursor protein substrate APP-REP 751.
XX KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;
XX KW substrate; muten; secretase; Alzheimer's disease; human;
XX KW APP-REP 751; pCLL602.
XX OS Chimeric Homo sapiens.
XX OS Chimeric synthetic.
XX FH Key Location/Qualifiers
XX FT Peptide 362..372
XX FT /label= SP
XX FT /note= "substance P reporter epitope"
XX FT Domain 389..430
XX FT /label= BAP
XX FT /note= "beta-amyloid protein"
XX FT Cleavage-site 404..405
XX FT /note= "secretase cleavage site"

```

FT Domain 417..440
 FT /label= Transmembrane
 FT Peptide 488..492
 FT /label= ME
 FT /note= "Met-enkephalin reporter epitope"
 XX
 PN US5652092-A.
 XX
 XX 29-JUL-1997.
 XX
 XX 01-MAY-1992; 92US-0877675.
 XX
 XX 20-SEP-1993; 93US-0123659.
 XX 01-MAY-1992; 92US-0877675.
 XX 05-JUN-1995; 95US-0462859.
 XX
 XX (AMCY) AMERICAN CYANAMID CO.
 XX
 XX Jacobsen JS, Vitek MP;
 XX WPI: 1997-392937/36.
 XX N-PSDB; AAT84561.
 XX
 PS Screening for compounds which reduce beta-amyloid protein formation
 PT - using cells which express a construct encoding a marker and an
 PT amyloid precursor mutin derived from APP isoforms
 XX
 PS Disclosure; Fig 7; 84pp; English.
 XX
 CC This polypeptide, designated APP-REP 761, comprises an amyloid
 CC precursor protein (APP) that has a 276-amino acid deletion of the
 CC native APP and which carries Substance P and Met-enkephalin epitope
 CC markers placed, respectively, on the N-terminal and C-terminal
 CC sites of the beta-amyloid protein (BAP) domain. APP-REP 751 can
 CC be used in a claimed method for screening for a compound which
 CC reduces the formation of beta-amyloid protein, determined by
 CC measuring the amount of marker in a medium containing transfected
 CC cells. The method is used to detect compounds which inhibit the
 CC activity of proteolytic enzymes which cleave APP to generate BAP
 CC fragments. Such compounds can be used in the treatment of e.g.
 CC Alzheimer's disease. The deletion of a 276 amino acid portion of
 CC APP distinguishes the construct from endogenously expressed APP,
 CC and beneficially increases the resolution of APP-REP fragments
 CC resulting from the proteolytic cleavage by secretase or other
 CC amyloidogenic, BAP-generating cleavage events.
 XX
 XX Sequence 492 AA;
 SQ
 Query Match 100.0%; Score 61; DB 18; Length 492;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RPKPQQFFGLM 11
 Db 362 rpkpqffgglm 372
 RESULT 80
 AAW4744
 ID AAW4744 standard; Protein; 492 AA.
 XX
 XX AAW4744;
 XX
 DT 01-JUN-1998 (first entry)
 XX
 DE APP-REP 751 protein from pCLL602.
 XX
 KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
 KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
 KW Alzheimer's disease; cleavage.
 XX
 OS Homo sapiens.

OS Synthetic.
 XX
 PN US5693478-A.
 XX
 XX 02-DEC-1997.
 PD
 XX
 XX 05-JUN-1995; 95US-0464247.
 XX
 XX 20-SEP-1993; 93US-0123659.
 XX 01-MAY-1992; 92US-0877675.
 XX 05-JUN-1995; 95US-0464247.
 XX
 XX (AMCY) AMERICAN CYANAMID CO.
 XX
 XX Jacobsen JS, Vitek MP;
 XX WPI: 1998-031744/03.
 XX N-PSDB; AAV05849.
 XX
 PS Amyloid precursor mutin reporter molecule assay containing antibody
 PT recognised marker - used to study pathways associated with
 PT Alzheimer's disease
 XX
 PS Disclosure; Fig 7; 84pp; English.
 XX
 CC This is the amino acid sequence of a novel amyloid precursor protein
 CC (APP) designated APP-REP 751, contained in construct pCLL602. The
 CC sequence comprises a mutant version of the APP 751 isoform of human APP
 CC which contains a deletion of 276 amino acids from the central region.
 CC The deleted region is replaced by a substrate P reporter epitope sequence
 CC (RPKPPQFFGLM) and a Met-enkephalin reporter epitope (YGGFM) is fused at
 CC the C-terminus. The shorter protein is generated for ease of detection
 CC based on size difference with the wild type APP protein and also by
 CC detection of the reporter epitopes. The mutant protein can be used in
 CC a method to study secretase and beta-amyloid protein (BAP)-generating
 CC pathways associated with Alzheimer's disease by studying proteolytic
 CC cleavage of the reporter polypeptides.
 XX
 XX Sequence 492 AA;
 SQ
 Query Match 100.0%; Score 61; DB 19; Length 492;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RPKPQQFFGLM 11
 Db 362 rpkpqffgglm 372
 RESULT 81
 AAW42978
 ID AAW42978 standard; Protein; 492 AA.
 XX
 XX AAW42978;
 XX
 DT 01-MAY-1998 (first entry)
 XX
 DE Amyloid precursor protein mutant APP-APP 751.
 XX
 KW Beta-amyloid peptide; BAP; extracellular BAP plaque;
 KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;
 KW amyloid precursor protein; APP; secretase; BAP aggregation;
 KW abnormal proteolytic cleavage.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Protein 1..487
 FT /note= "APP-APP 751"
 FT Peptide 488..492
 FT /note= "Met-enkephalin reporter epitope"

XX PN US5703209-A.
XX PD 30-DEC-1997.
XX PF 05-JUN-1995; 95US-0464248.
XX PR 20-SEP-1993; 93US-0123659.
XX PR 01-MAY-1992; 92US-0877675.
XX PA (AMCY) AMERICAN CYANAMID CO.
XX PI Jacobsen JS, Vitek MP;
XX DR WPI: 1998-076482/07.
XX DR N-PSDB; AAV04865.
XX PT Amyloid precursor protein fusion polypeptides - comprising APP
XX PT fragment and marker, useful for research and drug screening
XX PS Disclosure; Fig 7A-Q; 84pp; English.
XX CC The present sequence represents an amyloid precursor protein (APP),
XX CC which has a deletion of 276 amino acids to within 15 amino acids of the
XX CC beta-amyloid peptide (BAP) domain. The protein also contains the
XX CC Met-enkephalin reporter epitope at the carboxy terminus. Abnormal
XX CC accumulation of extracellular BAP in plaques and cerebrovascular deposits
XX CC is characteristic in brains of individuals suffering from Alzheimers
XX CC disease and Downs syndrome. BAP is a poorly soluble, self-aggregating
XX CC protein which is derived from a larger amyloid precursor protein (APP).
XX CC APP is expressed as an integral membrane protein, and is cleaved by
XX CC secretase, between BAP 16lys and 17Leu. Cleavage at this site precludes
XX CC amyloidogenesis and results in the release of the amino-terminal APP
XX CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and
XX CC APP-770. These isoforms are derived by alternative splicing. APP-RRP 751
XX CC is constructed by ligating restriction fragments representing N- and
XX CC C-terminal APP-751 cDNA and substrate P reporter epitope sequences.
XX CC APP can be used as a substrate for studying abnormal proteolytic cleavage
XX CC which results in the release of BAP, and also to screen for drugs that
XX CC will inhibit such cleavage.
SQ Sequence 492 AA;

Query Match 100.0%; Score 61; DB 19; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
Db 362 rpkpqgffglm 372
|||||

RESULT 82
AAR21934
ID AAR21934 standard; Protein; 11 AA.
XX AC AAR21934;
XX DT 25-JUN-1992 (first entry)
XX DE Substance P [Tyr7] and fragment (7-11) [Tyr 7].
XX KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX KW syndrome; hereditary cerebral haemorrhage.
XX OS Synthetic.
XX PN WO9202248-A.
XX PD 20-FEB-1992.
XX PF 29-JUL-1991; 91WO-US05323.
XX PR 27-JUL-1990; 90US-0559173.
XX PA (CHIL-) CHILDRENS MED CENT.
XX PI Yankner BA;
XX DR WPI: 1992-079804/10.

XX PR 27-JUL-1990; 90US-0559173.
XX PA (CHIL-) CHILDRENS MED CENT.
XX PI Yankner BA;
XX DR WPI: 1992-079804/10.
XX PT Treatment of neuronal accumulation of beta-amyloid - using
XX PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX PS Claim 10; Page 21; 35pp; English.
XX CC The peptide is the tachykinin agonist substance P with a Tyr
XX CC residue substituted at position 7. The peptide was synthesised
XX CC by standard solid phase synthesis. A N-terminal deleted peptide
XX CC (7-11) with the Tyr substitution was also synthesised. Neuronal
XX CC accumulation of beta-amyloid may be treated by administration
XX CC of tachykinin agonists. The peptides can reduce the neurotoxic
XX CC effects of a beta-amyloid related polypeptide on cultured neurons.
XX CC The peptide and its analogues are useful for controlling diseases
XX CC characterised by beta amyloid accumulation in the brain such as
XX CC Alzheimer's disease and Down's syndrome.
XX CC See also AAR21932-75.
SQ Sequence 11 AA;

Query Match 95.1%; Score 58; DB 13; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00095;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
Db 1 rpkpqgffglm 11
|||||

RESULT 83
AAR21937
ID AAR21937 standard; Protein; 11 AA.
XX AC AAR21937;
XX DT 25-JUN-1992 (first entry)
XX DE Substance P or (7-11) [Norleucine 11].
XX KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX KW syndrome; hereditary cerebral haemorrhage.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 11 /label= OTHER
XX FT /note= "OTHER = Nle"
XX PN WO9202248-A.
XX PD 20-FEB-1992.
XX PF 29-JUL-1991; 91WO-US05323.
XX PR 27-JUL-1990; 90US-0559173.
XX PA (CHIL-) CHILDRENS MED CENT.
XX PI Yankner BA;
XX DR WPI: 1992-079804/10.

PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
PS Claim 10; Page 21; 35pp; English.

XX The peptide is the tachykinin agonist substance P with a Norleucine
CC residue substituted at position 11. The peptide was synthesised
CC by standard solid phase synthesis. An N-terminal deleted peptide
CC (7-11) with the same substitution was also synthesised. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptides can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
SQ Sequence 11 AA;

Query Match 95.1%; Score 58; DB 13; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00095;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
| | | | | | | | | |
DB 1 rpkpqffgl 11

RESULT 84

AAR21951
ID AAR21951 standard; Peptide; 11 AA.

XX
AC AAR21951;

XX 25-JUN-1992 (first entry)

XX Substance P [Glu 3].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHTL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
PS Claim 10; Page 21; 35pp; English.

XX The peptide is the tachykinin agonist substance P with a glutamic
CC acid residue substituted at position 5. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as

CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.

SQ Sequence 11 AA;

Query Match 95.1%; Score 58; DB 13; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00095;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
| | | | | | | | | |
DB 1 rpkpqffglm 11

RESULT 85

AAR28445
ID AAR28445 standard; peptide; 11 AA.

XX
AC AAR28445;

XX 22-MAR-1993 (first entry)

XX Neurokinine 1 ligand #3.

XX NK1 receptor; tumour; malignant glioma; pheochromocytoma;
KW paraganglia; small cell lung cancer; nerve regeneration; lymphoma;
KW granuloma; Crohn's disease.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 11

FT /note= "amidated"

XX WO9218536-A.

XX 29-OCT-1992.

XX 22-APR-1992; 92WO-US03307.

XX 22-APR-1991; 91EP-0200955.

XX (MLCW) MALLINCKRODT MEDICAL INC.

XX Bakker WH, Hagen PM, Krenning EP, Lamberts SWJ, Visser TJ;

XX WPI; 1992-382047/46.

XX Detection and localisation of tissues with neurokinine-1 receptors
PT - for detecting and treating tumours having neurokinine-1
PT receptors e.g. malignant glioma, small cell lung cancer etc.

XX Disclosure; Page 4; 22pp; English.

XX This peptide or its Tyr0 deriv. is a preferred peptide having a
CC selective affinity to neurokinine-1 receptors which (when
CC labelled with a radioactive isotope) can be used in imaging methods.
CC A generic formula for preferred peptides is AAR28441. Such peptides
CC are thus useful in diagnosis and treatment of conditions that are
CC related to NK1 receptors and in visualising NK1 receptors on certain
CC tissues. See AAR28442-R28446.

SQ Sequence 11 AA;

Query Match 95.1%; Score 58; DB 13; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00095;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
| | | | | | | | | |
DB 1 rpkpqffglm 11

competitive inhibitor; receptor; neurogenic inflammation;
rheumatoid arthritis; ulcerative colitis; eczema; Crohn's disease;
anti-proliferative agent; small cell lung carcinoma; fibroblast.

RESULT 86
AAR42649

ID AAR42649 standard; peptide; 11 AA.
AC AAR42649;
DT 19-APR-1994 (first entry)
XX Neurokinin 1 receptor affinity-contg. peptide.

DE Neurokinin 1; somatostatin; receptor; cytokine; growth factor;
KW hormone; intra-operative; tumour; low energy gamma photon;
KW radionuclide.

XX Synthetic.
XX Key Location/Qualifiers
FT Modified-site 11
FT /note= "the C-terminal is amidated"

PN W09318797-A.

XX 30-SEP-1993.

XX 24-MAR-1993; 93WO-US02772.

XX 25-MAR-1992; 92EP-0200848.

XX (MLCW) MALLINCKRODT MEDICAL INC.

XX Doedens BJ, Ensing GJ, Panek KJ;

XX WPI; 1993-320461/40.

XX Intra-operatively detecting and locating tumour tissues - using
PT specific peptide(s) labelled with low energy gamma photon
PT emitting radionuclide

XX Disclosure; Page 5; 31pp; English.

XX The method of intraoperatively detecting and locating tumoral
CC tissues makes use of peptides having selective neurokinin 1
CC receptor affinity (AAR42644; generic formula; AAR42646-R42650;
CC specific examples), peptides having selective somatostatin
CC receptor affinity (AAR42645; generic formula; AAR42651-R42660;
CC specific examples), and peptides selected from cytokines,
CC growth factors and hormones.

XX Sequence 11 AA;

Query Match 95.1%; Score 58; DB 14; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00095;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RPKPQQFFGLM 11

Db 1 rpkpqfryglm 11

RESULT 87

AAW09003

ID AAW09003 standard; peptide; 11 AA.

AC AAW09003;

DT 03-MAR-1997 (first entry)

XX Substance P analogue, acts as substance P antagonist.

XX Analogue; substance P; spantide; non-peptide bond;

OS Synthetic.
XX Key Location/Qualifiers
FT Modified-site 6..7
FT /label= Gln-psi(CH2-NH)-Phe
FT /note= "Opt. non-peptide linkage"

FT Modified-site 7..8
FT /label= Phe-psi(CH2-NH)-Phe

FT Modified-site 8..9
FT /note= "Opt. non-peptide linkage"

FT Modified-site 9..10
FT /label= Phe-psi(CH2-NH)-Gly

FT Modified-site 11
FT /note= "Position of claimed non-peptide linkage"

FT /note= "Amidated C-terminal"

XX US5410019-A.

XX 25-APR-1995.

XX 24-SEP-1987; 87US-0100571.

XX 30-MAR-1992; 92US-0860675.

XX 24-SEP-1987; 87US-0100571.

XX 25-MAR-1988; 88US-0173311.

XX 08-JUN-1988; 88US-0204171.

XX 16-JUN-1988; 88US-0207759.

XX 23-SEP-1988; 88US-0248771.

XX 14-OCT-1988; 88US-0257998.

XX 09-DEC-1988; 88US-0282328.

XX 02-MAR-1989; 89US-0317941.

XX 16-AUG-1989; 89US-0394727.

XX (TULA) TULANE EDUCATIONAL FUND.

XX Coy DH, Moreau J;

XX WPI; 1995-169633/22.

XX Novel linear peptide substance P analogues - useful as substance P
PT antagonists, for treating neurogenic inflammation

XX Claim 3; Column 19; 16pp; English.

XX The sequences given in AAW09003-04 represent analogues of substance P
CC and spantide, respectively. These analogues comprise a non-peptide
CC bond between an amino acid residue of the active site, which occurs
CC in the C-terminal half of the peptide, and an adjacent amino acid
CC residue. They act as competitive inhibitors of the naturally
CC occurring peptide by binding to its receptor. These peptides may be
CC used in the treatment of diseases involving neurogenic inflammation,
CC e.g. rheumatoid arthritis, ulcerative colitis, eczema and Crohn's
CC disease. They are also useful as anti-proliferative agents, in
CC the treatment of small cell lung carcinoma or disorders involving the
CC proliferation of fibroblasts.

XX Sequence 11 AA;

Query Match 95.1%; Score 58; DB 16; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.00095;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RPKPQQFFGLM 11

Db 1 rpkpqgffgl 11
|||||

RESULT 88
AAW33181
ID AAW33181 standard; peptide; 11 AA.

AC AAW33181;

XX 29-JAN-1998 (first entry)

XX Mono-DTPA-Lys1 Substance P.

XX Substance P; radiolabel; diagnostic imaging; therapy;

XX mono-DTPA-Lys1.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT Modified-site /note= "DTPA-Lys"

FT Modified-site 11

FT Modified-site /note= "amidated"

XX WO9640292-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US09706.

XX 07-JUN-1995; 95US-0480372.

XX (MLCW) MALLINCKRODT MEDICAL INC.

XX Srinivasan A;

XX WPI; 1997-087027/08.

XX Prepn. of pure radio-labelled peptide, e.g. for diagnostic imaging -

XX by combining protected poly(amino:carboxylate) ligand with peptide

XX and forming complex with radionuclide

XX Example 4; Page 12; 20pp; English.

XX Preparing a radiolabelled peptide composition, comprises combining

XX a triamine or diamine chelating agent with a peptide, e.g. the

XX present peptide, in a solid phase peptide synthesiser, and

XX complexing a radionuclide with the chelate-peptide conjugate.

XX Radiolabelled peptides or peptidomimetics can be used as diagnostic

XX imaging agents, or in therapeutic applications, e.g. iodine(111)

XX labelled pentaerythritol can be used for somatostatin receptor

XX imaging of neuroendocrine tumours. The radiolabelled products are

XX obtained efficiently and inexpensively in high purity. The

XX protected polyaminocarboxylate ligands can be added to the peptide

XX by standard solution or solid phase peptide synthesis and

XX deprotected with conventional reagents to give only the

XX mono-addition product, free of di-addition product impurities. The

XX deprotected product can be labelled with medically useful

XX radionuclides, e.g. lanthanides or actinides, at any desired

Db 1 rpkpqgffgl 11
|||||

RESULT 88
AAW33181
ID AAW33181 standard; peptide; 11 AA.

AC AAW33181;

XX 29-JAN-1998 (first entry)

XX Mono-DTPA-Lys1 Substance P.

XX Substance P; radiolabel; diagnostic imaging; therapy;

XX mono-DTPA-Lys1.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT Modified-site /note= "DTPA-Lys"

FT Modified-site 11

FT Modified-site /note= "amidated"

XX WO9640292-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US09706.

XX 07-JUN-1995; 95US-0480372.

XX (MLCW) MALLINCKRODT MEDICAL INC.

XX Srinivasan A;

XX WPI; 1997-087027/08.

XX Prepn. of pure radio-labelled peptide, e.g. for diagnostic imaging -

XX by combining protected poly(amino:carboxylate) ligand with peptide

XX and forming complex with radionuclide

XX Example 4; Page 12; 20pp; English.

XX Preparing a radiolabelled peptide composition, comprises combining

XX a triamine or diamine chelating agent with a peptide, e.g. the

XX present peptide, in a solid phase peptide synthesiser, and

XX complexing a radionuclide with the chelate-peptide conjugate.

XX Radiolabelled peptides or peptidomimetics can be used as diagnostic

XX imaging agents, or in therapeutic applications, e.g. iodine(111)

XX labelled pentaerythritol can be used for somatostatin receptor

XX imaging of neuroendocrine tumours. The radiolabelled products are

XX obtained efficiently and inexpensively in high purity. The

XX protected polyaminocarboxylate ligands can be added to the peptide

XX by standard solution or solid phase peptide synthesis and

XX deprotected with conventional reagents to give only the

XX mono-addition product, free of di-addition product impurities. The

XX deprotected product can be labelled with medically useful

XX radionuclides, e.g. lanthanides or actinides, at any desired

Db 1 rpkpqgffgl 11
|||||

RESULT 89
AAW79775
ID AAW79775 standard; peptide; 11 AA.

AC AAW79775;

XX 07-JAN-1999 (first entry)

XX Substance P.

XX Tachykinin; neurokinin; NK1; receptor; antagonist; cystic fibrosis;

XX Substance P.

XX Mammalia.

XX US5830854-A.

XX 03-NOV-1998.

XX 14-DEC-1993; 93US-0166437.

XX 14-DEC-1992; 92GB-0026056.

XX 14-DEC-1992; 92GB-0026047.

XX (MERI) MERCK SHARP & DOHME LTD.

XX Hargreaves RJ;

XX WPI; 1998-609287/51.

XX Treatment of cystic fibrosis - comprises administration of

XX tachykinin receptor antagonist which is a neurokinin-1 receptor

XX antagonist

XX Disclosure; Column 1; 12pp; English.

XX The invention relates to the new use of tachykinin receptor antagonists

XX (particularly NK1 receptor antagonists) for the treatment of cystic

XX fibrosis. The present sequence is that of Substance P, one of three

XX known mammalian tachykinins.

XX Sequence 11 AA;

XX Query Match 95.1%; Score 58; DB 19; Length 11.

XX Best Local Similarity 90.9%; Pred. No. 0.00095;

XX Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11

DB 1 rpkpqgffgl 11

|||||

RESULT 90

AAW99689

ID AAW99689 standard; peptide; 11 AA.

XX AAW99689;

XX 03-JUN-1999 (first entry)

XX Substance P analogue #6.

XX Substance P receptor antagonist; analgesic; inhibitor; NMDA blocker;

XX nontoxic N-methyl-D-aspartate receptor antagonist; muscular pain;

Db 1 rpkpqgffgl 11
|||||

Query Match 95.1%; Score 58; DB 18; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.00095;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11

DB 1 rpkpqgffgl 11

|||||

Key Location/Qualifiers

FT Modified-site 1

FT Modified-site /note= "DTPA-Lys"

FT Modified-site 11

FT Modified-site /note= "amidated"

XX WO9640292-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US09706.

XX 07-JUN-1995; 95US-0480372.

XX (MLCW) MALLINCKRODT MEDICAL INC.

XX Srinivasan A;

XX WPI; 1997-087027/08.

XX Prepn. of pure radio-labelled peptide, e.g. for diagnostic imaging -

XX by combining protected poly(amino:carboxylate) ligand with peptide

XX and forming complex with radionuclide

XX Example 4; Page 12; 20pp; English.

XX Preparing a radiolabelled peptide composition, comprises combining

XX a triamine or diamine chelating agent with a peptide, e.g. the

XX present peptide, in a solid phase peptide synthesiser, and

XX complexing a radionuclide with the chelate-peptide conjugate.

XX Radiolabelled peptides or peptidomimetics can be used as diagnostic

XX imaging agents, or in therapeutic applications, e.g. iodine(111)

XX labelled pentaerythritol can be used for somatostatin receptor

XX imaging of neuroendocrine tumours. The radiolabelled products are

XX obtained efficiently and inexpensively in high purity. The

XX protected polyaminocarboxylate ligands can be added to the peptide

XX by standard solution or solid phase peptide synthesis and

XX deprotected with conventional reagents to give only the

XX mono-addition product, free of di-addition product impurities. The

XX deprotected product can be labelled with medically useful

XX radionuclides, e.g. lanthanides or actinides, at any desired

XX location. Pre-derivatisation of individual amino acids is not

FT Modified-site /note= "Leu-psi(CH2-NH)-Leu"
FT 11
XX /note= "amidated"
PN WO9907413-A1.
XX
PD 18-FEB-1999.
XX
XX
PF 26-MAY-1998; 98WO-US10707.
XX
PR 11-AUG-1997; 97US-0055233.
XX
PA (ALGO-) ALGOS PHARM CORP.
XX
PI Caruso FS;
XX
XX WPI; 1999-167216/14.
DR
XX
XX New analgesic composition comprises - a substance P receptor
PT antagonist with a substance P receptor antagonist potentiator, used
PT for the treatment of pain
XX
XX Claim 3; Page 29; 54pp; English.
XX
XX A method has been developed for treating pain with: (a) a substance P
CC receptor antagonist; and (b) a substance P receptor antagonist
CC potentiator, i.e. N-methyl-D-aspartate (NMDA) receptor antagonist or
CC substance that blocks at least 1 major intracellular consequence of
CC NMDA receptor activation. The method can be used for treating muscular,
CC musculoskeletal, chronic or neuropathic pain, or migraine. The present
CC sequence represents a substance P analogue for use in the method.
XX
SQ Sequence 11 AA;

Query Match 95.1%; Score 58; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00095;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKQQQFFGLM 11
DB |||||
1 rpkqqffgll 11

RESULT 91
AAW92679
ID AAW92679 standard; peptide; 11 AA.
XX
AC AAW92679;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #25.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX
OS Homo sapiens.
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #25.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX
OS Homo sapiens.
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX

DR WPI; 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Disclosure; Column 21-22; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage,
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

Query Match 95.1%; Score 58; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00095;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKQQQFFGLM 11
DB |||||
1 rpkqqffgll 11

RESULT 92
AAW92666
ID AAW92666 standard; peptide; 11 AA.
XX
AC AAW92666;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #12.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX
OS Homo sapiens.
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
XX WPI; 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Disclosure; Column 15-16; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage,
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human

CC beta-amyloid peptide fragments.

XX Sequence 11 AA;

Query Match 95.1%; Score 58; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00095;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
|||:|||||
Db 1 rpkpqyfglm 11

RESULT 93

AAB91402
ID AAB91402 standard; Peptide; 11 AA.

XX AC AAB91402;

XX DT 22-JUN-2001 (first entry)

XX DE Tachykinins peptide SEQ ID NO:578.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX KW blood component; modification; succinimidyl; maleimido group; amino;
XX KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US13576.

XX PR 17-MAY-1999; 99US-0134406.

XX PR 10-SEP-1999; 99US-0153406.

XX PR 15-OCT-1999; 99US-0159783.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX DR WPI; 2001-112059/12.

XX PT Modifying and attaching therapeutic peptides to albumin prevents
XX PT peptidase degradation, useful for increasing length of in vivo activity

XX PS Disclosure; Page 389; 733pp; English.

XX CC The present invention describes a modified therapeutic peptide (I)
XX CC comprising a therapeutically active amino acid region (III) and a
XX CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
XX CC a less therapeutically active amino acid region (IV), which covalently
XX CC bonds with amino/hydroxyl/thiol groups on blood components to form a
XX CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
XX CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX CC factors and neurotransmitters, to protect them from peptidase activity
XX CC in vivo for the treatment of various disorders. Endogenous therapeutic
XX CC peptides are not suitable as drug candidates as they require frequent
XX CC administration due to rapid degradation by peptidases in the body.
XX CC Modifying and attaching therapeutic peptides to albumin prevents or
XX CC reduces the action of peptidases to increase length of activity (half
XX CC life) and specificity as bonding to large molecules decreases
XX CC intracellular uptake and interference with physiological processes.
XX CC AAB90829 to AAB92441 represent peptides which can be used in the
XX CC exemplification of the present invention.

XX Sequence 11 AA;

Query Match 95.1%; Score 58; DB 22; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00095;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match 95.1%; Score 58; DB 22; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00095;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
|||:|||||
Db 1 rrpqgffglm 11

RESULT 94

AAB91409
ID AAB91409 standard; Peptide; 11 AA.

XX AC AAB91409;

XX DT 22-JUN-2001 (first entry)

XX DE Tachykinins peptide SEQ ID NO:585.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX KW blood component; modification; succinimidyl; maleimido group; amino;
XX KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US13576.

XX PR 17-MAY-1999; 99US-0134406.

XX PR 10-SEP-1999; 99US-0153406.

XX PR 15-OCT-1999; 99US-0159783.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX DR WPI; 2001-112059/12.

XX PT Modifying and attaching therapeutic peptides to albumin prevents
XX PT peptidase degradation, useful for increasing length of in vivo activity

XX PS Disclosure; Page 391; 733pp; English.

XX CC The present invention describes a modified therapeutic peptide (I)
XX CC comprising a therapeutically active amino acid region (III) and a
XX CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
XX CC a less therapeutically active amino acid region (IV), which covalently
XX CC bonds with amino/hydroxyl/thiol groups on blood components to form a
XX CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
XX CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX CC factors and neurotransmitters, to protect them from peptidase activity
XX CC in vivo for the treatment of various disorders. Endogenous therapeutic
XX CC peptides are not suitable as drug candidates as they require frequent
XX CC administration due to rapid degradation by peptidases in the body.
XX CC Modifying and attaching therapeutic peptides to albumin prevents or
XX CC reduces the action of peptidases to increase length of activity (half
XX CC life) and specificity as bonding to large molecules decreases
XX CC intracellular uptake and interference with physiological processes.
XX CC AAB90829 to AAB92441 represent peptides which can be used in the
XX CC exemplification of the present invention.

XX Sequence 11 AA;

QY 1 RPKPQQFFGLM 11
 |||||:||||
 Db 1 rpkpqffgglm 11

RESULT 95

AAAP50633
 ID AAP50633 standard; Peptide; 10 AA.

AC AAP50633;

XX 09-MAR-1992 (first entry)

XX Substance P-like peptide, P2-11.

XX Hair tonic; growth; regeneration.

XX Synthetic.

XX JP60202807-A.

PD 14-OCT-1985.

XX 28-MAR-1984; 84JP-0058390.

XX 28-MAR-1984; 84JP-0058390.

XX (WEIJ) MEIJI SEIKA KAISHA.

XX WPI; 1985-293619/47.

XX Hair tonic compen. - comprises peptide contg. pyroglutamic acid

PT or other aminoacid(s) residue

XX Disclosure; Page 2; 3pp; Japanese.

XX The C-terminal residues 1-4 may be absent (P6-11, P5-11, P4-11 and
 CC P3-11 respectively). The C-terminal is amidated. Substance P
 CC (H-RKPEEFGLM-NH2) or these peptides derived from it can be used in
 CC aq. soln. or suspension to promote hair growth and regeneration.
 CC See also AAP50632 and AAP50634.

XX Sequence 10 AA;

Query Match 91.8%; Score 56; DB 6; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PKPQQFFGLM 11
 |||||:||||
 Db 1 pkpqffgglm 10

RESULT 96

AAR21933

ID AAR21933 standard; Protein; 10 AA.

XX AAR21933;

XX 25-JUN-1992 (first entry)

XX Substance P (2-11) fragment.

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using

PT tachykinin agonists e.g. substance P, physalamin and neurokinin

PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX Claim 9; Page 21; 35pp; English.

XX The peptide is a tachykinin agonist consisting of residues 2-11 of

CC substance P. The peptide was synthesised by standard solid phase

CC synthesis. Analogues of the peptide, with N-terminal deletions down

CC to substance P (7-11) were also synthesised. Neuronal accumulation of

CC beta-amyloid may be treated by administration of these tachykinin

CC agonists. The peptides reduce the neurotoxic effects of a beta-

CC amyloid related polypeptide on cultured neurons. The peptide and

CC its analogues are useful for controlling diseases characterised by

CC beta amyloid accumulation in the brain such as Alzheimer's disease

CC and Down's syndrome.

CC See also AAR21932-75.

XX Sequence 10 AA;

Query Match 91.8%; Score 56; DB 13; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PKPQQFFGLM 11
 |||||:||||
 Db 1 pkpqffgglm 10

RESULT 97

AAW92663

ID AAW92663 standard; peptide; 10 AA.

XX AAW92663;

XX 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #9.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.

XX Homo sapiens.

XX US5876948-A.

XX 02-MAR-1999.

XX 27-JUL-1991; 91US-0737371.

XX 29-JUL-1991; 91US-0737371.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Yankner BA;

XX WPI; 1999-189630/16.

XX Screening for neurotoxin inhibitors - by testing compounds for their

PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

PS Disclosure; Column 13-14; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

XX Sequence 10 AA;

Query Match 91.8%; Score 56; DB 20; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PKPQOFFGLM 11

Db 1 pkpgqffglm 10

RESULT 98

AAB91423

ID AAB91423 standard; Peptide; 10 AA.

XX AC AAB91423;

XX DT 22-JUN-2001 (first entry)

XX DE Tachykinins peptide SEQ ID NO:599.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX blood component; modification; succinimidy; maleimido group; amino;
XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US13576.

XX PR 17-MAY-1999; 99US-0134406.

XX PR 10-SEP-1999; 99US-0153406.

XX PR 15-OCT-1999; 99US-0159783.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 395; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity

CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 10 AA;

Query Match 91.8%; Score 56; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKQOFFGL 10

Db 1 rpkgqffgl 10

RESULT 99

AAB91427

ID AAB91427 standard; Peptide; 10 AA.

XX AC AAB91427;

XX DT 22-JUN-2001 (first entry)

XX DE Tachykinins peptide SEQ ID NO:603.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX blood component; modification; succinimidy; maleimido group; amino;
XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US13576.

XX PR 17-MAY-1999; 99US-0134406.

XX PR 10-SEP-1999; 99US-0153406.

XX PR 15-OCT-1999; 99US-0159783.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 396; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or

CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 10 AA;

Query Match 91.8%; Score 56; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10

|||||

Db 1 rpkpqqffgl 10

RESULT 100

AAB91445

ID AAB91445 standard; Peptide; 10 AA.

XX

AC AAB91445;

XX

DT 22-JUN-2001 (first entry)

XX

DE Tachykinins peptide SEQ ID NO:621.

XX

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimide; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX

OS Homo sapiens.

XX

OS Synthetic.

XX

PN WO200069900-A2.

XX

PD 23-NOV-2000.

XX

PF 17-MAY-2000; 2000WO-US13576.

XX

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX

XX (CONJ-) CONJUCHEM INC.

XX

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX

XX WPI; 2001-112059/12.

XX

XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

PT

PT

XX

PS Disclosure; Page 402; 733pp; English.

XX

CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (iii) and a
CC reactive group (ii) (e.g. succinimide and maleimido groups) attached to
CC a less therapeutically active amino acid region (iv), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.

CC AAB90829 to AAB92441 represent peptides which can be used in the

CC exemplification of the present invention.

XX

SQ Sequence 10 AA;

Query Match

Best Local Similarity 91.8%; Score 56; DB 22; Length 10;

Matches 10; Conservative 100.0%; Pred. No. 0.0019;

Mismatches 0; Indels 0; Gaps 0;

QY 2 PKPQOFFGLM 11

|||||

Db 1 pkpqffglm 10

RESULT 101

AAR21945

ID AAR21945 standard; Protein; 11 AA.

XX

AC AAR21945;

XX

DT 25-JUN-1992 (first entry)

XX

DE Substance P [Pro 1].

XX

KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.

XX

OS Synthetic.

XX

PN WO9202248-A.

XX

PD 20-FEB-1992.

XX

PF 29-JUL-1991; 91WO-US05323.

XX

PR 27-JUL-1990; 90US-0559173.

XX

PA (CHIL-) CHILDRENS MED CENT.

XX

PI Yankner BA;

XX

XX WPI; 1992-079804/10.

XX

PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Down's syndrome, etc.

XX

PS Claim 10; Page 21; 35pp; English.

XX

CC The peptide is the tachykinin agonist substance P with a Proline
CC residue substituted at position 1. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.

XX Sequence 11 AA;

SQ

Query Match

Best Local Similarity 91.8%; Score 56; DB 13; Length 11;

Matches 10; Conservative 100.0%; Pred. No. 0.0021;

Mismatches 0; Indels 0; Gaps 0;

QY 2 PKPQOFFGLM 11

|||||

Db 2 pkpqffglm 11

RESULT 102

AAR21936
ID AAR21936 standard; Protein; 11 AA.

XX AAR21936;

XX 25-JUN-1992 (first entry)

XX Substance P or (7-11) [Ethionine 11].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 11
FT /label= OTHER
FT /note= "OTHER = Ethionine"

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX Claim 10; Page 21; 35pp; English.

XX The peptide is the tachykinin agonist substance P with an Ethionine
CC residue substituted at position 11. The peptide was synthesised
CC by standard solid phase synthesis. An N-terminal deleted peptide
CC (7-11) with the same substitution was also synthesised. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptides can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.

XX Sequence 11 AA;

Query Match 91.8%; Score 56; DB 13; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0021;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10

DB 1 rpkpqgffgl 10

RESULT 103

AAR21941
ID AAR21941 standard; Protein; 11 AA.

XX AAR21941;

XX 25-JUN-1992 (first entry)

XX Substance P [pGLU 1].

KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1
FT /label= OTHER
FT /note= "OTHER = pyro Glu"

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX Claim 10; Page 21; 35pp; English.

XX The peptide is the tachykinin agonist substance P with a pyro
CC glutamic acid residue substituted at position 1. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.

XX Sequence 11 AA;

Query Match 91.8%; Score 56; DB 13; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0021;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PKPQQFFGLM 11

DB 2 pkpqgffglm 11

RESULT 104

AAR21944
ID AAR21944 standard; Protein; 11 AA.

XX AAR21944;

XX 25-JUN-1992 (first entry)

XX Substance P [Pro 11].

KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

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XX PR 27-JUL-1990; 90US-0559173.
XX XX
XX PA (CHIL-) CHILDRENS MED CENT.
XX XX
XX PI Yankner BA;
XX XX
XX DR WPI; 1992-079804/10.
XX XX
XX XX Treatment of neuronal accumulation of beta-amyloid - using
XX PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX XX
XX PS Claim 10; Page 21; 35pp; English.
XX XX
XX CC The peptide is the tachykinin agonist substance P with a Proline
XX CC residue substituted at position 11. The peptide was
XX CC synthesised by standard solid phase synthesis. Neuronal
XX CC accumulation of beta-amyloid may be treated by administration of
XX CC tachykinin agonists. The peptide can reduce the neurotoxic effects
XX CC of a beta-amyloid related polypeptide on cultured neurons. The
XX CC peptide and its analogues are useful for controlling diseases
XX CC characterised by beta amyloid accumulation in the brain such as
XX CC Alzheimer's disease and Down's syndrome.
XX CC See also AAR21932-75.
XX XX
XX SQ Sequence 11 AA;

Query Match 91.8%; Score 56; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
DB 1 rpkpqffgl 10

RESULT 105
AAW92709
ID AAW92709 standard; peptide; 11 AA.
XX XX
XX AC AAW92709;
XX XX
XX DT 30-APR-1999 (first entry)
XX XX
XX DE Human tachykinin agonist beta-amyloid peptide fragment #55.
XX XX
XX KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX XX
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT Modified-site 9
XX FT /label= MeGly
XX FT /note= "N-methyl-glycine (sarcosine)"
XX FT Modified-site 11
XX FT /note= "Residue is Met(O2)"
XX XX
XX PN US5876948-A.
XX XX
XX PD 02-MAR-1999.
XX XX
XX PF 27-JUL-1991; 91US-0737371.
XX XX
XX PR 29-JUL-1991; 91US-0737371.
XX PR 27-JUL-1990; 90US-0559173.
XX XX
XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX XX
XX PI Yankner BA;

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XX XX WPI; 1999-189630/16.
XX XX
XX PT Screening for neurotoxin inhibitors - by testing compounds for their
XX PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX XX
XX PS Disclosure; Column 35-36; 28pp; English.
XX XX
XX CC This invention describes a method for screening compounds for inhibiting
XX CC a neurotoxin. The method involves incubating tachykinin agonists with
XX CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
XX CC used for identifying compounds for treating diseases characterised by an
XX CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
XX CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
XX CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
XX CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX CC beta-amyloid peptide fragments.
XX XX
XX SQ Sequence 11 AA;

Query Match 91.8%; Score 56; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
DB 1 rpkpqffgl 10

RESULT 106
AAW92717
ID AAW92717 standard; peptide; 11 AA.
XX XX
XX AC AAW92717;
XX XX
XX DT 30-APR-1999 (first entry)
XX XX
XX DE Human tachykinin agonist beta-amyloid peptide fragment #63.
XX XX
XX KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
XX XX
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT Modified-site 11
XX FT /label= MeMet
XX FT /note= "N-methyl-methionine"
XX XX
XX PN US5876948-A.
XX XX
XX PD 02-MAR-1999.
XX XX
XX PF 27-JUL-1991; 91US-0737371.
XX XX
XX PR 29-JUL-1991; 91US-0737371.
XX PR 27-JUL-1990; 90US-0559173.
XX XX
XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX XX
XX PI Yankner BA;
XX XX
XX DR WPI; 1999-189630/16.
XX XX
XX PT Screening for neurotoxin inhibitors - by testing compounds for their
XX PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX XX
XX PS Disclosure; Column 37-38; 28pp; English.
XX XX
XX CC This invention describes a method for screening compounds for inhibiting
XX CC a neurotoxin. The method involves incubating tachykinin agonists with

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